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OM nucleic - nucleic search, using sw model

Run on: March 12, 2005, 09:53:38 ; Search time 86 Seconds
(without alignments)
209.291 Million cell updates/sec

Title: US-10-070-588A-112
Perfect score: 11
Sequence: 1 cttggcacta 11

Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 1202784 seqs, 818138359 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Issued Patents_NA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	11	100.0	207	4	US-09-248-796A-8315, A
6	11	100.0	276	4	US-09-513-999C-27111, A
7	11	100.0	305	4	US-09-270-767-26937, A
8	11	100.0	321	4	US-09-543-681A-963, A
9	11	100.0	341	4	US-09-513-999C-3625, A
10	11	100.0	386	4	US-09-270-767-7666, A
11	11	100.0	386	4	US-09-270-767-22948, A
12	11	100.0	396	4	US-09-640-173-30, A
13	11	100.0	396	4	US-09-713-550-30, A
14	11	100.0	396	4	US-09-825-294-30, A
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18	11	100.0	477	4	US-09-248-796A-2902, A
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c 259	11	100.0	5009	2	US-08-478-433-3	Sequence 3, Appli	332	11	100.0	9416	3	US-08-823-895A-26	Sequence 26, Appli
c 260	11	100.0	5009	2	US-08-337-483-3	Sequence 3, Appli	333	11	100.0	9416	4	US-10-104-966-13	Sequence 13, Appli
c 261	11	100.0	5009	2	US-08-478-373-3	Sequence 3, Appli	334	11	100.0	9595	3	US-09-014-416-4	Sequence 4, Appli
c 262	11	100.0	5009	3	US-08-474-671-3	Sequence 3, Appli	335	11	100.0	9599	3	US-09-014-416-2	Sequence 2, Appli
c 263	11	100.0	5009	3	US-08-483-577A-3	Sequence 3, Appli	336	11	100.0	9599	3	US-09-014-416-6	Sequence 6, Appli
c 264	11	100.0	5009	3	US-08-897-438-3	Sequence 3, Appli	337	11	100.0	9646	3	US-08-811-566-1	Sequence 1, Appli
c 265	11	100.0	5009	3	US-08-637-654-3	Sequence 3, Appli	338	11	100.0	9646	4	US-09-034-756-1	Sequence 1, Appli
c 266	11	100.0	5033	1	US-08-649-518-3	Sequence 3, Appli	339	11	100.0	10818	4	US-09-949-016-13583	Sequence 13583, A
c 267	11	100.0	5033	1	US-08-487-890A-2	Sequence 2, Appli	340	11	100.0	11076	4	US-09-539-601-1	Sequence 1, Appli
c 268	11	100.0	5033	2	US-08-478-435-2	Sequence 2, Appli	341	11	100.0	11076	4	US-09-539-601-19	Sequence 19, Appli
c 269	11	100.0	5033	2	US-08-337-483-2	Sequence 2, Appli	342	11	100.0	11076	4	US-09-539-601-25	Sequence 25, Appli
c 270	11	100.0	5033	3	US-08-478-373-2	Sequence 2, Appli	343	11	100.0	11076	4	US-09-539-601-31	Sequence 31, Appli
c 271	11	100.0	5033	3	US-08-474-671-2	Sequence 2, Appli	c 344	11	100.0	11209	4	US-09-949-016-17514	Sequence 17514, A
c 272	11	100.0	5033	3	US-08-483-577A-2	Sequence 2, Appli	c 345	11	100.0	11261	4	US-09-949-016-14358	Sequence 14358, A
c 273	11	100.0	5033	3	US-08-897-438-2	Sequence 2, Appli	c 346	11	100.0	11261	4	US-09-949-016-14908	Sequence 14908, A
c 274	11	100.0	5033	3	US-08-637-654-2	Sequence 2, Appli	347	11	100.0	12232	4	US-09-949-016-12570	Sequence 12570, A
c 275	11	100.0	5033	3	US-08-649-518-2	Sequence 2, Appli	348	11	100.0	12240	4	US-09-949-016-16209	Sequence 16209, A
c 276	11	100.0	5099	1	US-08-487-890A-4	Sequence 4, Appli	349	11	100.0	12980	3	US-08-811-566-5	Sequence 5, Appli
c 277	11	100.0	5099	2	US-08-478-435-4	Sequence 4, Appli	350	11	100.0	12980	3	US-09-034-756-5	Sequence 5, Appli
c 278	11	100.0	5099	2	US-08-337-483-4	Sequence 4, Appli	c 351	11	100.0	14707	4	US-09-312-762A-3	Sequence 3, Appli
c 279	11	100.0	5099	3	US-08-478-373-4	Sequence 4, Appli	c 352	11	100.0	15192	4	US-09-949-016-15143	Sequence 15143, A
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c 281	11	100.0	5099	3	US-08-483-577A-4	Sequence 4, Appli	354	11	100.0	18227	4	US-09-949-016-12127	Sequence 12127, A
c 282	11	100.0	5099	3	US-08-897-438-4	Sequence 4, Appli	355	11	100.0	19328	4	US-09-949-016-16285	Sequence 16285, A
c 283	11	100.0	5099	3	US-08-637-654-4	Sequence 4, Appli	356	11	100.0	19332	2	US-08-477-451-25	Sequence 25, Appli
c 284	11	100.0	5099	3	US-08-649-518-4	Sequence 4, Appli	357	11	100.0	21862	4	US-09-949-016-17319	Sequence 17319, A
285	11	100.0	5125	1	US-08-453-553-11	Sequence 11, Appl	c 358	11	100.0	22281	4	US-09-949-016-14778	Sequence 14778, A
286	11	100.0	5125	2	US-08-710-637-11	Sequence 11, Appl	359	11	100.0	23757	4	US-09-949-016-12010	Sequence 12010, A
287	11	100.0	5125	5	PCT-US93-00907-11	Sequence 11, Appl	360	11	100.0	23792	4	US-09-949-016-16189	Sequence 16189, A
c 288	11	100.0	5144	1	US-08-487-890A-105	Sequence 105, App	361	11	100.0	26385	3	US-08-961-527-3	Sequence 3, Appli
c 289	11	100.0	5144	2	US-08-478-435-105	Sequence 105, App	c 362	11	100.0	31000	4	US-09-966-451-10	Sequence 10, Appli
c 290	11	100.0	5144	2	US-08-337-483-105	Sequence 105, App	c 363	11	100.0	32725	4	US-09-949-016-15239	Sequence 15239, A
c 291	11	100.0	5144	3	US-08-478-373-105	Sequence 105, App	c 364	11	100.0	35913	4	US-09-949-016-16586	Sequence 16586, A
c 292	11	100.0	5144	3	US-08-474-671-105	Sequence 105, App	c 365	11	100.0	36577	4	US-09-949-016-13176	Sequence 13176, A
c 293	11	100.0	5144	3	US-08-483-577A-105	Sequence 105, App	366	11	100.0	39489	4	US-09-949-016-13886	Sequence 13886, A
c 294	11	100.0	5144	3	US-08-897-438-105	Sequence 105, App	367	11	100.0	39686	4	US-09-949-016-13633	Sequence 13633, A
c 295	11	100.0	5144	3	US-08-637-654-105	Sequence 105, App	c 368	11	100.0	42954	4	US-09-949-016-17123	Sequence 17123, A
c 296	11	100.0	5144	3	US-08-649-518-105	Sequence 105, App	c 369	11	100.0	42954	4	US-09-949-016-17124	Sequence 17124, A
297	11	100.0	5199	4	US-09-949-016-5474	Sequence 5474, Ap	c 370	11	100.0	45613	4	US-09-596-002-22	Sequence 22, Appli
298	11	100.0	5323	1	US-08-453-552-9	Sequence 9, Appli	c 371	11	100.0	48499	4	US-09-949-016-14032	Sequence 14032, A
299	11	100.0	5323	2	US-08-710-637-9	Sequence 9, Appli	372	11	100.0	48313	4	US-09-949-016-17088	Sequence 17088, A
300	11	100.0	5323	5	PCT-US93-00907-9	Sequence 9, Appli	373	11	100.0	49487	4	US-09-949-016-11770	Sequence 11770, A
301	11	100.0	5475	4	US-09-543-681A-837	Sequence 837, App	374	11	100.0	52457	4	US-09-949-016-12418	Sequence 12418, A
c 302	11	100.0	5544	4	US-08-956-171E-110	Sequence 110, App	375	11	100.0	55851	4	US-09-949-016-13732	Sequence 13732, A
c 303	11	100.0	5544	4	US-08-781-986A-110	Sequence 110, App	c 376	11	100.0	57331	4	US-09-949-016-17277	Sequence 17277, A
304	11	100.0	5599	2	US-08-477-451-9	Sequence 9, Appli	377	11	100.0	63982	4	US-09-949-016-16769	Sequence 16769, A
c 305	11	100.0	5599	2	US-08-477-451-13	Sequence 13, Appli	378	11	100.0	65792	4	US-09-596-002-31	Sequence 31, Appli
306	11	100.0	5640	4	US-09-949-016-385	Sequence 385, App	379	11	100.0	66247	4	US-09-949-016-16009	Sequence 16009, A
307	11	100.0	5643	4	US-09-949-016-4543	Sequence 4543, Ap	380	11	100.0	66428	4	US-09-949-016-12917	Sequence 12917, A
c 308	11	100.0	5762	3	US-09-919-172-55	Sequence 55, Appli	c 381	11	100.0	68035	4	US-09-949-016-16219	Sequence 16219, A
c 309	11	100.0	6156	3	US-08-891-640-1	Sequence 1, Appli	c 382	11	100.0	80246	3	US-09-078-294-4	Sequence 4, Appli
c 310	11	100.0	6156	3	US-09-723-535-3	Sequence 3, Appli	383	11	100.0	80411	4	US-09-949-016-15777	Sequence 15777, A
c 311	11	100.0	6156	4	US-09-949-016-867	Sequence 867, App	c 384	11	100.0	80595	3	US-09-078-294-3	Sequence 3, Appli
312	11	100.0	7106	1	US-08-188-281B-8	Sequence 8, Appli	385	11	100.0	83697	4	US-09-949-016-16040	Sequence 16040, A
313	11	100.0	7106	1	US-08-453-552-5	Sequence 5, Appli	c 386	11	100.0	84761	4	US-09-949-016-11919	Sequence 11919, A
314	11	100.0	7106	1	US-08-710-637-5	Sequence 5, Appli	c 387	11	100.0	84763	4	US-09-949-016-13914	Sequence 13914, A
315	11	100.0	7106	5	PCT-US93-00907-5	Sequence 5, Appli	c 388	11	100.0	88240	4	US-09-949-016-15279	Sequence 15279, A
316	11	100.0	7106	5	PCT-US94-07280-8	Sequence 8, Appli	c 389	11	100.0	93689	4	US-09-949-016-13089	Sequence 13089, A
317	11	100.0	7106	5	PCT-US95-01087-8	Sequence 8, Appli	c 390	11	100.0	92581	4	US-09-949-016-12182	Sequence 12182, A
318	11	100.0	7298	1	US-08-453-552-3	Sequence 3, Appli	c 391	11	100.0	92581	4	US-09-949-016-16542	Sequence 16542, A
319	11	100.0	7298	2	US-08-710-637-3	Sequence 3, Appli	392	11	100.0	94095	4	US-09-949-016-14389	Sequence 14389, A

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C 394	11	100.0	96987	4	US-09-949-016-14429	Sequence 14429, A	C 467	11	100.0	524032	4	US-09-949-016-16930	Sequence 16930, A
C 395	11	100.0	98844	3	US-09-791-211-10	Sequence 10, Appl	C 468	11	100.0	524032	4	US-09-949-016-16931	Sequence 16931, A
C 396	11	100.0	99629	4	US-09-596-002-37	Sequence 37, Appl	C 469	11	100.0	529885	4	US-09-949-016-14340	Sequence 14340, A
C 397	11	100.0	108929	4	US-09-949-016-12060	Sequence 12060, A	C 470	11	100.0	529885	4	US-09-949-016-14341	Sequence 14341, A
C 398	11	100.0	108929	4	US-09-949-016-16618	Sequence 16618, A	C 471	11	100.0	529885	4	US-09-949-016-14342	Sequence 14342, A
C 399	11	100.0	107329	4	US-09-949-016-12663	Sequence 12663, A	C 472	11	100.0	529885	4	US-09-949-016-14343	Sequence 14343, A
C 400	11	100.0	107329	4	US-09-949-016-12664	Sequence 12664, A	C 473	11	100.0	529885	4	US-09-949-016-14344	Sequence 14344, A
C 401	11	100.0	107330	4	US-09-949-016-15408	Sequence 15408, A	C 474	11	100.0	529885	4	US-09-949-016-14345	Sequence 14345, A
C 402	11	100.0	107330	4	US-09-949-016-15409	Sequence 15409, A	C 475	11	100.0	529885	4	US-09-949-016-14346	Sequence 14346, A
C 403	11	100.0	107330	4	US-09-949-016-15410	Sequence 15410, A	C 476	11	100.0	529885	4	US-09-949-016-14347	Sequence 14347, A
C 404	11	100.0	107330	4	US-09-949-016-15411	Sequence 15411, A	C 477	11	100.0	635591	4	US-09-949-016-11808	Sequence 11808, A
C 405	11	100.0	107750	4	US-09-949-016-12662	Sequence 12662, A	C 478	11	100.0	635591	4	US-09-949-016-13388	Sequence 13388, A
C 406	11	100.0	107751	4	US-09-949-016-15412	Sequence 15412, A	C 479	11	100.0	678533	4	US-09-949-016-14577	Sequence 14577, A
C 407	11	100.0	107751	4	US-09-949-016-15413	Sequence 15413, A	C 480	11	100.0	678533	4	US-09-949-016-14578	Sequence 14578, A
C 408	11	100.0	107751	4	US-09-949-016-15414	Sequence 15414, A	C 481	11	100.0	767677	4	US-09-949-016-12147	Sequence 12147, A
C 409	11	100.0	107751	4	US-09-949-016-15415	Sequence 15415, A	C 482	11	100.0	767677	4	US-09-949-016-17361	Sequence 17361, A
C 410	11	100.0	107925	4	US-09-949-016-11875	Sequence 11875, A	C 483	11	100.0	786431	4	US-09-751-389-3	Sequence 3, Appl
C 411	11	100.0	107926	4	US-09-949-016-15404	Sequence 15404, A	C 484	11	100.0	1830121	4	US-09-557-884-1	Sequence 1, Appl
C 412	11	100.0	107926	4	US-09-949-016-15405	Sequence 15405, A	C 485	11	100.0	1830121	4	US-09-643-990A-1	Sequence 1, Appl
C 413	11	100.0	107926	4	US-09-949-016-15406	Sequence 15406, A	C 486	11	100.0	4403765	3	US-09-103-840A-2	Sequence 2, Appl
C 414	11	100.0	107926	4	US-09-949-016-15407	Sequence 15407, A	C 487	11	100.0	4411529	3	US-09-103-840A-1	Sequence 1, Appl
C 415	11	100.0	110402	4	US-09-949-016-17295	Sequence 17295, A	C 488	10	90.9	17	4	US-09-404-912-686	Sequence 686, App
C 416	11	100.0	110403	4	US-09-949-016-12741	Sequence 12741, A	C 489	10	90.9	20	3	US-09-662-250A-86	Sequence 86, Appl
C 417	11	100.0	111454	4	US-09-949-016-14196	Sequence 14196, A	C 490	10	90.9	20	3	US-08-936-107A-40	Sequence 40, Appl
C 418	11	100.0	111459	4	US-09-949-016-12337	Sequence 12337, A	C 491	10	90.9	20	3	US-09-300-008B-29	Sequence 29, Appl
C 419	11	100.0	1113379	4	US-09-949-016-17561	Sequence 17561, A	C 492	10	90.9	22	3	US-09-342-749-8	Sequence 8, Appl
C 420	11	100.0	113379	4	US-09-949-016-17562	Sequence 17562, A	C 493	10	90.9	22	3	US-09-691-840-8	Sequence 8, Appl
C 421	11	100.0	115592	4	US-09-818-512-3	Sequence 3, Appl	C 494	10	90.9	25	4	US-09-396-196G-20455	Sequence 20455, A
C 422	11	100.0	119981	4	US-09-949-016-11844	Sequence 11844, A	C 495	10	90.9	25	4	US-09-396-196G-20456	Sequence 20456, A
C 423	11	100.0	119982	4	US-09-949-016-13606	Sequence 13606, A	C 496	10	90.9	25	4	US-09-396-196G-25565	Sequence 25565, A
C 424	11	100.0	121970	4	US-09-949-016-17216	Sequence 17216, A	C 497	10	90.9	25	4	US-09-396-196G-26371	Sequence 26371, A
C 425	11	100.0	123513	4	US-09-949-016-15794	Sequence 15794, A	C 498	10	90.9	25	4	US-09-396-196G-26372	Sequence 26372, A
C 426	11	100.0	124264	4	US-09-949-016-16396	Sequence 16396, A	C 499	10	90.9	25	4	US-09-396-196G-26373	Sequence 26373, A
C 427	11	100.0	126200	4	US-09-949-016-11824	Sequence 11824, A	C 500	10	90.9	25	4	US-09-396-196G-26383	Sequence 26383, A
C 428	11	100.0	126200	4	US-09-949-016-13193	Sequence 13193, A	C 501	10	90.9	25	4	US-09-396-196G-26384	Sequence 26384, A
C 429	11	100.0	128175	4	US-09-949-016-16268	Sequence 16268, A	C 502	10	90.9	25	4	US-09-396-196G-26385	Sequence 26385, A
C 430	11	100.0	143776	4	US-09-949-001-29	Sequence 29, Appl	C 503	10	90.9	25	4	US-09-396-196G-26386	Sequence 26386, A
C 431	11	100.0	144034	4	US-09-949-001-35	Sequence 35, Appl	C 504	10	90.9	25	4	US-09-396-196G-26387	Sequence 26387, A
C 432	11	100.0	144922	4	US-09-949-016-15890	Sequence 15890, A	C 505	10	90.9	25	4	US-09-396-196G-26388	Sequence 26388, A
C 433	11	100.0	150032	4	US-09-949-016-14321	Sequence 14321, A	C 506	10	90.9	25	4	US-09-396-196G-26389	Sequence 26389, A
C 434	11	100.0	150394	4	US-09-949-016-13042	Sequence 13042, A	C 507	10	90.9	25	4	US-09-396-196G-26390	Sequence 26390, A
C 435	11	100.0	163181	4	US-09-949-016-13730	Sequence 13730, A	C 508	10	90.9	25	4	US-09-396-196G-40870	Sequence 40870, A
C 436	11	100.0	164061	4	US-09-949-016-17422	Sequence 17422, A	C 509	10	90.9	25	4	US-09-396-196G-45696	Sequence 45696, A
C 437	11	100.0	174259	4	US-09-949-016-11968	Sequence 11968, A	C 510	10	90.9	25	4	US-09-396-196G-58190	Sequence 58190, A
C 438	11	100.0	174262	4	US-09-949-016-14259	Sequence 14259, A	C 511	10	90.9	25	4	US-09-396-196G-58190	Sequence 58190, A
C 439	11	100.0	175265	4	US-09-949-016-16089	Sequence 16089, A	C 512	10	90.9	25	4	US-09-396-196G-12252	Sequence 125890
C 440	11	100.0	177669	4	US-09-949-016-13713	Sequence 13713, A	C 513	10	90.9	25	4	US-09-396-196G-125891	Sequence 125891, A
C 441	11	100.0	187580	4	US-09-949-016-13266	Sequence 13266, A	C 514	10	90.9	25	4	US-09-396-196G-125902	Sequence 125902, A
C 442	11	100.0	189560	4	US-09-949-016-17202	Sequence 17202, A	C 515	10	90.9	25	4	US-09-396-196G-125903	Sequence 125903, A
C 443	11	100.0	194935	4	US-09-949-016-15584	Sequence 15584, A	C 516	10	90.9	25	4	US-09-396-196G-125904	Sequence 125904, A
C 444	11	100.0	227390	4	US-09-949-016-12201	Sequence 12201, A	C 517	10	90.9	26	4	US-09-641-652-12	Sequence 12, Appl
C 445	11	100.0	227391	4	US-09-949-016-13365	Sequence 13365, A	C 518	10	90.9	29	2	US-08-687-080-168	Sequence 168, Appl
C 446	11	100.0	235452	4	US-09-949-016-13675	Sequence 13675, A	C 519	10	90.9	37	3	US-09-306-881-16	Sequence 16, Appl
C 447	11	100.0	238815	4	US-09-949-016-16274	Sequence 16274, A	C 520	10	90.9	47	4	US-09-422-978-1765	Sequence 1765, Ap
C 448	11	100.0	238815	4	US-09-949-016-16274	Sequence 16274, A	C 521	10	90.9	69	4	US-08-956-171E-2279	Sequence 2279, Ap
C 449	11	100.0	246240	2	US-08-724-394A-20	Sequence 20, Appl	C 522	10	90.9	69	4	US-08-781-986A-2279	Sequence 2279, Ap
C 450	11	100.0	246240	2	US-08-724-394A-21	Sequence 21, Appl	C 523	10	90.9	74	4	US-09-513-999C-31762	Sequence 31762, A
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C 452	11	100.0	247781	4	US-09-949-016-17189	Sequence 14193, A	C 525	10	90.9	89	4	US-09-513-999C-20042	Sequence 20042, A
C 453	11	100.0	2565679	4	US-09-949-016-17193	Sequence 17189, A	C 526	10	90.9	107	4	US-09-513-999C-20378	Sequence 20378, A
C 454	11	100.0	256287	4	US-09-949-016-14608	Sequence 14608, A	C 527	10	90.9	139	1	US-08-392-678-22	Sequence 22, Appl
C 455	11	100.0	269223	4	US-09-596-002-41	Sequence 41, Appl	C 528	10	90.9	139	1	US-08-457-304A-22	Sequence 22, Appl
C 456	11	100.0	343352	4	US-09-949-016-13498	Sequence 13498, A	C 529	10	90.9	139	1	US-08-456-701A-22	Sequence 22, Appl
C 457	11	100.0	363032	4	US-09-949-016-12415	Sequence 12415, A	C 530	10	90.9	139	3	US-08-684-932A-22	Sequence 22, Appl
C 458	11	100.0	363033	4	US-09-949-016-15754	Sequence 15754, A	C 531	10	90.9	145	4	US-09-513-999C-24159	Sequence 24159, A
C 459	11	100.0	373182	4	US-09-949-016-17371	Sequence 17371, A	C 532	10	90.9	155	4	US-09-513-999C-8530	Sequence 8530, Ap
C 460	11	100.0	373694	4	US-09-949-016-12062	Sequence 12062, A	C 533	10	90.9	160	4	US-09-513-999C-25659	Sequence 25659, A
C 461	11	100.0	421118	4	US-09-949-016-16297	Sequence 16297, A	C 534	10	90.9	165	4	US-09-513-999C-13384	Sequence 13384, A
C 462	11	100.0	422592	4	US-09-949-016-14182	Sequence 14182, A	C 535	10	90.9	169	4	US-09-313-294A-6543	Sequence 6543, Ap
C 463	11	100.0	462589	4	US-09-949-016-12900	Sequence 12900, A	C 536	10	90.9	175	4	US-09-471-276-303	Sequence 303, App
C 464	11	100.0	476044	4	US-09-949-016-12412	Sequence 12412, A	C 537	10	90.9	183	4	US-09-540-236-1531	Sequence 1531, Ap
C 465	11	100.0	524032	4	US-09-949-016-16928	Sequence 16928, A	C 538	10	90.9	190	2	US-08-687-080-87	Sequence 87, Appl

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541	10	90.9	201	4	US-09-248-796A-13168	Sequence 13168, A	c 614	10	90.9	449	4	US-09-270-767-6461	Sequence 6461, Ap
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546	10	90.9	244	4	US-09-513-999C-29328	Sequence 29328, A	619	10	90.9	451	4	US-09-215-681-51	Sequence 51, Appl
547	10	90.9	264	4	US-09-313-294A-469	Sequence 469, App	620	10	90.9	451	4	US-09-216-003A-51	Sequence 51, Appl
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554	10	90.9	286	4	US-09-621-976-11456	Sequence 11456, A	c 627	10	90.9	457	4	US-09-614-134B-685	Sequence 685, App
555	10	90.9	287	4	US-09-313-294A-4492	Sequence 4492, Ap	c 628	10	90.9	457	4	US-09-671-345-685	Sequence 685, App
556	10	90.9	288	4	US-09-313-294A-820	Sequence 820, App	c 629	10	90.9	457	4	US-09-589-184-685	Sequence 685, App
557	10	90.9	288	4	US-09-313-294A-8646	Sequence 8646, Ap	c 630	10	90.9	457	4	US-09-658-824-685	Sequence 685, App
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585	10	90.9	384	4	US-09-270-767-932	Sequence 932, App	c 658	10	90.9	492	4	US-09-270-767-20793	Sequence 20793, A
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595	10	90.9	415	4	US-09-513-999C-790	Sequence 790, App	c 668	10	90.9	519	4	US-09-270-767-11494	Sequence 11494, A
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597	10	90.9	420	4	US-09-540-236-1693	Sequence 1693, Ap	c 670	10	90.9	528	4	US-09-669-751-147	Sequence 147, App
598	10	90.9	423	3	US-09-513-999C-9224	Sequence 9224, Ap	c 671	10	90.9	528	4	US-09-134-000C-972	Sequence 972, App
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690	10	90.9	4	US-09-489-039A-3355	Sequence 3255, App	C 763
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692	10	90.9	4	US-10-012-542-123	Sequence 123, App	C 765
693	10	90.9	4	US-10-115-123-123	Sequence 123, App	C 766
694	10	90.9	4	US-09-252-991A-7519	Sequence 7519, App	C 767
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696	10	90.9	4	US-09-543-681A-2594	Sequence 2594, App	C 769
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742	10	90.9	4	US-09-949-016-44846	Sequence 44846, A	C 815
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ALIGNMENTS

RESULT 1

US-09-396-196G-49096
; Sequence 49096, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR FILING DATE: 1999-09-15
; PRIOR FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 49096
; LENGTH: 25
; TYPE: DNA
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US-09-396-196G-49096

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Best Local Similarity 100.0%; Pred. No. 5.2e+02;
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RESULT 2

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; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G

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; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
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US-09-396-196G-106030

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Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3

US-09-396-196G-106031
; Sequence 106031, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 106031
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-106031

Query Match 100.0%; Score 11; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11
| | | | | | | | | |
Db 3 CTTTGGCACTA 13

RESULT 4

US-09-513-999C-26159
; Sequence 26159, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59 US2,REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 26159
; LENGTH: 100
; TYPE: DNA
; ORGANISM: Homo sapiens

US-09-513-999C-26159

Query Match 100.0%; Score 11; DB 4; Length 100;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTGGCACTA 11
| | | | | | | | | |
Db 81 CTTTGGCACTA 91

RESULT 5

US-09-248-796A-8315/c
; Sequence 8315, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; PRIOR FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 8315
; LENGTH: 207
; TYPE: DNA
; ORGANISM: Candida albicans
US-09-248-796A-8315

Query Match 100.0%; Score 11; DB 4; Length 207;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTGGCACTA 11
| | | | | | | | | |
Db 178 CTTTGGCACTA 168

RESULT 6

US-09-513-999C-27111
; Sequence 27111, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59 US2 REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 27111
; LENGTH: 276
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 34
; OTHER INFORMATION: m=a or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 122
; OTHER INFORMATION: y=c or t
US-09-513-999C-27111

Query Match 100.0%; Score 11; DB 4; Length 276;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTGGCACTA 11
| | | | | | | | | |
Db 219 CTTTGGCACTA 229

RESULT 7

US-09-270-767-26937/c
; Sequence 26937, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26937
; LENGTH: 305
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-26937

Query Match 100.0%; Score 11; DB 4; Length 305;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTGGCACTA 11
| | | | | | | | | |
Db 105 CTTTGGCACTA 95

RESULT 8

US-09-543-681A-963
; Sequence 963, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETTON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 963
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Proteus mirabilis
US-09-543-681A-963

Query Match 100.0%; Score 11; DB 4; Length 321;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTGGCACTA 11
| | | | | | | | | |
Db 242 CTTTGGCACTA 252

RESULT 9

US-09-513-999C-3625
; Sequence 3625, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.

;; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.

;; Patent No. 6783961
 ;; FILE REFERENCE: 59.US2.REG
 ;; CURRENT APPLICATION NUMBER: US/09/513,999C
 ;; CURRENT FILING DATE: 2000-02-24
 ;; PRIOR APPLICATION NUMBER: US 60/122,487
 ;; PRIOR FILING DATE: 1999-02-26
 ;; NUMBER OF SEQ ID NOS: 36681
 ;; SOFTWARE: Patent.pm
 ;; SEQ ID NO 3625
 ;; LENGTH: 341
 ;; TYPE: DNA
 ;; ORGANISM: Homo sapiens
 ;; FEATURE:
 ;; NAME/KEY: CDS
 ;; LOCATION: 156..341
 ;; FEATURE:
 ;; NAME/KEY: misc_feature
 ;; LOCATION: 224
 ;; OTHER INFORMATION: w=a or t
 ;; FEATURE:
 ;; NAME/KEY: misc_feature
 ;; LOCATION: 298
 ;; OTHER INFORMATION: w=a or t
 ;; FEATURE:
 ;; NAME/KEY: misc_feature
 ;; LOCATION: 307
 ;; OTHER INFORMATION: r=a or g
 ;; FEATURE:
 ;; NAME/KEY: UNSURE
 ;; LOCATION: 23
 ;; OTHER INFORMATION: Xaa=Arg or Ser
 ;; FEATURE:
 ;; NAME/KEY: UNSURE
 ;; LOCATION: 48
 ;; OTHER INFORMATION: Xaa=Phe or Tyr
 ;; FEATURE:
 ;; NAME/KEY: UNSURE
 ;; LOCATION: 51
 ;; OTHER INFORMATION: Xaa=Asp or Gly
 US-09-513-999C-3625

Query Match 100.0%; Score 11; DB 4; Length 341;
 Best Local Similarity 100.0%; Pred. No. 5.4e+02;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11
 |||||
 Db 130 CTTTGGCACTA 140

RESULT 10

US-09-270-767-7666
 ;; Sequence 7666, Application US/09270767
 ;; Patent No. 6703491
 ;; GENERAL INFORMATION:
 ;; APPLICANT: Homburger et al.
 ;; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
 ;; FILE REFERENCE: File Reference: 7326-094
 ;; CURRENT APPLICATION NUMBER: US/09/270,767
 ;; CURRENT FILING DATE: 1999-03-17
 ;; NUMBER OF SEQ ID NOS: 62517
 ;; SOFTWARE: PatentIn Ver. 2.0
 ;; SEQ ID NO 7666
 ;; LENGTH: 386
 ;; TYPE: DNA
 ;; ORGANISM: Drosophila melanogaster
 US-09-270-767-7666

Query Match 100.0%; Score 11; DB 4; Length 386;
 Best Local Similarity 100.0%; Pred. No. 5.4e+02;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11
 |||||
 Db 98 CTTTGGCACTA 108

RESULT 11

US-09-270-767-22948
 ;; Sequence 22948, Application US/09270767
 ;; Patent No. 6703491
 ;; GENERAL INFORMATION:
 ;; APPLICANT: Homburger et al.
 ;; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
 ;; FILE REFERENCE: File Reference: 7326-094
 ;; CURRENT APPLICATION NUMBER: US/09/270,767
 ;; CURRENT FILING DATE: 1999-03-17
 ;; NUMBER OF SEQ ID NOS: 62517
 ;; SOFTWARE: PatentIn Ver. 2.0
 ;; SEQ ID NO 22948
 ;; LENGTH: 386
 ;; TYPE: DNA
 ;; ORGANISM: Drosophila melanogaster
 US-09-270-767-22948

Query Match 100.0%; Score 11; DB 4; Length 386;
 Best Local Similarity 100.0%; Pred. No. 5.4e+02;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11
 |||||
 Db 98 CTTTGGCACTA 108

RESULT 12

US-09-640-173-30
 ;; Sequence 30, Application US/09640173
 ;; Patent No. 6613515
 ;; GENERAL INFORMATION:
 ;; APPLICANT: Xu, Jiangchun
 ;; APPLICANT: Stolk, John A.
 ;; TITLE OF INVENTION: OVARIAN TUMOR SEQUENCES AND
 ;; METHODS OF USE THEREFOR
 ;; FILE REFERENCE: 210121.484C2
 ;; CURRENT APPLICATION NUMBER: US/09/640,173
 ;; CURRENT FILING DATE: 2000-08-15
 ;; NUMBER OF SEQ ID NOS: 196
 ;; SOFTWARE: FastSeq for Windows Version 3.0
 ;; SEQ ID NO 30
 ;; LENGTH: 396
 ;; TYPE: DNA
 ;; ORGANISM: Homo sapien
 ;; FEATURE:
 ;; NAME/KEY: misc_feature
 ;; LOCATION: (1)...(396)
 ;; OTHER INFORMATION: n = A,T,C or G
 US-09-640-173-30

Query Match 100.0%; Score 11; DB 4; Length 396;
 Best Local Similarity 100.0%; Pred. No. 5.4e+02;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11
 |||||
 Db 316 CTTTGGCACTA 326

RESULT 13

US-09-713-550-30
 ;; Sequence 30, Application US/09713550
 ;; Patent No. 6617109
 ;; GENERAL INFORMATION:
 ;; APPLICANT: Xu, Jiangchun
 ;; APPLICANT: Stolk, John A.
 ;; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE

```
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.484C4
; CURRENT APPLICATION NUMBER: US/09/713,550
; CURRENT FILING DATE: 2000-11-14
; NUMBER OF SEQ ID NOS: 205
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 30
; LENGTH: 396
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc_feature
; FEATURE:
; LOCATION: (1)...(396)
; OTHER INFORMATION: n = A,T,C or G
US-09-713-550-30

Query Match          100.0%; Score 11; DB 4; Length 396;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTGGCACTA 11
   |||||||
Db 316 CTTTGGCACTA 326

RESULT 14
US-09-825-294-30
; Sequence 30, Application US/09825294
; Patent No. 6710170
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolk, John A.
; APPLICANT: Algate, Paul A.
; APPLICANT: Fling, Steven P.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.484C5
; CURRENT APPLICATION NUMBER: US/09/825,294
; CURRENT FILING DATE: 2001-04-03
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 30
; LENGTH: 396
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc_feature
; LOCATION: (1)...(396)
; OTHER INFORMATION: n = A,T,C or G
US-09-825-294-30

Query Match          100.0%; Score 11; DB 4; Length 396;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTGGCACTA 11
   |||||||
Db 316 CTTTGGCACTA 326

RESULT 15
US-09-970-966-30
; Sequence 30, Application US/09970966
; Patent No. 6720146
; GENERAL INFORMATION:
; APPLICANT: Stolk, John A.
; APPLICANT: Moleseh, David Alan
; APPLICANT: Fling, Steven P.
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.484C6
; CURRENT APPLICATION NUMBER: US/09/970,966
```

```
; CURRENT FILING DATE: 2001-10-02
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 396
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc_feature
; LOCATION: 28, 83, 126, 138, 254, 275, 298, 310, 311, 353, 363, 374,
; LOCATION: 379, 393
; OTHER INFORMATION: n = A,T,C or G
US-09-970-966-30

Query Match          100.0%; Score 11; DB 4; Length 396;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTGGCACTA 11
   |||||||
Db 316 CTTTGGCACTA 326

RESULT 16
US-09-621-976-17465/c
; Sequence 17465, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 17465
; LENGTH: 424
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc_feature
; LOCATION: 422
; OTHER INFORMATION: n=a, g, c or t
US-09-621-976-17465

Query Match          100.0%; Score 11; DB 4; Length 424;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTGGCACTA 11
   |||||||
Db 274 CTTTGGCACTA 264

RESULT 17
US-09-621-976-2058/c
; Sequence 2058, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 2058
; LENGTH: 475
; TYPE: DNA
```



```

; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 88..312
; NAME/KEY: sig_peptide
; LOCATION: 88..198
; OTHER INFORMATION: Von Heijne matrix
; OTHER INFORMATION: score 3.5
; OTHER INFORMATION: seq FFFFSKLLPVFS/MM
US-09-621-976-2058

Query Match          100.0%; Score 11; DB 4; Length 475;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11
Db 353 CTTTGGCACTA 343

RESULT 18
US-09-248-796A-2902/c
; Sequence 2902, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 2902
; LENGTH: 477
; TYPE: DNA
; ORGANISM: Candida albicans
US-09-248-796A-2902

Query Match          100.0%; Score 11; DB 4; Length 477;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11
Db 160 CTTTGGCACTA 150

RESULT 19
US-09-621-976-15675/c
; Sequence 15675, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 15675
; LENGTH: 505
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-15675

Query Match          100.0%; Score 11; DB 4; Length 505;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11
Db 182 CTTTGGCACTA 172
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Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11
Db 170 CTTTGGCACTA 160

RESULT 20
US-09-647-224A-21/c
; Sequence 21, Application US/09647224A
; Patent No. 6482631
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Falco, Saverio Carl
; APPLICANT: Gutteridge, Steven
; APPLICANT: Hitz, William D.
; APPLICANT: Maxwell, Carl A.
; APPLICANT: Rafalski, J. Antoni
; APPLICANT: Tao, Yong
; APPLICANT: Vollmer, Steven J.
; TITLE OF INVENTION: TRYPTOPHAN BIOSYNTHETIC ENZYMES
; FILE REFERENCE: BB-1150-A
; CURRENT APPLICATION NUMBER: US/09/647,224A
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 60/079,386
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: PCT/US99/06046
; PRIOR FILING DATE: 1999-03-19
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 21
; LENGTH: 551
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (414)
; OTHER INFORMATION: n = a, c, t, or g
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (445)
; OTHER INFORMATION: n = a, c, t, or g
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (464)
; OTHER INFORMATION: n = a, c, t, or g
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (494)
; OTHER INFORMATION: n = a, c, t, or g
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (508)
; OTHER INFORMATION: n = a, c, t, or g
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (522)
; OTHER INFORMATION: n = a, c, t, or g
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (549)
; OTHER INFORMATION: n = a, c, t, or g
; OTHER INFORMATION: n = a, c, t, or g
US-09-647-224A-21

Query Match          100.0%; Score 11; DB 4; Length 551;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11
Db 182 CTTTGGCACTA 172
```

```
RESULT 21
US-09-134-000C-1129
; Sequence 1129, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1129
; LENGTH: 552
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-09-134-000C-1129

Query Match      100.0%; Score 11; DB 4; Length 552;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CTTTGGCACTA 11
      |||||
Db      435 CTTTGGCACTA 445

RESULT 22
US-09-517-790-3/c
; Sequence 3, Application US/09517790
; Patent No. 6544512
; GENERAL INFORMATION:
; APPLICANT: White, Jr., James F
; TITLE OF INVENTION: Use of Phoma glomerata as a Hyperparasite in the Biocontrol of Fu
; FILE REFERENCE: RU-0093
; CURRENT APPLICATION NUMBER: US/09/517,790
; CURRENT FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 60/123,099
; PRIOR FILING DATE: 1999-03-05
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 570
; TYPE: DNA
; ORGANISM: Ampelomyces quisqualis
US-09-517-790-3

Query Match      100.0%; Score 11; DB 4; Length 570;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CTTTGGCACTA 11
      |||||
Db      524 CTTTGGCACTA 514

RESULT 23
US-09-640-211A-264/c
; Sequence 264, Application US/09640211A
; Patent No. 6833446
; GENERAL INFORMATION:
; APPLICANT: Wood, Marion
; APPLICANT: Shenk, Michael A.
; APPLICANT: McGrath, Annette
; APPLICANT: Glenn, Matthew
; TITLE OF INVENTION: Compositions and Methods for the
; FILE REFERENCE: 11000.1021C1U
; CURRENT APPLICATION NUMBER: US/09/640,211A
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; CURRENT FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 2368
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 264
; LENGTH: 579
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-09-640-211A-264

Query Match      100.0%; Score 11; DB 4; Length 579;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CTTTGGCACTA 11
      |||||
Db      187 CTTTGGCACTA 177

RESULT 24
US-09-949-016-20441
; Sequence 20441, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20441
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-20441

Query Match      100.0%; Score 11; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CTTTGGCACTA 11
      |||||
Db      553 CTTTGGCACTA 563

RESULT 25
US-09-949-016-20442
; Sequence 20442, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20442
; LENGTH: 601
```

; TYPE: DNA
; ORGANISM: Human
US-09-949-016-20442

Query Match 100.0%; Score 11; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11
|||||
Db 549 CTTTGGCACTA 559

RESULT 26
US-09-949-016-23566/c
; Sequence 23566, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23566
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-23566

Query Match 100.0%; Score 11; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11
|||||
Db 540 CTTTGGCACTA 530

RESULT 27
US-09-949-016-25590/c
; Sequence 25590, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25590
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-25590

Query Match 100.0%; Score 11; DB 4; Length 601;

Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11
|||||
Db 88 CTTTGGCACTA 78

RESULT 28
US-09-949-016-29497/c
; Sequence 29497, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29497
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-29497

Query Match 100.0%; Score 11; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11
|||||
Db 484 CTTTGGCACTA 474

RESULT 29
US-09-949-016-35684
; Sequence 35684, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35684
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-35684

Query Match 100.0%; Score 11; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11
|||||

Db 553 CTTTGGCACTA 563

RESULT 30

US-09-949-016-35685

; Sequence 35685, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 35685

; LENGTH: 601

; TYPE: DNA

; ORGANISM: Human

US-09-949-016-35685

Query Match 100.0%; Score 11; DB 4; Length 601;

Best Local Similarity 100.0%; Pred. No. 5.5e+02;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11

|||||

Db 549 CTTTGGCACTA 559

RESULT 31

US-09-949-016-35718

; Sequence 35718, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 35718

; LENGTH: 601

; TYPE: DNA

; ORGANISM: Human

US-09-949-016-35718

Query Match 100.0%; Score 11; DB 4; Length 601;

Best Local Similarity 100.0%; Pred. No. 5.5e+02;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11

|||||

Db 553 CTTTGGCACTA 563

RESULT 32

US-09-949-016-35719

; Sequence 35719, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 35719

; LENGTH: 601

; TYPE: DNA

; ORGANISM: Human

US-09-949-016-35719

Query Match 100.0%; Score 11; DB 4; Length 601;

Best Local Similarity 100.0%; Pred. No. 5.5e+02;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11

|||||

Db 549 CTTTGGCACTA 559

RESULT 33

US-09-949-016-35752

; Sequence 35752, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 35752

; LENGTH: 601

; TYPE: DNA

; ORGANISM: Human

US-09-949-016-35752

Query Match 100.0%; Score 11; DB 4; Length 601;

Best Local Similarity 100.0%; Pred. No. 5.5e+02;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11

|||||

Db 553 CTTTGGCACTA 563

RESULT 34

US-09-949-016-35753

; Sequence 35753, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35753
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-35753

Query Match 100.0%; Score 11; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTGGCACTA 11
|||||
Db 549 CTTTGGCACTA 559

RESULT 35
US-09-949-016-36869
; Sequence 36869, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 36869
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-36869

Query Match 100.0%; Score 11; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTGGCACTA 11
|||||
Db 177 CTTTGGCACTA 187

RESULT 36
US-09-949-016-45724/c
; Sequence 45724, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 45724
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-45724

Query Match 100.0%; Score 11; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTGGCACTA 11
|||||
Db 63 CTTTGGCACTA 53

RESULT 37
US-09-949-016-49633/c
; Sequence 49633, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 49633
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-49633

Query Match 100.0%; Score 11; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTGGCACTA 11
|||||
Db 504 CTTTGGCACTA 494

RESULT 38
US-09-949-016-49634/c
; Sequence 49634, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498

; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 49634
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-49634

Query Match 100.0%; Score 11; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTGGCACTA 11
|||||
DB 331 CTTTGGCACTA 321

RESULT 39
US-09-949-016-56559
; Sequence 56559, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 56559
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-56559

Query Match 100.0%; Score 11; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTGGCACTA 11
|||||
DB 260 CTTTGGCACTA 270

RESULT 40
US-09-949-016-60165/c
; Sequence 60165, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 60165
; LENGTH: 601
; TYPE: DNA

; ORGANISM: Human
US-09-949-016-60165

Query Match 100.0%; Score 11; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTGGCACTA 11
|||||
DB 329 CTTTGGCACTA 319

RESULT 41
US-09-949-016-60166/c
; Sequence 60166, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 60166
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-60166

Query Match 100.0%; Score 11; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTGGCACTA 11
|||||
DB 337 CTTTGGCACTA 327

RESULT 42
US-09-949-016-66919
; Sequence 66919, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 66919
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-66919

Query Match 100.0%; Score 11; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11
Db 138 CTTTGGCACTA 148

RESULT 43

US-09-949-016-66920
; Sequence 66920, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 66920
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-66920

Query Match 100.0%; Score 11; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11
Db 31 CTTTGGCACTA 41

RESULT 44

US-09-949-016-67654
; Sequence 67654, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 67654
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-67654

Query Match 100.0%; Score 11; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11
Db 215 CTTTGGCACTA 225

RESULT 47

US-09-949-016-86386/c
; Sequence 86386, Application US/09949016

RESULT 45

US-09-949-016-67726
; Sequence 67726, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 67726
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-67726

Query Match 100.0%; Score 11; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11
Db 322 CTTTGGCACTA 332

RESULT 46

US-09-949-016-78261
; Sequence 78261, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 78261
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-78261

Query Match 100.0%; Score 11; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11
Db 177 CTTTGGCACTA 187

; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 86386
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-86386

Query Match 100.0%; Score 11; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11
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Db 367 CTTTGGCACTA 357

RESULT 48
US-09-949-016-86773/c
; Sequence 86773, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 86773
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-86773

Query Match 100.0%; Score 11; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11
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Db 481 CTTTGGCACTA 471

RESULT 49
US-09-949-016-87066/c
; Sequence 87066, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 87066
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-87066

Query Match 100.0%; Score 11; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11
|||
Db 484 CTTTGGCACTA 474

RESULT 50
US-09-949-016-88660/c
; Sequence 88660, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 88660
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-88660

Query Match 100.0%; Score 11; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11
|||
Db 229 CTTTGGCACTA 219

Search completed: March 12, 2005, 10:59:14
Job time : 111 secs

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OM nucleic - nucleic search, using sw model

Run on: March 12, 2005, 08:28:43 ; Search time 1733 Seconds
(without alignments)
241.608 Million cell updates/sec

Title: US-10-070-588A-112

Perfect score: 11

Sequence: 1 ctttggcacta 11

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 34239544 seqs, 19032134700 residues

Word size : 0

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : EST:*

- 1: gb_est1:*
- 2: gb_est2:*
- 3: gb_hc:*
- 4: gb_est3:*
- 5: gb_est4:*
- 6: gb_est5:*
- 7: gb_est6:*
- 8: gb_gss1:*
- 9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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CV071926	EST4087.Z	152	7	CV071926
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BH390901	AG-ND-138	162	5	BH390901
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BM739275	K-EST0008	183	4	BM739275
UI51H02.Y	UI51H02.Y	184	1	UI51H02.Y
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AW839614	RC6-LT007	186	2	AW839614
AL798169	AL798169	187	1	AL798169
AV254054	AV254054	187	1	AV254054
BF360904	QV4-OT006	188	2	BF360904
BI061095	IL3-UT011	188	4	BI061095
BI061096	IL3-UT011	188	4	BI061096
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AZ809365	2M0073016	192	8	AZ809365
AA617593	VJ78c04.r	193	1	AA617593
BB512999	BB512999	193	2	BB512999
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AL716876	AL716876	195	1	AL716876
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BG219764	RST39529	196	4	BG219764
AG198201	Pan trogl	197	9	AG198201
CE703371	tigr-g88-	197	9	CE703371
AA254378	va14g07.r	199	1	AA254378
BB835479	RC5-FN002	199	2	BB835479
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EX259889	EX259889	201	5	EX259889
AL361947	AL361947	202	1	AL361947
AV830393	AV830393	203	1	AV830393
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BE835498	RC5-FN002	203	2	BE835498
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BE714221	PM4-HT072	208	2	BE714221
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D58208	HUM355H12B	211	7	D58208
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C 136 11 100.0 244 5 BQ462859 BQ462859
C 137 11 100.0 245 1 A1205004 an03d03.x
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BB344234 257 11 100.0 173
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CO736506 258 7 CO736506
CL420622 258 9 CL420622
CL445669 258 9 CL445669
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CB274583 259 6 CB274583
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CV317089 260 5 CV317089
AV091828 260 7 AV091828
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BB472287 262 2 BB472287
CV085510 262 7 CV085510
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CO295958 263 7 CO295958
CV164625 263 7 CV164625
CC001232 263 8 CC001232
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CL445669 ZMMBBb046
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CB274583 mai71a07
F37070 HSPD35108 H
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CF505326 USDA-FP 1
CF505552 USDA-FP 1
CK386458 maj185905
AV767953 AV767953
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BB472287 BB472287
CV085510 MdFrt3078
CL231012 ZMMBBc016
AV134221 AV134221
AW806346 MR2-UM011
CO295958 EK212402
CV164625 rsmex1.00
CC001232 PUDIG39TD
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BM248905 K0824812
AV360928 AV360928
BB422099 BB422099
AG242810 Lotus cor
BB270022 BB270022
BB291762 BB291762
BR223056 ES7426825
BX2098P00 Single re
BM149234 TCRAEPQ11
BX639559 BX639559
CR772814 DKF2P468H
CV307980 tj48d10.g
CL138451 NDL 69C15
U82192 U82192 Reli
AA982454 u08C04.r
AZ120845 RPCI-23-2
BZ267043 CH230-262
CG279204 QG0B141TV
BF446889 7o65b01.x
BB496623 BB496623
BY568608 BY568608
CK224863 701617338
BF807688 RC2-C1006
F26756 HSPD14344 H
AA747868 nx31h02.s
AA517865 yb82e11.r
CK720341 20765 Swo
CR458213 CR458213
AJ592279 Arabidops
AV337794 AV337794
BB344936 BB344936
BG184361 RST3285 A
BB530888 BB530888
CG206676 TOS0297 T
AI867749 wb38a04.x
AV041343 AV041343
BB412060 BB412060
BF988152 IL0-GN019
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BH745618 gz68h05.b
BB178597 BB178597
CK504085 rswcc0_00

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250 11 100.0 281 1 AV294689 AV294689
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389 11 100.0 312 1 AA652533 AA652533

BY519020 BY519020
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L26666 MUSF035A 1a
AQ066997 HS 2228 A
AA685272 EST106757
AA853124 NHTBCae03
BF081252 RC6-AN006
BG211329 RST30889
BG58460 RH122 67
AV014176 AV014176
BG193786 RST12922
BG217204 RST36906
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CK327480 EST4790 Z
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AV128534 AV128534
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CC839792 ZMMBBBC049
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BE234950 RST34950
BG189086 RST8124 A
BG220252 RST40025
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AV560827 AV560827
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BG196792 RST16019
T63494 YC22901.61
BA655555 INRA PORC
BG191186 RST10273
AV136761 AV136761
BE787745 601482312
BG095930 EST460449
BG190695 RST9769 A
BG193275 RST12402
BG209794 RST29321
BU097041 tca-1526
C63255 C63255 YUJ1
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CL208080 ZMMBBBC055
CL430772 ZMMBBBC043
BF530312 602071496
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390	11	100.0	312	2	BF737539	CM4-KT003	C 463	11	100.0	323	5	BM979499	UI-CF-DU1
391	11	100.0	312	2	AM449138	UI-H-BI3-	464	11	100.0	323	6	CB177752	in95905.x
C 392	11	100.0	312	6	BI120310	FO13P35Y	465	11	100.0	324	9	CG855019	ZMMBBc022
C 393	11	100.0	312	6	CB176560	PI23G01.Y	466	11	100.0	324	1	AU057416	AU057416
C 394	11	100.0	313	1	AA907440	AO102f10.s	467	11	100.0	324	1	AU057829	AU057829
C 395	11	100.0	313	2	BB507275	BB507275	468	11	100.0	324	1	AA278991	z880e03.r
C 396	11	100.0	313	4	BG214014	RST33640	469	11	100.0	324	4	BK406478	sac32g11.
C 397	11	100.0	313	7	CV402237	QVA-SN002	470	11	100.0	324	7	CK345926	L0533F04-
C 398	11	100.0	313	8	AQ971209	RPCI-23-3	471	11	100.0	325	1	AA672787	vs38d07.r
C 399	11	100.0	314	1	AV259425	AV259425	472	11	100.0	325	1	AI493365	tg70g08.x
C 400	11	100.0	314	1	AV524633	AV524633	473	11	100.0	325	1	AV307357	AV307357
C 401	11	100.0	314	2	BF877747	601482314	474	11	100.0	325	2	BE923133	EST7426902
C 402	11	100.0	314	4	BF985447	QVA-GN014	475	11	100.0	325	4	BG146473	maB91f04.
C 403	11	100.0	314	6	CA929078	MTU2CA.P1	476	11	100.0	325	8	CK767183	naQ03-1cs
C 404	11	100.0	314	8	B533613	OGAKI67TM	477	11	100.0	325	8	AQ843287	nbxb0007C
C 405	11	100.0	315	2	BB122148	BB122148	478	11	100.0	326	1	AA277874	vaS092.2.r
C 406	11	100.0	315	2	BE503891	h235b06.x	479	11	100.0	326	8	AZ385162	IMO143F03
C 407	11	100.0	315	9	CL394030	ZMMBBb024	480	11	100.0	326	8	BZ675902	PUBEN43TD
C 408	11	100.0	316	1	AL673589	we76b07.x	481	11	100.0	327	2	BB122890	BB122890
C 409	11	100.0	316	4	BG146261	maB73e07.	482	11	100.0	327	2	BF062105	7k72a08.x
C 410	11	100.0	316	4	BG210824	RST30372	483	11	100.0	327	7	CK319294	X9P09b06
C 411	11	100.0	316	6	CP911508	G550.111F	484	11	100.0	327	7	CO867115	Mxdb5006h
C 412	11	100.0	316	7	CK687116	ZF101-P00	485	11	100.0	327	7	CO994343	UMC-pd12
C 413	11	100.0	316	7	CK779785	UMC-bend	486	11	100.0	328	2	BZ287023	SAUK_0203
C 414	11	100.0	316	7	CK776275	tae79c07-	487	11	100.0	328	2	BF226483	uz51e12.x
C 415	11	100.0	317	2	AW132076	xe72b01.x	488	11	100.0	328	2	BE933891	RCO-HT090
C 416	11	100.0	317	2	BG207041	BB207041	489	11	100.0	328	5	BP601545	BP601545
C 417	11	100.0	317	2	BG205712	RST25029	490	11	100.0	328	9	CG690277	ZMMBBc013
C 418	11	100.0	317	4	BG360949	gb42b10.Y	491	11	100.0	329	5	BQ495197	BQ495197
C 419	11	100.0	317	4	B1216362	RE23479.5	492	11	100.0	329	5	BQ761681	EBEm10.SQ
C 420	11	100.0	317	6	CA772796	ik63d03.x	493	11	100.0	329	5	BY518786	BY518786
C 421	11	100.0	317	7	CO728900	UMC-bend	494	11	100.0	329	7	CN942645	010921AVB
C 422	11	100.0	317	8	AZ257430	RPCI-23-1	495	11	100.0	330	2	BE954594	UI-M-CC1-
C 423	11	100.0	318	9	CC813094	ZMMBBc048	496	11	100.0	330	5	EX869232	EX869232
C 424	11	100.0	318	1	AV021902	AV021902	497	11	100.0	330	5	BY519713	BY519713
C 425	11	100.0	318	2	BB530435	BB530435	498	11	100.0	330	6	CA535472	C0319A02-
C 426	11	100.0	318	4	B1119675	FO03P36Y	499	11	100.0	330	7	CV230514	WS01916.B
C 427	11	100.0	319	1	AT395948	487010A04	500	11	100.0	330	8	AQ584397	RPCI-11-4
C 428	11	100.0	319	1	AA606812	vm90h11.r	501	11	100.0	330	9	CE655262	tigr-g8s-
C 429	11	100.0	319	2	BB097330	BB097330	502	11	100.0	331	4	AI871566	we2g11.x
C 430	11	100.0	319	2	BB530437	BB530437	503	11	100.0	331	4	BG193784	RS12520
C 431	11	100.0	319	4	BG214013	RST33639	504	11	100.0	331	6	CB641164	OSUNEa18B
C 432	11	100.0	319	4	BM226235	K0224G09	505	11	100.0	331	7	CK899267	SGP162856
C 433	11	100.0	319	9	CG867622	CG867622	506	11	100.0	331	8	AQ366205	nbxb0065M
C 434	11	100.0	319	9	CL398797	ZMMBBb040	507	11	100.0	331	9	BE222270	Danio rer
C 435	11	100.0	320	1	AA954082	on62g10.s	508	11	100.0	332	1	AA667156	vg89d10.r
C 436	11	100.0	320	1	AI205735	qg32c01.x	509	11	100.0	332	1	AI051099	ow38e03.s
C 437	11	100.0	320	1	AI559401	tq33b09.x	510	11	100.0	332	1	AI121373	uc31902.r
C 438	11	100.0	320	1	AI824623	wc19h05.x	511	11	100.0	332	2	BF226970	uz18h05.x
C 439	11	100.0	320	1	AL369106	MtBA28H09	512	11	100.0	332	4	BG199910	RST19206
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C 443	11	100.0	320	7	W35436	glg09fs.f	516	11	100.0	333	6	BY557359	BY557359
C 444	11	100.0	320	8	AQ425575	AO425575	517	11	100.0	333	6	CD632309	55125210J
C 445	11	100.0	320	8	AO544643	CITBI-E1-	518	11	100.0	333	7	CO591563	DG3-51g22
C 446	11	100.0	321	1	AJ686528	AJ686528	519	11	100.0	333	8	BH290157	CH230-207
C 447	11	100.0	321	2	BF840294	RC3-HT023	520	11	100.0	334	1	AI991901	wa42b06.x
C 448	11	100.0	321	4	BG209795	BG209795	521	11	100.0	334	1	AV737315	AV737315
C 449	11	100.0	321	6	CD674760	fs14d06.Y	522	11	100.0	334	4	BG204511	RST23916
C 450	11	100.0	321	9	CNS00020V	AL085285	523	11	100.0	334	7	CV081603	CV081603
C 451	11	100.0	322	1	AA981813	ua31h11.r	524	11	100.0	334	9	CL572176	OB_Ba001
C 452	11	100.0	322	1	AV303979	AV303979	525	11	100.0	334	9	CL572176	OB_Ba001
C 453	11	100.0	322	2	BE327051	hw06d06.x	526	11	100.0	335	2	AW192189	x1B1C04.x
C 454	11	100.0	322	2	BF148524	uy82d02.x	527	11	100.0	335	2	AW501859	UI-HF-BR0
C 455	11	100.0	322	5	BM579721	BM579721	528	11	100.0	335	5	BQ030573	UI-1-BA0-
C 456	11	100.0	322	8	AZ870193	1M0554B13	529	11	100.0	335	6	CK102723	MMV_SQ013
C 457	11	100.0	322	8	AZ870193	2M0182P01	530	11	100.0	335	7	CK694433	ZF101-P00
C 458	11	100.0	322	9	CG391423	ZMMBBc057	531	11	100.0	335	9	CG763261	ZF101-P00
C 459	11	100.0	323	1	AA846030	ak79b03.s	532	11	100.0	336	1	AV259568	ZMMBBc020
C 460	11	100.0	323	1	AA188850	zp79d08.r	533	11	100.0	336	2	AW347865	AV259568
C 461	11	100.0	323	2	BB140143	BB140143	534	11	100.0	336	2	BE549844	32157 MAR
C 462	11	100.0	323	4	BI276625	UI-R-CX0-	535	11	100.0	336	5	BY517671	7a20d07.x

536	11	100.0	336	7	CN866896	001026AAN	CN866896	001026AAN	11	100.0	349	1	AI243294	AI243294	qh35h12.x
537	11	100.0	337	8	AZ838754	2M0334P08	AZ838754	2M0334P08	11	100.0	349	1	AI895627	EST265070	AI895627
538	11	100.0	338	1	AL750352	AL750352	AL750352	AL750352	11	100.0	349	1	AA514907	nh72c02.8	AA514907
539	11	100.0	337	4	BG207686	RST27169	BG207686	RST27169	11	100.0	349	2	AW268388	xv50907.x	AW268388
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543	11	100.0	337	7	CF615600	CES013958	CF615600	CES013958	11	100.0	349	7	CO483057	G00198.TB	CO483057
544	11	100.0	337	7	CV368378	PM2-CT080	CV368378	PM2-CT080	11	100.0	349	7	C0937021	UNC-pd12c	C0937021
545	11	100.0	337	7	TE3065	Yb98e08.r1	TE3065	Yb98e08.r1	11	100.0	350	1	AA453089	x415g03.r	AA453089
546	11	100.0	337	8	BH106357	RPC1-24-3	BH106357	RPC1-24-3	11	100.0	350	2	BF733517	RC6-AN006	BF733517
547	11	100.0	337	9	CL890389	abg02h07.	CL890389	abg02h07.	11	100.0	350	2	AW628002	AI37B10.x	AW628002
548	11	100.0	338	1	AI141691	ot08e01.x	AI141691	ot08e01.x	11	100.0	350	2	CN867652	00118AAN	CN867652
549	11	100.0	338	1	AA277097	vc06h05.r	AA277097	vc06h05.r	11	100.0	351	1	AI183068	ub93d10.r	AI183068
550	11	100.0	338	7	CV500994	65479.1.M	CV500994	65479.1.M	11	100.0	351	2	BF591296	7h44b10.x	BF591296
551	11	100.0	338	9	CL317157	ZMBBbc052	CL317157	ZMBBbc052	11	100.0	351	4	BM117843	LO857A09-	BM117843
552	11	100.0	339	1	AA689502	ns66h06.8	AA689502	ns66h06.8	11	100.0	351	5	BY413554	BY413554	BY413554
553	11	100.0	339	1	AA923730	cm39c03.s	AA923730	cm39c03.s	11	100.0	351	6	CB867750	HC01B20w	CB867750
554	11	100.0	339	1	AA514256	ni56g11.8	AA514256	ni56g11.8	11	100.0	352	1	AI156011	ud86902.r	AI156011
555	11	100.0	339	2	BF171785	PCL3386.M	BF171785	PCL3386.M	11	100.0	352	1	AI410077	EST238370	AI410077
556	11	100.0	339	7	D66851	CELK124F1R	D66851	CELK124F1R	11	100.0	352	4	BM840085	K-EST0117	BM840085
557	11	100.0	340	2	AW474294	x824d09.x	AW474294	x824d09.x	11	100.0	352	5	BQ565673	gi43e07.y	BQ565673
558	11	100.0	340	5	BY103527	BY103527	BY103527	BY103527	11	100.0	352	5	HU158393	AGENCOURT	HU158393
559	11	100.0	340	7	CO941320	UMC-peov3	CO941320	UMC-peov3	11	100.0	352	7	CN999200	UMC-bend	CN999200
560	11	100.0	341	2	BE185420	IL5-HT073	BE185420	IL5-HT073	11	100.0	352	7	CO955760	UMC-pputa	CO955760
561	11	100.0	341	4	BM150979	TCBAP1D13	BM150979	TCBAP1D13	11	100.0	352	7	CO989217	UMC-pd3en	CO989217
562	11	100.0	341	5	BP655258	BP655258	BP655258	BP655258	11	100.0	353	1	AI287981	qv01d08.x	AI287981
563	11	100.0	341	5	BY398234	BY398234	BY398234	BY398234	11	100.0	353	1	AI311564	G094d04.x	AI311564
564	11	100.0	341	1	AI219361	qg14e07.x	AI219361	qg14e07.x	11	100.0	353	1	AV815300	AV815300	AV815300
565	11	100.0	342	6	CA535165	C0214G08-	CA535165	C0214G08-	11	100.0	353	2	AW264770	xq35d08.x	AW264770
566	11	100.0	342	6	CD979936	QAH2B03.x	CD979936	QAH2B03.x	11	100.0	353	2	BE629131	uu32f07.y	BE629131
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870	11	100.0	378	5	BY416940	BY416940	C 943	11	100.0	385	1	AA583439	AA583439 nt38b03.s
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876	11	100.0	378	8	B69095	CIT-HSP-205	C 949	11	100.0	385	5	BY527310	BY527310 BY527310
877	11	100.0	378	9	CC811547	ZMMBBc047	C 950	11	100.0	385	6	BY659434	BY659434 BY659434
878	11	100.0	379	1	AA792995	VP54e10.r	C 951	11	100.0	385	6	BY678356	BY678356 BY678356
879	11	100.0	379	1	AI933724	wn43a08.x	C 952	11	100.0	385	6	BY701711	BY701711 BY701711
880	11	100.0	379	1	AU023286	AU023286	C 953	11	100.0	385	7	CO304289	CO304289 EK244256.
881	11	100.0	379	1	AV523891	AV523891	C 954	11	100.0	386	1	AA636558	AA636558 q86h02.s
882	11	100.0	379	1	AV888317	AV888317	C 955	11	100.0	386	1	AA675643	AA675643 vt63f04.s
883	11	100.0	379	1	AA398664	2t64h09.s	C 956	11	100.0	386	1	AI342284	AI342284 qt33q04.x
884	11	100.0	379	1	AA467712	ve02g05.x	C 957	11	100.0	386	1	AI476083	AI476083 t197f12.x
885	11	100.0	379	2	BE646751	UI-M-BH1-	C 958	11	100.0	386	1	AI826973	AI826973 wk55a09.x
886	11	100.0	379	4	BI657476	603281810	C 959	11	100.0	386	1	AA570787	AA570787 tm37e08.s
887	11	100.0	379	5	BY440948	BY440948	C 960	11	100.0	386	2	AM008543	AM008543 wb70a01.x
888	11	100.0	379	7	CO239333	WS00725.B	C 961	11	100.0	386	2	AW016950	AW016950 xq05a01.x
889	11	100.0	379	8	AZ239862	RPCI-23-B	C 962	11	100.0	386	2	AM664727	AM664727 h132h10.x
890	11	100.0	379	9	CR099940	Forward.s	C 963	11	100.0	386	2	BB836689	BB836689 BB836689
891	11	100.0	379	9	CE068356	tigr-g88-	C 964	11	100.0	386	5	BY420317	BY420317 BY420317
892	11	100.0	379	9	CL420253	ZMMBBb042	C 965	11	100.0	386	5	BY442065	BY442065 BY442065
893	11	100.0	380	1	AI032492	ow97a02.s	C 966	11	100.0	386	5	BY449302	BY449302 BY449302
894	11	100.0	380	1	AI841651	UI-M-AO0-	C 967	11	100.0	386	7	CK693317	CK693317 ZF101-P00
895	11	100.0	380	2	BF805741	OV1-CI017	C 968	11	100.0	386	7	CO320702	CO320702 EK287247.
896	11	100.0	380	7	CO360347	DR-ATE.SU	C 969	11	100.0	386	8	B05078	B05078 CSRL-54a6-u
897	11	100.0	380	8	BZ892946	UP-506-21	C 970	11	100.0	386	8	B56253	B56253 CIT-HSP-200
898	11	100.0	381	1	AA774108	ac36d01.s	C 971	11	100.0	386	9	CC601015	CC601015 ZMMBSC040
899	11	100.0	381	1	AA826611	of34d10.s	C 972	11	100.0	386	9	CL605882	CL605882 CH240.1B3
900	11	100.0	381	1	AL382590	MLBC08E11	C 973	11	100.0	387	1	AA706382	AA706382 eg97a03.s

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c 974      11 100.0      387 1 AA881812
c 975      11 100.0      387 1 A1049540
c 976      11 100.0      387 1 AA099542
c 977      11 100.0      387 1 AJ690317
c 978      11 100.0      387 1 AA180213
c 979      11 100.0      387 1 AA062730
c 980      11 100.0      387 1 AA598477
c 981      11 100.0      387 4 BM313705
c 982      11 100.0      387 6 BY644484
c 983      11 100.0      387 7 CN917937
c 984      11 100.0      387 7 CN952033
c 985      11 100.0      388 2 BE824747
c 986      11 100.0      388 4 BG583821
c 987      11 100.0      388 5 BM899081
c 988      11 100.0      388 6 BY644485
c 989      11 100.0      388 6 BY672036
c 990      11 100.0      388 6 BY684940
c 991      11 100.0      388 7 CN944620
c 992      11 100.0      388 7 CV351671
c 993      11 100.0      388 7 D54869
c 994      11 100.0      388 8 A0266797
c 995      11 100.0      388 8 B2408816
c 996      11 100.0      388 9 CG011634
c 997      11 100.0      388 9 CG702278
c 998      11 100.0      388 9 CL260354
c 999      11 100.0      389 1 AA834175
c1000     11 100.0      389 1 AA185175

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ALIGNMENTS

```

RESULT 1
AZ636663      43 bp  DNA      linear      GSS 13-DEC-2000
LOCUS      IM0495D12R Mouse 10kb plasmid UUGCLM library Mus musculus genomic
DEFINITION      Clone UUGCLM0495D12 R, genomic survey sequence.
ACCESSION      AZ636663
VERSION      AZ636663.1 GI:11758853
KEYWORDS      GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM      Mus musculus
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmod,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D. Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
Plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0495 row: D column: 12
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 43.
Location/Qualifiers
1. .43
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGCLM0495D12"
/sex="Male"

FEATURES
source
1. .68
/organism="Mus x domestica"
/mol_type="mRNA"
/db_xref="taxon:3750"
/clone="Mdfrc3046b04"
/lab_host="DH10B ampicillin resistant"

/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCLM library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 100.0%; Score 11; DB 8; Length 43;
Best Local Similarity 100.0%; Pred. No. 1.6e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11
Db 2 CTTTGGCACTA 12

RESULT 2
CO866272/c
LOCUS      Mdfrc3046b04.y1 Mdfrc Malus x domestica cDNA clone Mdfrc3046b04 5',
DEFINITION      mRNA sequence.
ACCESSION      CO866272
VERSION      CO866272.1 GI:51096422
KEYWORDS      EST.
SOURCE      Malus x domestica (cultivated apple)
ORGANISM      Malus x domestica
REFERENCE      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS      Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosids; eurosids I; Rosales; Rosaceae; Maloideae; Malus.
Korban,S., Vodkin,L., Liu,L., Gasic,K., Gonzales,O., Hernandez,A.,
Aldwinckle,H., Malnoy,M., Carroll,N., Goldsborough,P., Orvis,K.,
Clifton,S., Pape,D., Marra,M., Hillier,L., Martin,J., Wylie,T.,
Dante,M., Theising,B., Bowers,Y., Gibbons,M., Ritter,E., Ronko,I.,
Tsagarishvili,R., Kennedy,S., Waterston,R. and Wilson,R.
Apple Functional Genomics grant - NSF 0321702
Unpublished (2004)
Contact: Schuyler S. Korban
Apple Functional Genomics grant - NSF 0321702
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Library materials provided by: Schuyler S. Korban Library
constructed by: K. Gasic Library sequenced by: Washington
University Genome Sequencing Center
WashU EST name: aa152a02.y1
Seq primer: -40UP from Gibco
High quality sequence stop: 68.
Location/Qualifiers
1. .68
/organism="Malus x domestica"
/mol_type="mRNA"
/db_xref="taxon:3750"
/clone="Mdfrc3046b04"
/lab_host="DH10B ampicillin resistant"

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TITLE Zhu, Q., Person, C. and Sands, A.T.
JOURNAL Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap
COMMENT screen to identify potential targets for therapeutic intervention
 Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
 Contact: Zambrowicz BP
 OmniBank

Lexicon Genetics Incorporated
 4000 Research Forest Drive, The Woodlands, TX 77381, USA
 Email: materials@lexgen.com

Gene trap sequence tag generated by 3' RACE from mouse ES cells as
 described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
 Class: Gene Trap.

FEATURES Location/Qualifiers
 source 1..87

/organism="Mus musculus"
 /mol_type="mRNA"
 /strain="129Sv/Ev"
 /db_xref="taxon:10090"
 /clone="OST465420"
 /cell_type="embryonic stem cell"
 /clone_lib="Mus musculus 129Sv/Ev"

ORIGIN

Query Match 100.0%; Score 11; DB 9; Length 87;
 Best Local Similarity 100.0%; Pred. No. 1.7e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11
 |||||
 Db 51 CTTTGGCACTA 61

RESULT 5

LOCUS A1631958 88 bp mRNA linear EST 26-APR-1999
DEFINITION wa38b09.x1 NCI CGAP Kid11 Homo sapiens cDNA clone IMAGE:2300345 3'
 similar to gb:M98326 VALYL-TRNA SYNTHETASE (HUMAN);, mRNA sequence.

ACCESSION A1631958
VERSION A1631958.1 GI:4683288
KEYWORDS EST.

ORGANISM

Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 88)

REFERENCE NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT

Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 cDNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
 Seq primer: -40UP from Gibco
 High quality sequence stop: 1.

FEATURES Location/Qualifiers
 source 1..88

/organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2300345"
 /lab_host="PH10B"
 /clone_lib="NCI CGAP Kid11"

/note="Organ: kidney; Vector: p7T7D-Pac (Pharmacia) with
 a modified polylinker; Site_1: Not I; Site_2: Eco RI;

Plasmid DNA from the normalized library NCI CGAP Kid3 was
 prepared, and ss circles were made in vitro. Following HAP
 purification, this DNA was used as tracer in a subtractive
 hybridization reaction. The driver was PCR-amplified cDNAs
 from a pool of 5,000 clones made from the same library
 (cloneIDs 132376-1323911, 1456007-1456775, and
 1500552-1502855). Subtraction by Bento Soares and M.
 Fatima Bonaldo. "

ORIGIN

Query Match 100.0%; Score 11; DB 1; Length 88;
 Best Local Similarity 100.0%; Pred. No. 1.7e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11
 |||||
 Db 17 CTTTGGCACTA 7

RESULT 6

LOCUS BZ662266/c 88 bp DNA linear GSS 31-JAN-2003
DEFINITION SALIK_025751.28.05.x Arabidopsis thaliana TDNA insertion lines
 Arabidopsis thaliana genomic clone SALIK_025751.28.05.x, genomic
 survey sequence.

ACCESSION BZ662266
VERSION BZ662266.1 GI:28176379
KEYWORDS GSS.

ORGANISM

Arabidopsis thaliana (thale cress)
 Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE

1 (bases 1 to 88)

AUTHORS Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R.,
 Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L.,
 Shinn, P., Zimmermann, J. and Ecker, J.R.

TITLE A Sequence-Indexed Library of Insertion Mutations in the

JOURNAL Arabidopsis Genome

COMMENT

Unpublished (2001)
 Contact: Joseph R. Ecker
 Salk Institute Genomic Analysis Laboratory (SIGnAL)
 The Salk Institute for Biological Studies
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
 Tel: 858 453 4100 x1752
 Fax: 858 558 6379
 Email: ecker@salk.edu
 This is single pass sequence recovered from the left border of
 TDNA.

Class: TDNA tagged.

FEATURES Location/Qualifiers

source

1..88
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /ecotype="Col-0"
 /db_xref="taxon:3702"
 /clone="SALIK_025751.28.05.x"
 /clone_lib="Arabidopsis thaliana TDNA insertion lines"
 /note="PCR was performed on Arabidopsis thaliana lines
 each of which contains one or more TDNA insertion
 elements. The resultant fragment for each line was
 directly sequenced to determine the genomic sequence at
 the site of insertion. Details of the protocols used can
 be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN

Query Match 100.0%; Score 11; DB 8; Length 88;
 Best Local Similarity 100.0%; Pred. No. 1.7e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11
 |||||
 Db 68 CTTTGGCACTA 58

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RESULT 7
BG409256
LOCUS
DEFINITION
  91 bp mRNA linear EST 13-MAR-2001
  9b89g12.y1 Moss EST library PPG Physcomitrella patens cDNA clone
  PEP_SOURCE_ID:PPG_CopyA-121423 5', mRNA sequence.
ACCESSION
  BG409256
VERSION
  BG409256.1 GI:13315601
KEYWORDS
  EST.
SOURCE
  Physcomitrella patens
  Physcomitrella patens
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
  Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.
REFERENCE
  1 (bases 1 to 91)
  Quatrano, R., Bashardes, S., Cove, D., Cuming, A., Knight, C.,
  Clifton, S., Marra, M., Hillier, L., Pape, D., Martin, J., Wylie, T.,
  Underwood, K., Theising, B., Allen, M., Bowers, Y., Person, B.,
  Swaller, T., Steptoe, M., Gibbons, M., Harvey, N., Ritter, E.,
  Jackson, Y., McCann, R., Waterston, R. and Wilson, R.
  Leeds/Wash U Moss EST Project
  Unpublished (1999)
  Contact: Ralph Quatrano
  Leeds/Wash U Moss EST Project
  Washington University School of Medicine
  4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
  Tel: 314 286 1800
  Fax: 314 286 1810
  Email: estwatson.wustl.edu
  Libraries were constructed by Dr. Stavros Bashardes as part of the
  Physcomitrella EST program (PEP) at the Univ. of Leeds (UK) and
  Washington Univ. in St. Louis (USA) DNA sequencing by: Washington
  University Genome Sequencing Center For information on obtaining a
  clone please contact: Celia Knight (c.d.knight@leeds.ac.uk)
  Putative full length read
  vector to vector length is 92
  Seq primer: -40RP from Gibco.
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    1..91
      /organism="Physcomitrella patens"
      /mol_type="mRNA"
      /db_xref="taxon:3218"
      /clone="PEP_SOURCE_ID:PPG_CopyA-121423"
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      ammonium-grown"
      /lab_host="DH10B"
      /clone_lib="Moss EST library PPG"
      /note="Vector: pAMP1; Construction of the cDNA library was
      performed by Dr. W. Gregg Clark using a modification of
      the cDNA synthesis protocol developed in the laboratory of
      Dr. Michael Lovett by Dr. Yulia Korshunova (personal
      communication). First polyA + RNA was isolated from total
      gametophore RNA using oligo dT magnetic beads. Following
      this, first strand cDNA synthesis was performed on the
      bead-bound polyA + RNA, during which an oligonucleotide
      anchor sequence was incorporated onto the 5'-ends of the
      cDNA. PCR amplification was then used to synthesize the
      second strand, to amplify the double stranded DNA, and to
      incorporate dUTP containing sequences into the ends of the
      double stranded cDNA. This DNA was size selected and
      cloned into pAMP1 using the CloneAMP pAMP1 System (Life
      Technologies, GibcoBRL) for cloning amplification products
      by a non-restriction site dependant process. The cloning
      was directional based on sequence asymmetry introduced at
      the ends during PCR amplification. The 3' cDNA ends are
      proximal to the NotI site of the multiple cloning site in
      pAMP1. This annealing mixture was transformed into
      chemically competent DH10B cells and selected for
      ampicillin resistant growth. The resulting clones (about
      330,000) were pooled to make the library."
FEATURES
  source
    1..91
      /organism="Physcomitrella patens"
      /mol_type="mRNA"
      /db_xref="taxon:3218"
      /clone="PEP_SOURCE_ID:PPG_CopyA-121423"
      /tissue_type="gametophore: 30 day old tissue,
      ammonium-grown"
      /lab_host="DH10B"
      /clone_lib="Moss EST library PPG"
      /note="Vector: pAMP1; Construction of the cDNA library was
      performed by Dr. W. Gregg Clark using a modification of
      the cDNA synthesis protocol developed in the laboratory of
      Dr. Michael Lovett by Dr. Yulia Korshunova (personal
      communication). First polyA + RNA was isolated from total
      gametophore RNA using oligo dT magnetic beads. Following
      this, first strand cDNA synthesis was performed on the
      bead-bound polyA + RNA, during which an oligonucleotide
      anchor sequence was incorporated onto the 5'-ends of the
      cDNA. PCR amplification was then used to synthesize the
      second strand, to amplify the double stranded DNA, and to
      incorporate dUTP containing sequences into the ends of the
      double stranded cDNA. This DNA was size selected and
      cloned into pAMP1 using the CloneAMP pAMP1 System (Life
      Technologies, GibcoBRL) for cloning amplification products
      by a non-restriction site dependant process. The cloning
      was directional based on sequence asymmetry introduced at
      the ends during PCR amplification. The 3' cDNA ends are
      proximal to the NotI site of the multiple cloning site in
      pAMP1. This annealing mixture was transformed into
      chemically competent DH10B cells and selected for
      ampicillin resistant growth. The resulting clones (about
      330,000) were pooled to make the library."
ORIGIN
  Query Match
  Best Local Similarity 100.0%; Score 11; DB 4; Length 91;
  Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  QY 1 CTTTGGCACTA 11
  DB 24 CTTTGGCACTA 34
  RESULT 9
  CF776000/c
  Query Match
  Best Local Similarity 100.0%; Score 11; DB 2; Length 106;
  Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  QY 1 CTTTGGCACTA 11
  DB 24 CTTTGGCACTA 34
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  BE165421
  LOCUS
  DEFINITION
    106 bp mRNA linear EST 21-JUN-2000
    QV1-HT0474-070300-098-g07 HT0474 Homo sapiens cDNA, mRNA sequence.
  ACCESSION
    BE165421
  VERSION
    BE165421.1 GI:8628142
  KEYWORDS
    EST.
  SOURCE
    Homo sapiens (human)
  ORGANISM
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  REFERENCE
    1 (bases 1 to 106)
    Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
    Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
    Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
    Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V.,
    O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
    Simpson, A.J.
    Shotgun sequencing of the human transcriptome with ORF expressed
    sequence tags
  TITLE
    Shotgun sequencing of the human transcriptome with ORF expressed
    sequence tags
  JOURNAL
    Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  MEDLINE
    20202663
  PUBMED
    10737800
  COMMENT
    Contact: Simpson A.J.G.
    Laboratory of Cancer Genetics
    Ludwig Institute for Cancer Research
    Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
    Brazil
    Tel: +55-11-2704922
    Fax: +55-11-2707001
    Email: asimpson@ludwig.org.br
    This sequence was derived from the FAPESP/LICR Human Cancer Genome
    Project. This entry can be seen in the following URL
    (http://www.ludwig.org.br/scripts/gethtml2.pl?c1=4t2=QV1-HT0474-070
    300-098-g07&t3=2000-03-07&t4=1)
    Seq primer: puc 18 forward
    High quality sequence start: 9
    High quality sequence stop: 106.
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    source
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        /organism="Homo sapiens"
        /mol_type="mRNA"
        /db_xref="taxon:9606"
        /dev_stage="Adult"
        /clone_lib="HT0474"
        /note="Organ: head neck; Vector: puc18; Site: 1; SmaI;
        Site 2: SmaI; A mini-library was made by cloning products
        derived from ORESTES PCR (U.S. Letters Patent application
        No. 196.716 - Ludwig Institute for Cancer Research)
        profiles into the pUC 18 vector. Reverse transcription of
        tissue mRNA and cDNA amplification were performed under
        low stringency conditions."
  ORIGIN
    Query Match
    Best Local Similarity 100.0%; Score 11; DB 2; Length 106;
    Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
    QY 1 CTTTGGCACTA 11
    DB 24 CTTTGGCACTA 34
  RESULT 9
  CF776000/c
  Query Match
  Best Local Similarity 100.0%; Score 11; DB 4; Length 91;
  Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  QY 1 CTTTGGCACTA 11
  DB 24 CTTTGGCACTA 34

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LOCUS CF776000 107 bp mRNA linear EST 20-OCT-2003
DEFINITION jaa28e10.y1 Anolis sagrei limb bud 2 Anolis sagrei cDNA 5' similar
to TR:095630 O95630 AMSH. ;, mRNA sequence.

ACCESSION CF776000
VERSION CF776000.1 GI:37762717
KEYWORDS EST.
SOURCE Anolis sagrei (brown anole)
ORGANISM Anolis sagrei
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Iguania; Polychrotinae; Anolis.
1 (bases 1 to 107)

REFERENCE
AUTHORS Loos, J., Gibson-Brown, J., Sanger, T.J., Langwith, S., Murphy, C.,
Clifton, S., Pape, D., Marra, M., Hillier, L., Martin, J., Wylie, T.,
Dante, M., Theising, B., Bowers, Y., Gibbons, M., Ritter, E.,
Bennett, J., Ronko, I., Tsagareishvili, R., Maguire, L., Kennedy, S.,
Waterston, R. and Wilson, R.
Packard/Washington University Lizard Limb Bud EST Project
Unpublished (2003)
Contact: Jeremy Gibson-Brown
Packard/Washington University Lizard Limb Bud EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Library was constructed by Jeremy Gibson-Brown DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Jeremy Gibson-Brown
(gibbro@biology.wustl.edu)
Seq primer: T7.

FEATURES
source
1..107
/organism="Anolis sagrei"
/mol_type="mRNA"
/db_xref="taxon:38937"
/lab_host="DH10B"
/clone_lib="Anolis sagrei limb bud 2"
/note="Vector: Bluescript SK+; Site 1: EcoRI; Site 2:
BamHI; 1st strand primed with an oligo (dT) primer; double
stranded cDNA was cloned into the EcoRI and BamHI sites of
the pBluescript SK+ vector. Primary library;
non-amplified."

ORIGIN
Query Match 100.0%; Score 11; DB 7; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.7e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTGGCACTA 11
|||||
Db 26 CTTTGGCACTA 16

RESULT 10
AZ517183/c 113 bp DNA linear GSS 16-OCT-2000
LOCUS RPCI-11-5P24.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-5P24,
genomic survey sequence.

ACCESSION AZ517183
VERSION AZ517183.1 GI:10826158
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 113)
AUTHORS Zhao, S., Adams, M.D., Nierman, W., Malek, J., de Jong, P. and
Venter, J.C.
BAC end sequences of library RPCI-11
Unpublished (1997)
TITLE Other_GSSs: RPCI11-5P24.TVB
COMMENT Contact: Shaying Zhao
Department of Eukaryotic Genomics

The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhac@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genet cs (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
This BAC end was generated during the R&D process and may have
higher chance of clone tracking errors.
Seq primer: SP6
Class: BAC ends

FEATURES
Location/Qualifiers
1..113
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="GDB:7501919"
/db_xref="taxon:9606"
/clone="RPCI-11-5P24"
/sex="Male"
/cell_type="Lymphocytes"
/clone_lib="RPCI-11"
/notes="Vector: pBACe3.6; Site 1: EcoRI; Site 2: EcoRI;
RPCI11 Human Male BAC Library"

ORIGIN
Query Match 100.0%; Score 11; DB 8; Length 113;
Best Local Similarity 100.0%; Pred. No. 1.7e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTGGCACTA 11
|||||
Db 94 CTTTGGCACTA 84

RESULT 11
B1130927 116 bp mRNA linear EST 31-DEC-2001
LOCUS G112P81Y Populus cambium cDNA library Populus tremula x Populus
tremuloides cDNA, mRNA sequence.

ACCESSION B1130927
VERSION B1130927.1 GI:18014898
KEYWORDS EST.
SOURCE Populus tremula x Populus tremuloides
ORGANISM Populus tremula x Populus tremuloides
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Malpighiales; Salicaceae; Saliceae; Populus.
1 (bases 1 to 116)
AUTHORS Hertzberg, M., Aspeborg, H., Erlandsson, R., Bjorkbacka, H.,
Hiltunen, T., Karlsson, J., Teeri, T., Gustafsson, P., Bahlara, R.,
Jansson, S., Nilsson, O., Sundberg, B., Nilsson, P., Uhlen, M.,
Sandberg, G. and Lundberg, J.
Gene expression in Populus
Unpublished (2001)
Contact: Erlandsson R
Department of Biotechnology
Royal Institute of Technology
Teknikringen 30, Stockholm S-10044, Sweden
Tel: 46 8 790 8287
Fax: 46 8 245452
Email: rikeri@biochem.kth.se.

FEATURES
Location/Qualifiers
1..116
/organism="Populus tremula x Populus tremuloides"
/mol_type="mRNA"
/db_xref="taxon:47664"
/clone_lib="Populus cambium cDNA library"
/note="Organ: cambium"

ORIGIN


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Query Match      100.0%; Score 11; DB 4; Length 116;
Best Local Similarity 100.0%; Pred. No. 1.7e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CTTTGGCACTA 11
      |||||
Db      32 CTTTGGCACTA 42

RESULT 12
LOCUS      BF901301/c
DEFINITION      IL2-MT0179-081200-288-B12_1 MT0179 Homo sapiens cDNA, mRNA
ACCESSION      BF901301
VERSION      BF901301.1 GI:12292760
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
REFERENCE      1 (bases 1 to 120)
AUTHORS      Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
      Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
      Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V.,
      O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F.F., de Souza, S.J. and
      Simpson, A.J.
TITLE      Shotgun sequencing of the human transcriptome with ORF expressed
      sequence tags
JOURNAL      Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE      20202663
PUBMED      10737800
COMMENT      Contact: Simpson A.J.G.
      Laboratory of Cancer Genetics
      Ludwig Institute for Cancer Research
      Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
      Brazil
      Tel: +55-11-2704922
      Fax: +55-11-2707001
      Email: asimpson@ludwig.org.br
      This sequence was derived from the FAPESP/LICR Human Cancer Genome
      Project. This entry can be seen in the following URL
      (http://www.ludwig.org.br/scripts/gethtml2.pl?c1=IL2&t2=IL2-MT0179-081200-288-B12.1&t3=2000-12-08&t4=1)
      Seq primer: puc 18 forward
      High quality sequence stop: 116.
FEATURES      source
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      /organism="Homo sapiens"
      /mol_type="mRNA"
      /db_xref="taxon:9606"
      /dev_stage="Adult"
      /clone_lib="MT0179"
      /note="Organ: marrow; Vector: puc18; Site 1: SmaI; Site 2:
      SmaI; A mini-library was made by cloning products derived
      from ORESTES PCR (U.S. Letters Patent application No.
      196,716 - Ludwig Institute for Cancer Research) profiles
      into the puc 18 vector. Reverse transcription of tissue
      mRNA and cDNA amplification were performed under low
      stringency conditions."
ORIGIN
Query Match      100.0%; Score 11; DB 2; Length 120;
Best Local Similarity 100.0%; Pred. No. 1.7e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CTTTGGCACTA 11
      |||||
Db      19 CTTTGGCACTA 9

Query Match      100.0%; Score 11; DB 2; Length 120;
Best Local Similarity 100.0%; Pred. No. 1.7e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CTTTGGCACTA 11
      |||||
Db      19 CTTTGGCACTA 9

RESULT 13
LOCUS      AW551508
DEFINITION      L0079H06-3 NIA Mouse E12.5 Female Mesonephros and Gonads cDNA
ACCESSION      AW551508
VERSION      AW551508.2 GI:31566650
KEYWORDS      EST.
SOURCE      Mus musculus (house mouse)
ORGANISM      Mus musculus
REFERENCE      1 (bases 1 to 120)
AUTHORS      Tanaka, T.S., Jaradat, S.A., Lim, M.K., Kargul, G.J., Wang, X.,
      Grahovac, M.J., Pantano, S., Sano, Y., Piao, Y., Nagatsuma, R., Doi, H.,
      Wood, W.H. III, Becker, K.G. and Ko, M.S.H.
TITLE      Genome-wide expression profiling of mid-gestation placenta and
      embryo using a 15,000 mouse developmental cDNA microarray
JOURNAL      Proc. Natl. Acad. Sci. U.S.A. 97 (16), 9127-9132 (2000)
MEDLINE      20381348
PUBMED      10922068
COMMENT      On Mar 7, 2000 this sequence version replaced gi:7196936.
      Contact: George J. Kargul
      Laboratory of Genetics
      National Institute on Aging/National Institutes of Health
      333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
      Email: cdna@gsun.grc.nia.nih.gov
      Plate: L0079 row: H column: 06
      Seq primer: -21M13 Forward
      High quality sequence stop: 120
      POLYA=Yes.
FEATURES      Location/Qualifiers
      1..120
      /organism="Mus musculus"
      /mol_type="mRNA"
      /strain="C57BL/6J"
      /db_xref="niabst:L0079H06-3"
      /db_xref="taxon:10090"
      /clone="L0079H06"
      /sex="female"
      /dev_stage="12.5dpc"
      /lab_host="DH10B"
      /clone_lib="NIA Mouse E12.5 Female Mesonephros and Gonads
      cDNA Library"
      /note="Vector: pSPORT1 (Gibco/BRL Life Technology);
      Site 1: SalI; Site 2: NotI; Total RNAs were extracted from
      2 Mesonephros. The double-stranded cDNA was synthesized
      by Gibco's kit with an Oligo(dT) primer [NotI
      primer-adaptor from Gibco/BRL]
      [5'-PGACTAGTCTAGATCGAGCGCGCCCTTTTCTTTT-3'] from
      3.42ug of total RNA. The double-stranded cDNAs were
      treated with T4 DNA polymerase and purified by
      ethanol-precipitation. The cDNAs were ligated to
      lone-linker L1-Sal3 (include SalI sequence). The cDNAs
      were purified by phenol/chloroform and separated from
      free linkers by Centricon 100. Then, cDNAs were amplified
      by long-range high fidelity PCR using Takara's Ex Taq
      polymerase. Then, the cDNAs were purified by
      phenol/chloroform and by Centricon 100. The cDNAs were
      digested with SalI and NotI enzymes. Then, the cDNAs were
      size selected by Gibco's Size Fractionation Column. The
      cDNAs were cloned into SalI/NotI site of pSPORT1 plasmid
      vector. The DH10B E. coli host was transformed with the
      ligation mixture by chemical method. The library was
      constructed by Xiaohong Wang."
ORIGIN
Query Match      100.0%; Score 11; DB 2; Length 120;
Best Local Similarity 100.0%; Pred. No. 1.7e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CTTTGGCACTA 11
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```

```

Db          45 CTTTGGCACTA 55

RESULT 14
LOCUS      CK105615
DEFINITION UA25DPA07.5pR Populus dormant cambium cDNA library Populus tremula
            cDNA clone UA25DPA07 5', mRNA sequence.
ACCESSION  CK105615
VERSION     CK105615.1 GI:38589940
KEYWORDS   EST.
SOURCE     Populus tremula
ORGANISM   Populus tremula
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosids; eurosids I; Malpighiales; Salicaceae; Populus.
REFERENCE  1 (bases 1 to 120)
AUTHORS    Sterky,F., Bhalarao,R.R., Unneberg,P., Segerman,B., Nilsson,P.,
            Brunner,A.M., Campaa,L., Jonsson-Lindvall,J., Tandre,K.,
            Strauss,S.H., Sundberg,B., Gustafsson,P., Uhlen,M., Bhalarao,R.P.,
            Nilsson,O., Sandberg,G., Karlsson,J., Lundberg,J. and Jansson,S.
            A Populus EST resource for functional genomics
            Other ESTs: UA25DPA07
            Unpublished (2003)
TITLE      Contact: Bo Segerman
JOURNAL    Umea Plant Science Center, Department of Plant Physiology
COMMENT    Umea University
            901 87 Umea, Sweden
            Tel: +46 90 786 5279
            Fax: +46 90 786 6676
            Email: bo.segerman@plantphys.umu.se.

FEATURES   source
            1..120
            /organism="Populus tremula"
            /mol_type="mRNA"
            /db_xref="taxon:113636"
            /clone="UA25DPA07"
            /tissue_type="Dormant cambium"
            /clone_lib="Populus dormant cambium cDNA library"

ORIGIN
Query Match      100.0%; Score 11; DB 7; Length 120;
Best Local Similarity 100.0%; Pred. No. 1.7e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CTTTGGCACTA 11
        |||||
        58 CTTTGGCACTA 68

Db

RESULT 15
BF352764
LOCUS      BF352764
DEFINITION IL3-HT0619-050700-199-D07 HT0619 Homo sapiens cDNA, mRNA sequence.
ACCESSION  BF352764
VERSION     BF352764.1 GI:113111838
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 121)
AUTHORS    Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
            O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
            Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
TITLE      Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
JOURNAL    20202663
MEDLINE    10737800
PUBMED

CONTACT: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL3&tl2=IL3-HT0619-
050700-199-D07&tl3=2000-07-05&tl4=1)
Seq primer: puc 18 forward
High quality sequence start: 15
High quality sequence stop: 121.
Location/Qualifiers
1..121
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="HT0619"
/notes="Organ: head neck; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

ORIGIN
Query Match      100.0%; Score 11; DB 2; Length 121;
Best Local Similarity 100.0%; Pred. No. 1.7e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CTTTGGCACTA 11
        |||||
        18 CTTTGGCACTA 28

Db

RESULT 16
A2759838
LOCUS      A2759838
DEFINITION 1M0552P23R Mouse 10kb plasmid UUGCM library Mus musculus genomic
            clone UUGC1M0552P23 R, genomic survey sequence.
ACCESSION  A2759838
VERSION     A2759838.1 GI:12867034
KEYWORDS   GSS.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE  1 (bases 1 to 122)
AUTHORS    Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausen,A. and Wright,D., Weiss,R.
            Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
TITLE      Unpublished (2000)
JOURNAL    Contact: Robert B. Weiss
COMMENT    University of Utah
            Genome Center
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112 USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0552 row: P column: 23
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 122.

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FEATURES
source

Location/Qualifiers
1. .129
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0552P23"
/sex="Male"
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 100.0%; Score 11; DB 8; Length 122;
Best Local Similarity 100.0%; Pred. No. 1.7e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTGGCACTA 11
|||||
Db 14 CTTTGGCACTA 24

RESULT 17

CA345114/c
LOCUS 127 bp mRNA linear EST 05-NOV-2002
DEFINITION 675650 NCCOWA 1RT Oncorhynchus mykiss cDNA clone 1RT85B06_D_A03 5', mRNA sequence.
ACCESSION CA345114
VERSION CA345114.1 GI:24590285
KEYWORDS EST.
SOURCE Oncorhynchus mykiss (rainbow trout)
ORGANISM Oncorhynchus mykiss
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
1 (bases 1 to 127)
Koop, B., Gahr, S.A., Palti, Y., and Quackenbush, J.
Rexroad, C.E. 3rd, Lee, Y., Keele, J.W., Karamycheva, S., Brown, G., et al.
Sequence analysis of a rainbow trout cDNA library and creation of a gene index
Cytogenet. Genome Res. 102 (1-4), 347-354 (2003)
Contact: Rexroad CE
USDA, ARS, National Center for Cool and Cold Water Aquaculture
11876 Leetown Road, Kearneysville, WV 25430, USA
Tel: 304 724 8340 x2129
Fax: 304 725 0351
Email: crexroad@nccowa.ars.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and trimmed with the aid of the trim_alt option. Vector identified by cross match v0.990329.
Seq primer: ACGGATACAAATTCACACAGGA.

FEATURES

source
1. .129
/organism="Oncorhynchus mykiss"
/mol_type="mRNA"

FEATURES
source

/db_xref="taxon:8022"
/clone="1RT85B06_D_A03"
/tissue type="pooled"
/lab host="DH10B"
/clone lib="NCCOWA 1RT"
/note="Vector: PCMV SPORT6; Site 1: NotI; Site 2: SalI; library made from pooled tissue from brain, gill, liver, spleen, muscle, and kidney."

ORIGIN

Query Match 100.0%; Score 11; DB 6; Length 127;
Best Local Similarity 100.0%; Pred. No. 1.7e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTGGCACTA 11
|||||
Db 39 CTTTGGCACTA 29

RESULT 18

CB352552/c
LOCUS 129 bp mRNA linear EST 10-NOV-2003
DEFINITION ZF001-P00003-DPB-F2-D.H03 GISZF001 Danio rerio cDNA clone IMAGE:6892759 5' similar to fd56h03.y1 Zebrafish Washu WPIWG EST
Danio rerio cDNA clone IMAGE:3733781 5' similar to SW:ACDM_RAI
P08503 ACYL-COA DEHYDROGENASE, MEDIUM-CHAIN SPECIFIC PRECURSOR, mRNA sequence.
ACCESSION CB352552
VERSION CB352552.1 GI:28989293
KEYWORDS EST.
SOURCE Danio rerio (zebrafish)

ORIGIN

Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 129)
Mathavan, S., Wei, C., Thoreau, H., Chia, J.M. and Ruan, Y.
Genome Institute of Singapore, Zebrafish EST Collection
Unpublished (2003)
Contact: Ruan Y
Cloning and Sequencing
Genome Institute of Singapore
60 Biopolis Street, #02-01, Genome, Singapore 138672
Tel: +65 6478 8073
Fax: +65 6478 9059
Email: ruanyj@gis.a-star.edu.sg
GIS Clone ID: ZF001-P00003-PP_P06
PCR Primers
FORWARD: M13
BACKWARD: M13
Plate: ZF001-P00003-DPB-F2-D
Seq primer: CCGCATACCTGTATAGCA
High quality sequence stop: 129.
Location/Qualifiers
1. .129
/organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
/clone="IMAGE:6892759"
/tissue type="Embryo"
/dev stages="7 Different embryonic stages (From just fertilized Embryos to 72 hours just hatched baby fish)"
/lab host="DH10B"
/clone lib="GISZF001"
/note="Vector: pDNR-LIB; Site 1: Sfi A (GGCCATTAGGCC); Site 2: Sfi B (GGCCGCTCGGCC); Priming method: Sfi-(drr)30
Primed; Priming sequence: 5'ATTCTAGA GGCCGAGCGGCC
GACATG(T)30VN; Directionally cloned, 5' cloning site:
Sfi A site GGCCATTAGGCC; 5' linker/adaptor sequence:
5'AGCAGTGTATCAACGACAGTGGCC; 3' cloning site: Sfi B
site GGCCGCTCGGCC; 3' linker/adaptor sequence: same
as the priming sequence; Average insert size: 2kb; For
PCR insert analysis: Use M13 Forward and reverse primers;

FEATURES

source

1. .129
/organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
/clone="IMAGE:6892759"
/tissue type="Embryo"
/dev stages="7 Different embryonic stages (From just fertilized Embryos to 72 hours just hatched baby fish)"
/lab host="DH10B"
/clone lib="GISZF001"
/note="Vector: pDNR-LIB; Site 1: Sfi A (GGCCATTAGGCC); Site 2: Sfi B (GGCCGCTCGGCC); Priming method: Sfi-(drr)30
Primed; Priming sequence: 5'ATTCTAGA GGCCGAGCGGCC
GACATG(T)30VN; Directionally cloned, 5' cloning site:
Sfi A site GGCCATTAGGCC; 5' linker/adaptor sequence:
5'AGCAGTGTATCAACGACAGTGGCC; 3' cloning site: Sfi B
site GGCCGCTCGGCC; 3' linker/adaptor sequence: same
as the priming sequence; Average insert size: 2kb; For
PCR insert analysis: Use M13 Forward and reverse primers;

Library Amplified Recombinants (inserts): 98* ; Library complexity: 5x10⁶ ; Full-length construction (method): SMART, a Clontech method ; Library constructed by: S. Mathavan, Chia-Lin Wei, and Yijun Ruan Genome Institute of Singapore"

ORIGIN

Query Match 100.0%; Score 11; DB 6; Length 129;
Best Local Similarity 100.0%; Pred. No. 1.7e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11
|||||
Db 95 CTTTGGCACTA 85

RESULT 19

CG918048/c
LOCUS CG918048 130 bp DNA linear GSS 12-DEC-2003
DEFINITION CH240_137A21.TJ CHORI-240 Bos taurus genomic clone CH240_137A21,
genomic survey sequence.

ACCESSION CG918048
VERSION CG918048
KEYWORDS GSS.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus

REFERENCE

1 (bases 1 to 130)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.

AUTHORS

Costa J.N., Mota M. and Caetano A.R.
Brazil's Contribution to End-Sequencing the Bovine BAC Library
CHORI-240

JOURNAL

Unpublished (2003)
Other_GSSs: CH240_137A21.TV
Contact: Caetano AR
Department of Biotechnology
Embrapa Recursos Geneticos e Biotecnologia
Parque Estacao Biologicas, Final Av. W/5 Norte, Brasilia-DF C.P.
02372, 70770-900 Brasil
Tel: 55 61 448 4778
Fax: 55 61 340 3658
Email: acetano@cenargen.embrapa.br

Clones are derived from the bovine BAC library CHORI-240
(<http://www.chori.org/bacpac/bovine240.htm>).

Bases shown have Phred quality value equal to or higher than 20.
Bases with quality value below 20 were masked with 'N'.
For BAC library availability, please contact Pieter de Jong
(pdejong@mail.cho.org).

Clones may be purchased from BACPAC Resources
(<http://www.chori.org/bacpac/ordering/information.htm>).
This work was undertaken as part of the International Bovine BAC
Mapping Consortium (IBBMC) by Embrapa Recursos Geneticos e
Biotecnologia with financing from Conselho Nacional de
Desenvolvimento Cientifico e Tecnologico (CNPq), Brazil
Plate: 137 row: A column: 21
Seq primer: SP6
Class: BAC ends

FEATURES

High quality sequence stop: 130.

source

Location/Qualifiers
1..130
/organism="Bos taurus"
/mol_type="genomic DNA"
/strain="breed: Hereford"
/db_xref="taxon:9913"
/clone="CH240_137A21"
/sex="Male"
/cell_type="Blood"
/clone_lib="CHORI-240"
/note="Vector: pTARBAC1.3; Site 1: MboI; Site 2: MhoI;
Hereford bull LI Domino 99375; CHORI-240 Bovine BAC
library (Male) produced by Pieter de Jong"

ORIGIN

Query Match 100.0%; Score 11; DB 9; Length 130;
Best Local Similarity 100.0%; Pred. No. 1.7e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11
|||||
Db 113 CTTTGGCACTA 103

RESULT 20

AA508728/c
LOCUS AA508728 138 bp mRNA linear EST 18-AUG-1997
DEFINITION nh88d08.sl NCI_CGAP_Pr8 Homo sapiens cDNA clone IMAGE:957519, mRNA
sequence.

ACCESSION AA508728
VERSION AA508728.1 GI:2246231
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

1 (bases 1 to 138)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David G. Bostwick, M.D., Rodrigo F. Chuasqui,
M.D., Michael R. Emmert-Buck, M.D., Ph.D.

CNA Library Preparation: David B. Krizman, Ph.D.
CNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone Distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 346 Std Error: 0.00
Seq primer: -40ml3 fwd.ET from Amersham.
Location/Qualifiers
1..138
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:957519"
/sex="male"
/tissue_type="prostate"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Pr8"
/note="Vector: PAMP10; mRNA made from invasive prostate
tumor, cDNA made by oligo-dT priming. Non-directionally
cloned. Size-selected on agarose gel, average insert
size 600 bp."

FEATURES

Location/Qualifiers
1..138
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:957519"
/sex="male"
/tissue_type="prostate"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Pr8"
/note="Vector: PAMP10; mRNA made from invasive prostate
tumor, cDNA made by oligo-dT priming. Non-directionally
cloned. Size-selected on agarose gel, average insert
size 600 bp."

ORIGIN

Query Match 100.0%; Score 11; DB 1; Length 138;
Best Local Similarity 100.0%; Pred. No. 1.7e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11
|||||
Db 18 CTTTGGCACTA 8

RESULT 21

BF545856
LOCUS BF545856 138 bp mRNA linear EST 11-DEC-2000
DEFINITION UI-R-BT0-qe-c-01-0-UI-r1 UI-R-BT0 Rattus norvegicus cDNA clone
BF545856
ACCESSION BF545856
VERSION BF545856.1 GI:11636963
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)

ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE 1 (bases 1 to 138)
AUTHORS Bonaldo,M.F., Lemmon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
discovery

JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 9704477
PUBMED 889548

COMMENT Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
cDNA Library Preparation: M.B. Soares Lab Clone distribution:
clones will be available through Research Genetics (www.regen.com)
This clone is also available through the I.M.A.G.E. Consortium at
LLNL (info@image.llnl.gov). IMAGE ID= 1788637
Seq primer: M13 Forward.

FEATURES
Location/Qualifiers
1..138
/organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-B70-qe-c-01-0-UI"
/dev_stage="adult"
/lab_host="DHI0B (Life Technologies)"
/clone_lib="UI-R-B70"
/note="Vector: pTT3D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; This library
(UI-R-B70) consists of a mixture of individually tagged
normalized libraries constructed from rat hippocampus,
thalamus, mid-brain, medulla, corpus striatum, cerebral
cortex and testis. The tag used to identify the source
tissue is a string of 3-6 nucleotides present between the
Not I site and the oligo-dT track which allows
identification of the library of origin of a clone within
the mixture. This library was then subtracted using a
driver consisting of a mixture of all clones from UI-R-A0,
UI-R-A1, UI-R-E0, UI-R-E1, UI-R-C0, UI-R-C1, UI-R-C2 and
UI-R-C2p."

ORIGIN
Query Match 100.0%; Score 11; DB 2; Length 138;
Best Local Similarity 100.0%; Pred. No. 1.7e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTGGCCTA 11
|||||
DB 127 CTTTGGCCTA 137

RESULT 22
BH055493/c
LOCUS BH055493 140 bp DNA linear GSS 18-JUL-2001
DEFINITION RPCI-24-278115.TJ RPCI-24 Mus musculus genomic clone
RPCI-24-278115, genomic survey sequence.

ACCESSION BH055493
VERSION BH055493.1 GI:14862399
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 140)
Zhaio,S., Nierman,W., Malek,J., Shatsman,S., Akinret,B., Levins,M.,
Tsegaye,G., Geer,K., Krol,M., Shvartsbeyn,A., Gebregeorgis,E.,
Russell,D., de Jong,P. and Fraser,C.M.

TITLE Mouse BAC End Sequences from Library RPCI-24
Unpublished (1999)
Other GSSs: RPCI-24-278115.TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-24. For BAC
library availability, please contact Pieter de Jong
(pdejong@mail.cho.org). Clones may be purchased from BACPAC
Resources (<http://www.tigr.org/bacpac/orderingframe.htm>). BAC end
plate: 278 row: I column: 15
Seq primer: SP6
Class: BAC ends.

FEATURES
Location/Qualifiers
1..140
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-24-278115"
/sex="Male"
/cell_type="Spleen/Brain"
/clone_lib="RPCI-24"
/note="Vector: pTARBAC1; Site 1: BamHI; Site 2: BamHI;
RPCI-24 Mouse BAC Library produced by Pieter de Jong. The
library was cloned in the pTARBAC1 cloning vector at the
BamHI sites using MboI partially digested male C57BL/6J
DNA."

ORIGIN
Query Match 100.0%; Score 11; DB 8; Length 140;
Best Local Similarity 100.0%; Pred. No. 1.7e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTGGCCTA 11
|||||
DB 93 CTTTGGCCTA 83

RESULT 23
AI965679/c
LOCUS AI965679 141 bp mRNA linear EST 12-JUL-2004
DEFINITION sc76h06.y1 Gm-cl018 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
Gm-cl018-852 5', mRNA sequence.

ACCESSION AI965679
VERSION AI965679.1 GI:5760388
KEYWORDS EST.

SOURCE Glycine max (soybean)
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1 (bases 1 to 141)
Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V.,
Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J.,
Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M.,
Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N.,
Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,
McCann,R., Waterston,R. and Wilson,R.
Public Soybean EST Project
Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810

TITLE Public Soybean EST Project
JOURNAL Unpublished (1999)
COMMENT Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810

Email: est@watson.wustl.edu
 When it has been determined, an EST from the other end of this clone is listed in the 'Other ESTs on clone' field. This clone is available through: Biogenetic Services, 801 32nd Ave. Brookings, SD 57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com)
 Insert length: 821 Std Error: 0.00
 High quality sequence stop: 119.

FEATURES

Location/Qualifiers
 1..141
 /organism="Glycine max"
 /mol_type="mRNA"
 /cultivar="Williams 82"
 /db_xref="taxon:3847"
 /clone="GENOME SYSTEMS CLONE ID: Gm-cl018-852"
 /tissue_type="leaves of greenhouse grown plants"
 /dev_stage="2-3 weeks old"
 /lab_host="DH10B (Gibco BRL)"
 /clone_lib="Gm-cl018"
 /note="Vector: pBluescript II XE; Site 1: EcoRI; Site 2: XhoI; This cDNA library was constructed from mRNA isolated from 2-3 week old greenhouse grown plants. The cDNA library was prepared using the Stratagene pBluescript II XE library construction kit. Complementary DNA was synthesized from mRNA using a primer consisting of a poly (dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (Gibco BRL). This library was constructed by Dr. Randy Shoemaker and Dr. John Expelding."

ORIGIN

Query Match 100.0%; Score 11; DB 1; Length 141;
 Best Local Similarity 100.0%; Pred. No. 1.7e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CTTTGGCACTA 11
 |||||
 Db 120 CTTTGGCACTA 110

RESULT 24

AA717598/c
 LOCUS
 DEFINITION
 vp94a07.r1 Stratagene mouse diaphragm (#937303) Mus musculus cDNA clone IMAGE:1092372 5' similar to gb:M12866 Mouse skeletal muscle actin mRNA, complete cds (MOUSE); mRNA sequence.

ACCESSION

AA717598

VERSION

AA717598.1 GI:2729872

KEYWORDS

EST.

SOURCE

Mus musculus (house mouse)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 146)
 Marra M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.

TITLE

The WashU-HMI Mouse EST Project

JOURNAL

Unpublished (1996)

COMMENT

Contact: Marra M/Mouse EST Project
 WashU-HMI Mouse EST Project
 Washington University School of MedicineP
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810

Email: mouseest@watson.wustl.edu
 This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:598604

Trace considered overall poor quality
 Seq primer: -28ml3 revl ET from Amersham
 High quality sequence stop: 1.

FEATURES

source

Location/Qualifiers
 1..146
 /organism="Mus musculus"
 /mol_type="mRNA"
 /db_xref="taxon:10090"
 /clone="IMAGE:1092372"
 /tissue_type="diaphragm"
 /dev_stage="adult"
 /lab_host="SOLR (kanamycin resistant)"
 /clone_lib="Stratagene mouse diaphragm (#937303)"
 /note="Organ: diaphragm; Vector: pBluescript SK-; Site 1: EcoRI; Site 2: XhoI; Cloned unidirectionally from mRNA prepared from diaphragm muscle. Primer: Oligo dT. Average insert size: 1.5 kb. Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTGGCACGAG 3' -3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTT 3"

ORIGIN

Query Match 100.0%; Score 11; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 1.7e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CTTTGGCACTA 11
 |||||
 Db 109 CTTTGGCACTA 99

RESULT 25

CCS16068/c

LOCUS

CH240_361F11.TARBAC13P2 CHOR1-240 Bos taurus genomic clone
 CH240_361F11, genomic survey sequence.

ACCESSION

CCS16068

VERSION

CCS16068.1 GI:31834356

KEYWORDS

GSS.

SOURCE

Bos taurus (cow)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
 1 (bases 1 to 147)
 Holt, R., Stott, J., Yang, G., Barber, S., Smailus, D., Prabhu, A., L., Teal, M., Cloutier, A., Lee, D., Girn, N., Olson, T., Mayo, M., Butterfield, Y., Kirkpatrick, R., Liu, J., Guin, R., Chan, A., Chiu, R., Mathewson, C., Wye, N., Masson, A., Brown-John, M., Jones, S., Schein, J., Marra, M., de Jong, P., McWilliam, S., Barris, W., Dalrymple, B. P. and Tellam, R.

REFERENCE

AUTHORS

Bovine BAC End Sequences from Library CHORI-240, PLATES 294 to 398

TITLE

Unpublished (2003)

JOURNAL

Other GSSs: CH240_361F11.T7

COMMENT

Contact: Rob Holt
 The British Columbia Cancer Agency Genome Science Centre
 600 W. 10th Ave, Vancouver, British Columbia, Canada V5Z 4E6
 Tel: 604-877-6085
 Fax: 604-877-6276
 Email: rholt@bccsc.ca
 Clones are derived from the bovine BAC library CHORI-240
 (http://www.chori.org/bacpac/bovine240.htm). For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources
 (http://www.chori.org/bacpac/ordering/information.htm). This work was undertaken as part of the International Bovine BAC Mapping Consortium (IBBMC) by CSIRO Livestock Industries, Australia and the British Columbia Genome Sciences Centre, Canada.
 Plate: 361 row: F column: 11
 Seq primer: SP6
 Class: BAC ends.

FEATURES

Location/Qualifiers

source

1..147
 /organism="Bos taurus"
 /mol_type="genomic DNA"
 /strain="breed: Hereford"
 /db_xref="taxon:9913"
 /clone="CH240_361F11"
 /sex="Male"
 /cell_type="Blood"
 /clone_lib="CHORI-240"
 /note="Vector: pTARBAC1.3; Site 1: MboI; Site 2: MboI;
 Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC
 library (Male) produced by Pieter de Jong"

ORIGIN

Query Match 100.0%; Score 11; DB 9; Length 147;
 Best Local Similarity 100.0%; Pred. No. 1.7e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11
 |||||
 Db 41 CTTTGGCACTA 31

RESULT 26

BM113996
 LOCUS
 DEFINITION EST561532 potato roots Solanum tuberosum cDNA clone cPRO2013 5',
 end, mRNA sequence.

ACCESSION BM113996
 VERSION BM113996.1 GI:17077044
 KEYWORDS
 SOURCE

ORGANISM Solanum tuberosum (potato)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; lamids; Solanales; Solanaceae; Solanum.

REFERENCE

AUTHORS
 1 (bases 1 to 149)
 van der Hoeven, R., Sun, H., Karamycheva, S.A., Tsai, J., Van Aken, S.,
 Tanksley, S. and Baker, B.

TITLE

Generation of ESTs from potato roots

JOURNAL

Unpublished (2001)

COMMENT

Contact: Robin Buell
 The Institute for Genomic Research
 9712 Medical Center Dr, Rockville, MD 20850, USA
 Email: potato-array@tigr.org
 This clone can be obtained from the University of Arizona Genomics
 Institute. Orders can be made through URL:
 http://genome.arizona.edu/orders/
 Seq primer: T3.

FEATURES

source

1..149
 /organism="Solanum tuberosum"
 /mol_type="mRNA"
 /cultivar="Kennebec"
 /db_xref="taxon:4113"
 /clone="cPRO2013"
 /tissue_type="roots"
 /dev_stages="in vitro grown stem cuttings"
 /lab_host="SOLR"

/clone_lib="potato roots"
 /note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2:
 XhoI; supplier: Cornell University, Tanksley lab;
 sequencing; The Institute for Genomic Research. Roots were
 isolated from in vitro grown stem cuttings on CM medium.
 Roots were isolated two weeks after placing the stem
 cuttings from in vitro grown plants on medium."

ORIGIN

Query Match 100.0%; Score 11; DB 4; Length 149;
 Best Local Similarity 100.0%; Pred. No. 1.7e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11
 |||||
 Db 17 CTTTGGCACTA 27

RESULT 27

BM405670
 LOCUS
 DEFINITION EST579997 potato roots Solanum tuberosum cDNA clone cPRO24J20 5',
 end, mRNA sequence.

ACCESSION BM405670
 VERSION BM405670.1 GI:18257257
 KEYWORDS
 SOURCE

ORGANISM Solanum tuberosum (potato)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; lamids; Solanales; Solanaceae; Solanum.

REFERENCE

AUTHORS
 1 (bases 1 to 149)
 van der Hoeven, R., Sun, H., Karamycheva, S.A., Tsai, J., Van Aken, S.,
 Tanksley, S. and Baker, B.

TITLE

Generation of ESTs from potato roots

JOURNAL

Unpublished (2001)

COMMENT

Contact: Robin Buell
 The Institute for Genomic Research
 9712 Medical Center Dr, Rockville, MD 20850, USA
 Email: potato-array@tigr.org
 This clone can be obtained from the University of Arizona Genomics
 Institute. Orders can be made through URL:
 http://genome.arizona.edu/orders/
 Seq primer: T3.

FEATURES

source

1..149
 /organism="Solanum tuberosum"
 /mol_type="mRNA"
 /cultivar="Kennebec"
 /db_xref="taxon:4113"
 /clone="cPRO24J20"
 /tissue_type="roots"
 /dev_stages="in vitro grown stem cuttings"
 /lab_host="SOLR"

/clone_lib="potato roots"

/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2:
 XhoI; supplier: Cornell University, Tanksley lab;
 sequencing; The Institute for Genomic Research. Roots were
 isolated from in vitro grown stem cuttings on CM medium.
 Roots were isolated two weeks after placing the stem
 cuttings from in vitro grown plants on medium."

ORIGIN

Query Match 100.0%; Score 11; DB 4; Length 149;

Best Local Similarity 100.0%; Pred. No. 1.7e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11
 |||||
 Db 17 CTTTGGCACTA 27

RESULT 28

R57383/c
 LOCUS
 DEFINITION F2971 Petal heart Homo sapiens cDNA clone F2971 5' end, mRNA
 sequence.

ACCESSION R57383
 VERSION R57383.1 GI:827441
 KEYWORDS
 SOURCE

ORGANISM Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 150)


```

melanogaster cDNA clone EK297249 5, mRNA sequence.
CO331019
VERSION CO331019.1 GI:49391294
KEYWORDS EST.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephyrdoidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 155)
AUTHORS Kopczynski,C., Platt,D., Campbell,J., Muzong,C., Laufer,A.,
Peterson,E. and Swimmer,C.
TITLE Exelixis Flytag EST Project CK01 Library
JOURNAL Unpublished (2004)
COMMENT Contact: Stapleton, M.
BDGP
Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
Based upon one or more reads of this clone where vector sequence
was present at both ends, this clone has been determined to contain
contain a cDNA insert on the order of 600-1000 bases.
Plate: EK.2972 row: E column: 1
High quality sequence stop: 154.
Location/Qualifiers
1..155
/organism="Drosophila melanogaster"
/mol_type="mRNA"
/db_xref="taxon:7227"
/clone="EK297249"
/note="Organ: mixed stage embryos, imaginal disks, and
adult heads; Vector: pCDNA-SK+; Site_1: NotI; Site_2:
XhoI; Random primed, normalized library from mixed stage
embryos, imaginal disks, and adult heads."

ORIGIN
Query Match 100.0%; Score 11; DB 7; Length 155;
Best Local Similarity 100.0%; Pred. No. 1.7e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTGGCACTA 11
|||||
Db 69 CTTTGGCACTA 79

RESULT 32
CD054495
LOCUS HO01E06r HO Hordeum vulgare cDNA clone HO01E06 5-PRIME, mRNA
DEFINITION CD054495
ACCESSION CD054495
VERSION CD054495.1 GI:30595488
KEYWORDS EST.
SOURCE Hordeum vulgare
ORGANISM Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 156)
AUTHORS Zierold,U. and Schweizer,P.
TITLE Barley ESTs from pathogen-attacked leaf epidermis
JOURNAL Unpublished (2003)
COMMENT Contact: Patrick Schweizer
Transcriptome Analysis, Cytogenetics Department
Institute of Plant Genetics and Crop Plant Research (IPK)
Corrensstr. 3, D-06466 Gatersleben, Germany
Tel: 0049 (0)39482-5660
Fax: 0049 (0)39482-5595
Email: schweiz@ipk-gatersleben.de
Insert Length: 156 Std Error: 0.00
Plate: 1 row: E column: 6

```

```

Seq primer: M13rev.
Location/Qualifiers
1..156
/organism="Hordeum vulgare"
/mol_type="mRNA"
/cultivar="Ingrid BC mlo-5"
/db_xref="GABI:703789"
/db_xref="taxon:4513"
/clone="HO01E06"
/tissue_type="leaf epidermis, 6 h and 24 h post
inoculation with Blumeria graminis"
/dev_stage="7 d after germination"
/lab_host="XL10-Gold"
/clone_lib="HO"
/note="Vector: pBluescript SK+; Site_1: EcoRI (5'-end of
cDNA); Site_2: XhoI (3'-end of cDNA); Approximately 5 % of
the clones correspond to cDNA from the fungi B. graminis
hordei and tritici, respectively. Due to a cloning
artefact caused by the kit, in most cases the EcoRI site
is NOT present, as well as the EcoRI adapter used for
cloning. To excise the insert, restriction sites upstream
EcoRI should be used (e.g. BamHI, SalI, PstI). NOTE: Also
due to the cloning system used Blue/white selection for
recombinants is not 100% reliable. Average insert size is
1.2 kb"

ORIGIN
Query Match 100.0%; Score 11; DB 6; Length 156;
Best Local Similarity 100.0%; Pred. No. 1.7e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTGGCACTA 11
|||||
Db 103 CTTTGGCACTA 113

RESULT 33
BZ654414/c
LOCUS OGAMR91TM ZM_0.7_1.5_KB Zea mays genomic clone ZMMBma0096014,
DEFINITION BZ654414
ACCESSION BZ654414
VERSION BZ654414.1 GI:28123674
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 156)
AUTHORS Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
TITLE Consortium for Maize Genomics
JOURNAL Other GSSs: OGAMR91TC
COMMENT Unpublished (2002)
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TR
Class: sheared ends.
Location/Qualifiers
1..156
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMMBma0096014"
/clone_lib="ZM 0.7_1.5_KB"
/note="Vector: pBGSK-; Site_1: HincII; 0.7-1.5 kb

```

```

methylation filtered genomic DNA library"

ORIGIN
  Query Match      100.0%; Score 11; DB 8; Length 156;
  Best Local Similarity 100.0%; Pred. No. 1.7e+04;
  Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11
   |||||
Db 71 CTTTGGCACTA 61

RESULT 34
AV013351
LOCUS
DEFINITION AV013351 Mus musculus 18-day embryo C57BL/6J Mus musculus cDNA
clone 1110046M18, mRNA sequence.
ACCESSION AV013351
VERSION AV013351.1 GI:4790343
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
  1 (bases 1 to 159)
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS Carninci, P., Shibata, K., Ozawa, Y., Konno, H., Itoh, M., Aizawa, K.,
Akahira, S., Akiyama, J., Fukuda, S., Fukunishi, Y., Funayama, T.,
Hara, A., Hayatsu, N., Hori, F., Ishikawa, T., Itoh, M., Izawa, M.,
Kawai, J., Kikuchi, N., Kojima, Y., Matsuyama, T., Niitsuma, H., Oda, H.,
Owa, C., Sato, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y.,
Sugahara, Y., Suzuki, H., Suzuki, H., Tateno, M., Tomaru, Y.,
Tomimaga, N., Watanabe, S., Yagame, M., Yamamura, T., Yokota, T.,
Yoshino, M., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.

TITLE RIKEN Mouse ESTs
JOURNAL Unpublished (1999)
COMMENT Contact: Chie Owa
Genome Science Laboratory
RIKEN
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-9145
Fax: 81-298-36-9098
Email: genome-res@rtc.riken.go.jp
Thermotabilization and thermoactivation of thermostable enzymes by
trehalose and its application for the synthesis of full length cDNA
(Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA
polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for
further details.

FEATURES
  source
    Location/Qualifiers
      1..159
        /organism="Mus musculus"
        /mol_type="mRNA"
        /strain="C57BL/6J"
        /db_xref="taxon:10090"
        /clone="1110046M18"
        /sex="mixed"
        /dev_stage="18-day embryo"
        /clone_lib="Mus musculus 18-day embryo C57BL/6J"

ORIGIN
  Query Match      100.0%; Score 11; DB 1; Length 159;
  Best Local Similarity 100.0%; Pred. No. 1.7e+04;
  Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11
   |||||
Db 2 CTTTGGCACTA 12

RESULT 35
BP671035/C
LOCUS
DEFINITION BP671035 Arabidopsis thaliana cDNA clone RAFL21-37-K01 3',
mRNA sequence.
ACCESSION BP671035
VERSION BP671035.1 GI:49322538
KEYWORDS EST.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana

REFERENCE
  1 (bases 1 to 162)
  Seki, M., Narusaka, M., Kamiya, A., Ishida, J., Satou, M., Sakurai, T.,
  Nakajima, M., Enju, A., Akiyama, K., Oono, Y., Muramatsu, M.,
  Hayashizaki, Y., Kawai, J., Carninci, P., Itoh, M., Ishii, Y.,
  Arakawa, T., Shibata, K., Shinagawa, A. and Shinozaki, K.
  Functional annotation of a full-length Arabidopsis cDNA collection
  Science 296 (5565), 141-145 (2002)

JOURNAL Science 296
MEDLINE 21932900
PUBMED 11910074
COMMENT Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
Fax: 81-298-36-9060
Email: msek@rtc.riken.go.jp
reversed clone; Please visit our web site
(http://pfweb.gsc.riken.go.jp/) for further details.

FEATURES
  source
    Location/Qualifiers
      1..162
        /organism="Arabidopsis thaliana"
        /mol_type="mRNA"
        /db_xref="taxon:3702"
        /clone="RAFL21-37-K01"
        /lab_host="DH10B"
        /clone_lib="RAFL21"
        /note="Site 1: BamHI; Site 2: SalI; Subtraction Library.
        The sequence was obtained from samples subjected to
        various stress and plant hormones-treated"

ORIGIN
  Query Match      100.0%; Score 11; DB 5; Length 162;
  Best Local Similarity 100.0%; Pred. No. 1.7e+04;
  Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11
   |||||
Db 136 CTTTGGCACTA 126

RESULT 36
BH390901
LOCUS
DEFINITION AG-ND-138122.TR ND-TAM Anopheles gambiae genomic clone
AG-ND-138122, genomic survey sequence.
ACCESSION BH390901
VERSION BH390901.1 GI:17337042
KEYWORDS GSS.
SOURCE Anopheles gambiae (African malaria mosquito)
ORGANISM Anopheles gambiae

REFERENCE
  1 (bases 1 to 162)
  Hong, Y.S., Hogan, J.R., Wang, X., Sarkar, A., Sim, C., Loftus, B.J.,
  Ren, C., Huff, E.R., Carlile, J.L., Black, K., Zhang, H.-B.,
  Gardner, M.J. and Collins, F.H.
  Construction of a BAC library and generation of BAC end
  sequence-tagged connectors for genome sequencing of the African
  malaria mosquito Anopheles gambiae
  Mol. Genet. Genomics 268 (6), 720-728 (2003)

JOURNAL Mol. Genet. Genomics 268
MEDLINE 22542063
PUBMED 12655398

```

COMMENT Other_GSSs: AG-ND-138L22.TF
 Contact: Brendan J Loftus
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0208
 Fax: 301 838 3543
 Email: bjloftus@tigr.org
 This clone is from an A. gambiae BAC library (ND-TAM) provided by
 P.H. Collins and sequenced by The Institute for Genomic Research
 (TIGR). The BAC library was generated from A. gambiae PEST strain
 DNA. All DNA was extracted from newly hatched first instar larvae
 to minimize the inclusion of DNA from microorganisms that inhabit
 the gut. The DNA is derived from mixed sexes of larvae. The BAC
 library was constructed at Texas A&M University BAC Center
 University, College Station, Texas 77843-2123, USA using a HindIII
 partial digest.
 Seq primer: M13 Rev
 Class: BAC ends.

FEATURES source
 Location/Qualifiers
 1..162
 /organism="Anopheles gambiae"
 /mol_type="genomic DNA"
 /strain="PEST"
 /db_xref="taxon:7165"
 /clone="AG-ND-138L22"
 /clone_lib="ND-TAM"
 /note="Vector: pECBAC1; Site_1: HindIII"

ORIGIN
 Query Match 100.0%; Score 11; DB 8; Length 162;
 Best Local Similarity 100.0%; Pred. No. 1.7e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11
 |||||
 Db 53 CTTTGGCACTA 63

RESULT 37
 BW485387 164 bp mRNA linear EST 11-JUN-2004
 LOCUS BW485387 Nori Satoh unpublished cDNA library, mature adult whole
 DEFINITION animal Ciona intestinalis cDNA clone cima050g08 5', mRNA sequence.
 ACCESSION BW485387
 VERSION BW485387.1 GI:48621251
 KEYWORDS EST.
 SOURCE Ciona intestinalis
 ORGANISM Ciona intestinalis
 Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
 Phlebobranchia; Cionidae; Ciona.
 1 (bases 1 to 164)
 Satou, Y., Shin-i, T., Kohara, Y. and Satoh, N.
 TITLE Expressed genes in Ciona intestinalis (2004)
 JOURNAL Unpublished (2004)
 COMMENT Contact: Nori Satoh
 Department of Zoology
 Kyoto University
 Sakyo-Ku, Kyoto, Kyoto 606-8502, Japan
 Tel: 81-75-753-4081
 Fax: 81-75-705-1113
 Email: satoh@ascidian.zool.kyoto-u.ac.jp.

FEATURES source
 Location/Qualifiers
 1..164
 /organism="Ciona intestinalis"
 /mol_type="mRNA"
 /db_xref="taxon:7719"
 /clone="cima050g08"
 /tissue_type="whole animal"
 /dev_stage="mature adult"
 /clone_lib="Nori Satoh unpublished cDNA library, mature
 adult whole animal"

ORIGIN

Query Match 100.0%; Score 11; DB 5; Length 164;
 Best Local Similarity 100.0%; Pred. No. 1.7e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11
 |||||
 Db 136 CTTTGGCACTA 146

RESULT 38
 BZ654404 168 bp DNA linear GSS 29-JAN-2003
 LOCUS OGAMR91TC ZM 0.7 1.5 KB Zea mays genomic clone ZMMBMA0096014,
 DEFINITION genomic survey sequence.
 ACCESSION BZ654404
 VERSION BZ654404.1 GI:28123664
 KEYWORDS GSS.
 SOURCE Zea mays
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 168)
 Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
 Resnick, A., Fraser, C.M., Buddiman, M.A., Bedell, J.A., Rohlfing, T.,
 Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.
 TITLE Consortium for Maize Genomics
 JOURNAL Unpublished (2002)
 COMMENT Other_GSSs: OGAMR91TM
 Contact: Cathy Whitelaw
 TIGR
 9712 Medical Center Drive, Rockville, MD 20850, USA
 Tel: 301-838-5843
 Fax: 301-838-0208
 Email: whitelaw@tigr.org
 Seq primer: Tf
 Class: sheared ends.

FEATURES source
 Location/Qualifiers
 1..168
 /organism="Zea mays"
 /mol_type="genomic DNA"
 /strain="B73"
 /db_xref="taxon:4577"
 /clone="ZMMBMA0096014"
 /clone_lib="ZM 0.7 1.5 KB"
 /note="Vector: pBCSK-; Site_1: HincII; 0.7-1.5 kb
 methylation filtered genomic DNA library"

ORIGIN
 Query Match 100.0%; Score 11; DB 8; Length 168;
 Best Local Similarity 100.0%; Pred. No. 1.7e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11
 |||||
 Db 69 CTTTGGCACTA 79

RESULT 39
 CL954906 168 bp DNA linear GSS 21-SEP-2004
 LOCUS OsIRUA005118 Oryza sativa Express Library Oryza sativa (indica
 DEFINITION cultivar-group) genomic, genomic survey sequence.
 ACCESSION CL954906
 VERSION CL954906.1 GI:52367015
 KEYWORDS GSS.
 SOURCE Oryza sativa (indica cultivar-group)
 ORGANISM Oryza sativa (indica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 168)

AUTHORS Ma,L., Wang,J., Chen,C., Liu,X., Su,N., Li,L., Wang,X., Cao,M.,
Jiao,Y., Sun,N., Zhang,X., Bao,J., Sun,D., Zhao,H., Yuan,L.,
Wong,G.K.S., Deng,X.W. and Wang,J.
TITLE An analysis of transcriptional regulation of the rice genome and
its comparison to Arabidopsis

JOURNAL Unpublished (2004)
COMMENT Contact: Chen Chen
Department of Bioinformatic
Beijing Institute of Genomics
Chinese Academy of Sciences, Beijing 101300, China
Tel: 86-10-80481559
Fax: 86-10-80488676
Email: chenchen@genomics.org.cn
Rice genomic sequence.
Class: exon-trapped.

FEATURES Location/Qualifiers
source
1..168
/organism="Oryza sativa (indica cultivar-group)"
/mol_type="genomic DNA"
/db_xref="taxon:39946"
/clone_lib="Oryza sativa Express Library"
/note="Oryza sativa exon trapped genomic sequences"

ORIGIN

Query Match 100.0%; Score 11; DB 9; Length 168;
Best Local Similarity 100.0%; Pred. No. 1.7e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTGGGCACTA 11
|||||

Db 18 CTTGGGCACTA 8

RESULT 40
CG869416/c
LOCUS CG869416 172 bp mRNA linear GSS 26-NOV-2003
DEFINITION AE0323 Sanger Institute Gene Trap Library pGT01xr Mus musculus
CDNA, mRNA sequence.
ACCESSION CG869416
VERSION CG869416.1 GI:38533096
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 172)
AUTHORS Sanger Institute Gene Trap Resource - SIGTR.
TITLE http://www.sanger.ac.uk/PostGenomics/genetrap/
JOURNAL Unpublished (2003)
COMMENT Contact: Sanger Institute Gene Trap Resource - SIGTR
Wellcome Trust Sanger Institute
Email: info.genetrap@sanger.ac.uk
Sequence tag generated by 5' RACE of total RNA from gene trap ES
cell line. ES cell lines harboring insertion mutation of target
gene are available upon request from Sanger Institute Gene Trap
Resource. Annotation information available from
http://www.sanger.ac.uk/PostGenomics/genetrap/
Class: Gene trap.

FEATURES Location/Qualifiers

source
1..172
/organism="Mus musculus"
/mol_type="mRNA"
/strains="129 OLA"
/db_xref="taxon:10090"
/sex="Male"
/cell_type="Embryonic Stem Cell"
/clone_lib="Sanger Institute Gene Trap Library pGT01xr"
/note="Vector: pGT01xr"

ORIGIN

Query Match 100.0%; Score 11; DB 9; Length 172;
Best Local Similarity 100.0%; Pred. No. 1.7e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTGGGCACTA 11
|||||

Db 121 CTTGGGCACTA 111

RESULT 41
BQ294074/c
LOCUS BQ294074 174 bp mRNA linear EST 15-MAY-2002
DEFINITION 1091026B01.y2 1091 - Immature ear with common ESTs screened by
Schmidt lab Zea mays cDNA, mRNA sequence.

ACCESSION BQ294074
VERSION BQ294074.1 GI:20803024
KEYWORDS EST.

SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 174)

AUTHORS Walbot V.

TITLE Maize ESTs from various cDNA libraries sequenced at Stanford

JOURNAL University
COMMENT Unpublished (1999)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 1091026 row: B column: 01.

FEATURES Location/Qualifiers

source

1..174
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="OH43"
/db_xref="taxon:4577"
/tissue_type="Inflorescence meristem - floral organ
primordia"
/dev_stage="0.5 cm to 2 cm"
/lab_host="Stratagene XL0LR"
/clone_lib="1091 - Immature ear with common ESTs screened
by Schmidt lab"
/note="Organ: Immature ear; Vector: pAD-GAL4; Site 1:
EcoRI; Site 2: XhoI; RNA from library 606 was filtered for
common ESTs found in 606."

ORIGIN

Query Match 100.0%; Score 11; DB 5; Length 174;
Best Local Similarity 100.0%; Pred. No. 1.7e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTGGGCACTA 11
|||||

Db 75 CTTGGGCACTA 65

RESULT 42

BQ080480

LOCUS BQ080480

DEFINITION san33g10.y1 Gm-cl084 Glycine max cDNA clone SOYBEAN CLONE ID:
Gm-cl084-5708 5', similar to TR:Q9SVES Q9SVES PUTATIVE POLLEN
ALLERGEN. ;, mRNA sequence.

ACCESSION BQ080480

VERSION BQ080480.1 GI:19935539

KEYWORDS EST.

SOURCE Glycine max (soybean)

ORGANISM Glycine max

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.

```

REFERENCE
AUTHORS
1 (bases 1 to 175)
Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V.,
Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J.,
Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M.,
Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N.,
Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,
McCann,R., Waterston,R. and Wilson,R.
Public Soybean EST Project
Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
When it has been determined, an EST from the other end of this
clone is listed in the 'Other ESTs on clone' field. This clone is
available through: Biogenetic Services, 801 32nd Ave. Brookings, SD
57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com)
Trace considered overall poor quality
Seq primer: -40RP from Gibco
High quality sequence stop: 1.

FEATURES
source
1..175
/organism="Glycine max"
/mol_type="mRNA"
/cultivar="Williams 82"
/db_xref="taxon:3847"
/clone="SOYBEAN CLONE ID: Gm-cl084-5708"
/tissue_type="Etiolated hypocotyls (Williams 82)"
/lab_host="DH10B"
/clone_lib="Gm-cl084"
/note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2:
XhoI; The cDNA library was constructed by M. Bhattacharyya
from mRNA isolated from etiolated hypocotyls from the
cultivar Williams 82. Tissue was inoculated with
Phytophthora soyae race 1 and tissues were harvested 2 and
4 hours following infection. The library is the pool of
these two time points. Complementary DNA was synthesized
from mRNA using a primer consisting of a poly(dT) sequence
with a XhoI restriction site. EcoRI adapters were ligated
to the blunt-ended cDNA fragments followed by XhoI
digestion. The cDNA fragments were directionally cloned
into the EcoRI-XhoI restriction site of the pBluescript
vector. The ligated cDNA fragments were transformed into
DH10B host cells (Gibco BRL). This library was constructed
by M. Bhattacharyya in the laboratory of Dr. Randy
Shoemaker at Iowa State University."

ORIGIN
Query Match 100.0%; Score 11; DB 5; Length 175;
Best Local Similarity 100.0%; Pred. No. 1.7e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTGGCACTA 11
|||||
Db 120 CTTTGGCACTA 130

RESULT 43
AZ113246/c
LOCUS
DEFINITION
RPCI-23-475G2-TV RPCI-23 Mus musculus genomic clone RPCI-23-475G2,
genomic survey sequence.
ACCESSION
AZ113246
VERSION
AZ113246.1 GI:7772594
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 177)

AUTHORS
Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S.,
Akinret,B., Levins,M., McGann,S., Tsegaye,G., Geer,K., Krol,M., de
Jong,P. and Fraser,C.M.
Mouse BAC End Sequences from Library RPCI-23
Unpublished (1999)
Other GSSs: RPCI-23-475G2.TJ
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (http://info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac\_ends/mouse/bac\_end\_intro.html
Plate: 475 row: G column: 2
Seq primer: T7
Class: BAC ends.

FEATURES
Location/Qualifiers
1..177
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-23-475G2"
/sex="Female"
/lab_host="DH10B"
/clone_lib="RPCI-23"
/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site 1:
EcoRI; Site 2: EcoRI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
EcoRI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies)."

ORIGIN
Query Match 100.0%; Score 11; DB 8; Length 177;
Best Local Similarity 100.0%; Pred. No. 1.7e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTGGCACTA 11
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Db 73 CTTTGGCACTA 63

RESULT 44
AA065630/c
LOCUS
DEFINITION
mm42ell.r1 StrataGene mouse melanoma (#937312) Mus musculus CDNA
clone IMAGE:524204 5', mRNA sequence.
ACCESSION
AA065630
VERSION
AA065630.1 GI:1563210
KEYWORDS
EST.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 178)
AUTHORS
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
The WashU-HMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine

```

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:318052
Seq primer: -28ml3 rev1 ET from Amersham
High quality sequence stop: 160.

FEATURES
source
1. 178
/lab_host="S9SNU601"
/clone_lib="Mus musculus"
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/db_xref="taxon:10090"
/clone="IMAGE:524204"
/tissue_type="melanoma"
/dev_stage="M2 cells"
/lab_host="SOLR (kanamycin resistant)"
/clone_lib="Stratagene mouse melanoma (#937312)"
/note="Organ: skin; Vector: pBluescript SK-; Site_1:
EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer:
Oligo dt. From M2 cells, a highly metastatic derivative of
the K-1735 (mouse) melanoma. Average insert size: 1.0 kb;
Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGGACGAG
3' -3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3' "

ORIGIN
Query Match 100.0%; Score 11; DB 1; Length 178;
Best Local Similarity 100.0%; Pred. No. 1.7e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CTTTGGCACTA 11
|||||
Db 134 CTTTGGCACTA 124

RESULT 45
BM829109/c
LOCUS
DEFINITION BM829109.1 Homo sapiens cDNA clone S9SNU601-56-A12 5',
mRNA sequence.
ACCESSION BM829109
VERSION BM829109.1 GI:19185518
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 178)
REFERENCE Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
21C Frontier Korean EST Project 2001
Unpublished (2002)
CONTACT: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Boeun-dong Yuseong-gu, Daejeon 305-339, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 56 row: A column: 12
High quality sequence stop: 178.

FEATURES
source
1. 178
/lab_host="S9SNU601"
/clone_lib="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S9SNU601-56-A12"
/sex="M"
/tissue_type="Ascites"
/cell_type="Epithelial"
/cell_line="SNU-601"

ORIGIN
Query Match 100.0%; Score 11; DB 4; Length 178;
Best Local Similarity 100.0%; Pred. No. 1.7e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CTTTGGCACTA 11
|||||
Db 155 CTTTGGCACTA 145

RESULT 46
BM406539/c
LOCUS
DEFINITION BM406539 Yutaka Satou unpublished cDNA library, embryo whole animal
Ciona intestinalis cDNA clone ciem851106 3', mRNA sequence.
ACCESSION BM406539
VERSION BM406539.1 GI:47822367
KEYWORDS EST.
SOURCE Ciona intestinalis
ORGANISM Ciona intestinalis
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Cionidae; Ciona.
1 (bases 1 to 178)
REFERENCE Satou,Y., Shin,I.T., Kohara,Y. and Satoh,N.
Expressed genes in Ciona intestinalis (2004)
Unpublished (2004)
CONTACT: Yutaka Satou
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4095
Fax: 81-75-705-1113
Email: yutaka@ascidian.zool.kyoto-u.ac.jp.

FEATURES
source
1. 178
/lab_host="S9SNU601"
/clone_lib="Ciona intestinalis"
/mol_type="mRNA"
/db_xref="taxon:7719"
/clone="ciem851106"
/tissue_type="whole animal"
/dev_stage="embryo"
/clone_lib="Yutaka Satou unpublished cDNA library, embryo
whole animal"

ORIGIN
Query Match 100.0%; Score 11; DB 5; Length 178;
Best Local Similarity 100.0%; Pred. No. 1.7e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CTTTGGCACTA 11
|||||
Db 111 CTTTGGCACTA 101

RESULT 47
BM829109/c
LOCUS
DEFINITION BM829109.1 Homo sapiens cDNA clone S9SNU601-56-A12 5',
mRNA sequence.
ACCESSION BM829109
VERSION BM829109.1 GI:19185518
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 178)
REFERENCE Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
21C Frontier Korean EST Project 2001
Unpublished (2002)
CONTACT: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Boeun-dong Yuseong-gu, Daejeon 305-339, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 56 row: A column: 12
High quality sequence stop: 178.

FEATURES
source
1. 178
/lab_host="S9SNU601"
/clone_lib="Homo sapiens"
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/clone="S9SNU601-56-A12"
/sex="M"
/tissue_type="Ascites"
/cell_type="Epithelial"
/cell_line="SNU-601"

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CE643587
LOCUS tigr-gss-dog-1700036685068 linear DNA 180 bp GSS 29-SEP-2003
DEFINITION genomic survey sequence.
ACCESSION CE643587
VERSION CE643587.1 GI:36961833
KEYWORDS GSS.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (bases 1 to 180)
AUTHORS Kirschner, E.F., Batra, V., Halpern, A.L., Levy, S., Remington, K.,
Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and
Venter, J.C.
TITLE The dog genome: survey sequencing and comparative analysis
JOURNAL Science 301 (5641), 1898-1903 (2003)
MEDLINE 22875432
PUBMED 14512627
COMMENT Contact: Kirkness EF
The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0208
Fax: 301-838-0208
Email: ekirknes@tigr.org
Class: shotgun.
Location/Qualifiers
1..180
/organism="Canis familiaris"
/mol_type="genomic DNA"
/strain="Standard Poodle"
/db_xref="taxon:9615"
/clone_lib="Dog Library"
/note="Site 1: BSKXI; Libraries were prepared from
peripheral blood"

ORIGIN
Query Match 100.0%; Score 11; DB 9; Length 180;
Best Local Similarity 100.0%; Pred. No. 1.7e+04; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11
|||||
Db 101 CTTTGGCACTA 111

FEATURES
source
BM110364
LOCUS EST557900 potato roots Solanum tuberosum cDNA clone cPRO7P9 5' end,
DEFINITION mRNA sequence.
ACCESSION BM110364
VERSION BM110364.1 GI:17072035
KEYWORDS EST.
SOURCE Solanum tuberosum (potato)
ORGANISM Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiales; Solanales; Solanaceae; Solanum.
REFERENCE 1 (bases 1 to 181)
AUTHORS van der Hoeven, R., Sun, H., Karameycheva, S.A., Tsai, J., Van Aken, S.,
Utterback, T., Chiemiango, A., Bougri, O., Buell, C.R., Ronning, C.,
Tanksley, S. and Baker, B.
TITLE Generation of ESTs from potato roots
JOURNAL Unpublished (2001)
COMMENT Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
This clone can be obtained from the University of Arizona Genomics
Institute. Orders can be made through URL:
http://genome.arizona.edu/orders/

CE643587
LOCUS tigr-gss-dog-1700036685068 linear DNA 180 bp GSS 29-SEP-2003
DEFINITION genomic survey sequence.
ACCESSION CE643587
VERSION CE643587.1 GI:36961833
KEYWORDS GSS.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (bases 1 to 180)
AUTHORS Kirschner, E.F., Batra, V., Halpern, A.L., Levy, S., Remington, K.,
Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and
Venter, J.C.
TITLE The dog genome: survey sequencing and comparative analysis
JOURNAL Science 301 (5641), 1898-1903 (2003)
MEDLINE 22875432
PUBMED 14512627
COMMENT Contact: Kirkness EF
The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0208
Fax: 301-838-0208
Email: ekirknes@tigr.org
Class: shotgun.
Location/Qualifiers
1..180
/organism="Canis familiaris"
/mol_type="genomic DNA"
/strain="Standard Poodle"
/db_xref="taxon:9615"
/clone_lib="Dog Library"
/note="Site 1: BSKXI; Libraries were prepared from
peripheral blood"

ORIGIN
Query Match 100.0%; Score 11; DB 9; Length 180;
Best Local Similarity 100.0%; Pred. No. 1.7e+04; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11
|||||
Db 101 CTTTGGCACTA 111

FEATURES
source
BM110364
LOCUS EST557900 potato roots Solanum tuberosum cDNA clone cPRO7P9 5' end,
DEFINITION mRNA sequence.
ACCESSION BM110364
VERSION BM110364.1 GI:17072035
KEYWORDS EST.
SOURCE Solanum tuberosum (potato)
ORGANISM Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiales; Solanales; Solanaceae; Solanum.
REFERENCE 1 (bases 1 to 181)
AUTHORS van der Hoeven, R., Sun, H., Karameycheva, S.A., Tsai, J., Van Aken, S.,
Utterback, T., Chiemiango, A., Bougri, O., Buell, C.R., Ronning, C.,
Tanksley, S. and Baker, B.
TITLE Generation of ESTs from potato roots
JOURNAL Unpublished (2001)
COMMENT Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
This clone can be obtained from the University of Arizona Genomics
Institute. Orders can be made through URL:
http://genome.arizona.edu/orders/

```

```

Seq primer: T3.
Location/Qualifiers
1..181
/organism="Solanum tuberosum"
/mol_type="mRNA"
/cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="cPRO7P9"
/tissue_type="roots"
/dev_stage="in vitro grown stem cuttings"
/lab_host="SOLR"
/clone_lib="potato roots"
/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2:
XhoI; supplier: Cornell University, Tanksley lab;
sequencing: The Institute for Genomic Research. Roots were
isolated from in vitro grown stem cuttings on CM medium.
Roots were isolated two weeks after placing the stem
cuttings from in vitro grown plants on medium."

ORIGIN
Query Match 100.0%; Score 11; DB 4; Length 181;
Best Local Similarity 100.0%; Pred. No. 1.7e+04; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11
|||||
Db 17 CTTTGGCACTA 27

FEATURES
source
CF206632
LOCUS RR890915I0007 IIIC Rc H08 Vitis sp. RR890915I Vitis hybrid cultivar
DEFINITION cDNA clone RR890915I0007 IIIC Rc_H08 3', mRNA sequence.
ACCESSION CF206632
VERSION CF206632.1 GI:33401005
KEYWORDS EST.
SOURCE Vitis hybrid cultivar
ORGANISM Vitis hybrid cultivar
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; Vitaceae; Vitis.
REFERENCE 1 (bases 1 to 181)
AUTHORS Goes da Silva, F., Iandolino, A., Lim, H., Baek, J., Leslie, A., Xu, J.,
Jones, K. and Cook, D.
TITLE Transcriptional responses of a Pierce's Disease resistant Vitis sp.
to infection by Xylella fastidiosa
JOURNAL Unpublished (2003)
COMMENT Contact: Douglas Cook, PhD
CAES Genome Facility
UC Davis, Plant Pathology
One Shields Ave, Davis, CA 95616, USA
Tel: 530 754 6561
Fax: 530 754 6617
Email: drcook@ucdavis.edu
Seq primer: GCCAAACGAATGCTGAG.
Location/Qualifiers
1..181
/organism="Vitis hybrid cultivar"
/mol_type="mRNA"
/db_xref="taxon:241073"
/clone="RR890915I0007 IIIC Rc_H08"
/lab_host="DH5alpha"
/clone_lib="Vitis sp. RR890915I"
/note="Organ: Leaf; Vector: pDNR; Site 1: SfiI; Site 2:
SfiI; RR890915I is a cDNA library of leaves from the F1 of
Vitis rupestris 'A. de Serres' x V. spp. 'b42-26'
(8909-15) showing resistance to Xylella fastidiosa under
greenhouse experimental conditions (M. Andrew Walker and
Alan Krivanek, U C Davis). Samples were collected from
17-week old greenhouse grown plants, nine weeks after
inoculation with the bacterial pathogen Xylella
fastidiosa. cDNAs were made by oligo-dT priming and

```

directionally cloned. 5' and 3' adaptors were used in cloning as follows:
5'-RAGCAGTGTATCAGCAGAGTGGCCATTACGGCCGG-3' and
5'-ATTCAGAGCGGAGCGCCGACATG-dt(30)NN-3'. Library was constructed using the Clontech Creator SMART kit and size-selected to contain the 0.5-3 kb size fraction."

ORIGIN

Query Match 100.0%; Score 11; DB 7; Length 181;
Best Local Similarity 100.0%; Pred. No. 1.7e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11
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Db 41 CTTTGGCACTA 51

RESULT 50
BM748955/c
LOCUS BM748955 182 bp mRNA linear EST 04-MAR-2002
DEFINITION K-EST0024004 S2SNU668 Homo sapiens cDNA clone S2SNU668-2-G06 5',
mRNA sequence.

ACCESSION BM748955
VERSION BM748955.1 GI:19078573
KEYWORDS EST.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 182)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.

TITLE 21C Frontier Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS

Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 2 row: G column: 06
High quality sequence stop: 182.

FEATURES

source

1..182
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S2SNU668-2-G06"
/sex="M"
/tissue_type="Ascites"
/cell_type="Epithelial"
/cell_line="SNU-668"
/lab_host="Top10P"
/clone_lib="S2SNU668"
/note="Organ: Stomach; Vector: pcms; Site_1: EcoRI;
Site_2: NotI; The poly (A)+ RNA was decapped with tobacco
acid pyrophosphatase (TAP) and ligated with DNA-RNA linker
including EcoRI site by treatment of T4 RNA ligase. The
first strand cDNA was synthesized from oligo dt-selected
mRNA by priming with dt-tailed vector. The dt-tailed
vector was adjusted to have about 60nt. The cDNA vector
was circularized with E. coli DNA ligase after digestion
of EcoRI which site is also included in vector. An RNA
strand converted to a DNA strand by Okayama-Berg method.
The obtained cDNA vectors were used for transfection of
competent cells E. coli Top10P' by electroporation
method."

ORIGIN

Query Match 100.0%; Score 11; DB 4; Length 182;
Best Local Similarity 100.0%; Pred. No. 1.7e+04;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CTTTGGCACTA 11
|||||||
Db 141 CTTTGGCACTA 131

Search completed: March 12, 2005, 10:58:15
Job time : 1792 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 12, 2005, 07:19:17 ; Search time 1429 Seconds
(without alignments)
372.993 Million cell updates/sec

Title: US-10-070-588A-112
Perfect score: 11
Sequence: 1 ctttggcacta 11

Scoring table: OLIGO NUC
Gapop 50.0 , Gapext 60.0

Searched: 4708233 seqs, 24227607955 residues

Word size : 0

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

GenEmbl: *
1: gb_ba: *
2: gb_htg: *
3: gb_in: *
4: gb_om: *
5: gb_ov: *
6: gb_pat: *
7: gb_ph: *
8: gb_pl: *
9: gb_pr: *
10: gb_ro: *
11: gb_scs: *
12: gb_sy: *
13: gb_un: *
14: gb_vi: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	11	100.0	11	6	AX099049 Sequence
2	11	100.0	11	6	AX099050 Sequence
3	11	100.0	18	6	AX201811 Sequence
4	11	100.0	22	6	AX003312 Sequence
5	11	100.0	23	6	BD095189 Sequence
6	11	100.0	47	6	AX427666 Sequence
7	11	100.0	77	6	CQ057099 Sequence
8	11	100.0	77	6	CQ076362 Sequence
9	11	100.0	77	6	CQ107351 Sequence
10	11	100.0	77	6	CQ146017 Sequence
11	11	100.0	77	6	CQ205816 Sequence
12	11	100.0	77	6	CQ229223 Sequence
13	11	100.0	77	6	CQ267352 Sequence
14	11	100.0	77	6	CQ304373 Sequence
15	11	100.0	77	6	CQ341641 Sequence
16	11	100.0	100	6	AX310296 Sequence
17	11	100.0	100	6	BD045829 Sequence
18	11	100.0	121	6	AX325267 Sequence
19	11	100.0	121	6	AX325268 Sequence

20	11	100.0	129	11	G00343	G00343	SMSS785 Eri
21	11	100.0	149	11	BX284306	BX284306	Arabidops
c 22	11	100.0	150	6	CQ659646	CQ659646	Sequence
c 23	11	100.0	153	6	CQ058212	CQ058212	Sequence
c 24	11	100.0	153	6	CQ077548	CQ077548	Sequence
c 25	11	100.0	153	6	CQ108562	CQ108562	Sequence
c 26	11	100.0	153	6	CQ147196	CQ147196	Sequence
c 27	11	100.0	153	6	CQ182574	CQ182574	Sequence
c 28	11	100.0	153	6	CQ206983	CQ206983	Sequence
c 29	11	100.0	153	6	CQ230434	CQ230434	Sequence
c 30	11	100.0	153	6	CQ268567	CQ268567	Sequence
c 31	11	100.0	153	6	CQ305599	CQ305599	Sequence
c 32	11	100.0	153	6	CQ342787	CQ342787	Sequence
33	11	100.0	198	8	ATH553769	ATH553769	Arabidops
34	11	100.0	201	11	BV201964	BV201964	sqm20783
c 35	11	100.0	204	6	AX618370	AX618370	Sequence
c 36	11	100.0	207	6	AX553184	AX553184	Sequence
c 37	11	100.0	226	8	ATH526781	ATH526781	Arabidops
38	11	100.0	232	11	BV084044	BV084044	sc1275_p3
39	11	100.0	234	11	BX467061	BX467061	Arabidops
40	11	100.0	245	11	BX467053	BX467053	Arabidops
c 41	11	100.0	246	6	CQ450823	CQ450823	Sequence
42	11	100.0	250	11	BV084038	BV084038	sc1275_p3
43	11	100.0	250	11	BV084041	BV084041	sc1275_p3
44	11	100.0	250	11	BV084045	BV084045	sc1275_p3
45	11	100.0	250	11	BV084046	BV084046	sc1275_p3
46	11	100.0	250	11	G15461	G15461	human STS S
c 47	11	100.0	251	6	CQ675738	CQ675738	Sequence
48	11	100.0	251	11	BV084034	BV084034	sc1275_p3
49	11	100.0	251	11	BV084035	BV084035	sc1275_p3
50	11	100.0	251	11	BV084036	BV084036	sc1275_p3
51	11	100.0	251	11	BV084039	BV084039	sc1275_p3
52	11	100.0	251	11	BV084040	BV084040	sc1275_p3
53	11	100.0	251	11	BV084047	BV084047	sc1275_p3
c 54	11	100.0	252	8	CUSCC	CUSCC	Sequence
55	11	100.0	252	11	BV084037	BV084037	sc1275_p3
56	11	100.0	252	11	BV084042	BV084042	sc1275_p3
57	11	100.0	252	11	BV084043	BV084043	sc1275_p3
58	11	100.0	254	11	G74797	G74797	STS6-213-Sm
c 59	11	100.0	255	6	AX210840	AX210840	Sequence
c 60	11	100.0	273	6	CQ749145	CQ749145	Sequence
c 61	11	100.0	273	6	AX413144	AX413144	Sequence
62	11	100.0	273	14	AF289535	AF289535	Hepatitis
63	11	100.0	273	14	AF289538	AF289538	Hepatitis
64	11	100.0	276	6	AX911248	AX911248	Sequence
65	11	100.0	276	6	BD046781	BD046781	Sequence
66	11	100.0	282	5	AF274899	AF274899	Dicamptod
67	11	100.0	284	6	CQ430504	CQ430504	Sequence
c 68	11	100.0	286	6	AX284825	AX284825	Sequence
c 69	11	100.0	289	6	CQ701125	CQ701125	Sequence
c 70	11	100.0	293	6	CQ703610	CQ703610	Sequence
c 71	11	100.0	293	6	AX284452	AX284452	Sequence
c 72	11	100.0	297	6	CQ465756	CQ465756	Sequence
73	11	100.0	299	6	CQ674265	CQ674265	Sequence
74	11	100.0	300	6	CQ674069	CQ674069	Sequence
75	11	100.0	303	6	BD095187	BD095187	Novel pol
c 76	11	100.0	305	6	AR521977	AR521977	Sequence
77	11	100.0	306	8	AY504063	AY504063	Sorghum b
78	11	100.0	306	8	AY504064	AY504064	Sorghum b
79	11	100.0	306	8	AY504074	AY504074	Sorghum b
80	11	100.0	309	6	CQ057931	CQ057931	Sequence
81	11	100.0	309	6	CQ077243	CQ077243	Sequence
82	11	100.0	309	6	CQ108240	CQ108240	Sequence
83	11	100.0	309	6	CQ146868	CQ146868	Sequence
84	11	100.0	309	6	CQ182280	CQ182280	Sequence
85	11	100.0	309	6	CQ206674	CQ206674	Sequence
86	11	100.0	309	6	CQ230099	CQ230099	Sequence
87	11	100.0	309	6	CQ268243	CQ268243	Sequence
88	11	100.0	309	6	CQ305278	CQ305278	Sequence
89	11	100.0	309	6	CQ342476	CQ342476	Sequence
90	11	100.0	312	8	AY504058	AY504058	Sorghum b
91	11	100.0	313	8	AY504057	AY504057	Sorghum b
92	11	100.0	313	8	AY504059	AY504059	Sorghum b

93	11	100.0	313	8	AY504062	Sorghum b	166	11	100.0	396	6	AR489642	Sequence
94	11	100.0	313	8	AY504069	Sorghum a	167	11	100.0	396	6	AR493883	Sequence
95	11	100.0	313	8	AY504075	Sorghum b	168	11	100.0	396	6	AX093212	Sequence
c 96	11	100.0	314	8	AX285139	Sequence	169	11	100.0	398	11	HSBE77C7	AL010088 H.sapiens
97	11	100.0	314	8	AY504051	Sorghum b	c 170	11	100.0	399	6	CQ678040	Sequence
98	11	100.0	314	8	AY504052	Sorghum b	171	11	100.0	399	6	CQ684483	Sequence
99	11	100.0	314	8	AY504053	Sorghum b	172	11	100.0	400	6	CQ676175	Sequence
100	11	100.0	314	8	AY504054	Sorghum b	173	11	100.0	400	11	G19234	G19234 human STS S
101	11	100.0	314	8	AY504055	Sorghum b	174	11	100.0	401	11	BV194428	sgm18101
102	11	100.0	314	8	AY504056	Sorghum a	175	11	100.0	401	11	G70004	G70004 713510831FN
103	11	100.0	314	8	AY504060	Sorghum b	c 176	11	100.0	403	11	BV006439	OKS 1059
104	11	100.0	314	8	AY504061	Sorghum b	177	11	100.0	404	11	AL773193	Arabidops
105	11	100.0	314	8	AY504065	Sorghum b	178	11	100.0	405	5	AF282408	Hiodon al
106	11	100.0	314	8	AY504066	Sorghum b	c 179	11	100.0	406	9	AB050779	Homo sapi
107	11	100.0	314	8	AY504067	Sorghum b	180	11	100.0	408	11	G70079	G70079 713510831FN
108	11	100.0	314	8	AY504068	Sorghum a	181	11	100.0	408	11	G70174	G70174 713500831FP
109	11	100.0	314	8	AY504070	Sorghum b	182	11	100.0	409	11	G69796	713510831FC
110	11	100.0	314	8	AY504071	Sorghum b	183	11	100.0	413	11	HSU29001	Human chrom
111	11	100.0	314	8	AY504072	Sorghum b	184	11	100.0	419	6	CQ691551	Sequence
112	11	100.0	314	8	AY504073	Sorghum b	185	11	100.0	419	11	G37103	SHGC-56874
113	11	100.0	316	3	AF356475	Sequence	186	11	100.0	423	6	CQ052927	Sequence
114	11	100.0	321	6	AR375957	Sequence	187	11	100.0	423	6	CQ068025	Sequence
c 115	11	100.0	329	6	AX150032	Sequence	188	11	100.0	423	6	CQ095081	Sequence
116	11	100.0	332	3	AF356478	Chironomu	189	11	100.0	423	6	CQ133828	Sequence
c 117	11	100.0	332	6	CQ681594	Sequence	190	11	100.0	423	6	CQ172367	Sequence
118	11	100.0	332	6	AX208846	Sequence	191	11	100.0	423	6	CQ201537	Sequence
119	11	100.0	333	3	AF356474	Chironomu	192	11	100.0	423	6	CQ217070	Sequence
120	11	100.0	333	3	AF356477	Chironomu	193	11	100.0	423	6	CQ255644	Sequence
121	11	100.0	333	6	CQ453591	Sequence	194	11	100.0	423	6	CQ292741	Sequence
122	11	100.0	338	6	CQ673855	Sequence	195	11	100.0	423	6	CQ329724	Sequence
123	11	100.0	340	6	CQ674468	Sequence	196	11	100.0	424	6	AX099111	Sequence
124	11	100.0	340	9	AF240680S3	Homo sapi	c 197	11	100.0	424	6	AX425968	Sequence
125	11	100.0	341	6	AX887762	Sequence	c 198	11	100.0	424	6	AX986662	Sequence
126	11	100.0	341	6	BD027372	Sequence	c 199	11	100.0	424	6	BD121521	EST and e
127	11	100.0	342	6	AX198282	Sequence	200	11	100.0	430	6	CQ673965	Sequence
128	11	100.0	346	8	NTA538651	Nicotiana	201	11	100.0	433	14	HPCE2A	M86771 Hepatitis C
129	11	100.0	347	9	HS268XE1	H. sapiens	202	11	100.0	435	6	CQ671892	Sequence
130	11	100.0	352	8	NTA538759	Nicotiana	c 203	11	100.0	441	6	CQ726193	Sequence
131	11	100.0	352	11	G69887	G69887 713500831FH	c 204	11	100.0	444	6	AX427662	Sequence
132	11	100.0	353	11	G05931	G05931 human STS W	c 205	11	100.0	445	6	CQ506128	Sequence
c 133	11	100.0	354	14	AF451287	AF451287 Vaccinia	206	11	100.0	446	5	AB117556	Xyrichtys
c 134	11	100.0	354	14	AF455803	AF455803 Vaccinia	c 207	11	100.0	446	6	CQ500790	Sequence
c 135	11	100.0	354	14	AF455804	AF455804 Vaccinia	c 208	11	100.0	448	6	CQ460471	Sequence
c 136	11	100.0	354	14	AF455805	AF455805 Vaccinia	c 209	11	100.0	449	11	G70149	AY049756 Human pap
c 137	11	100.0	354	14	AF455806	AF455806 Vaccinia	c 210	11	100.0	449	14	AY049756	Sequence
c 138	11	100.0	355	6	CQ485573	CQ485573 Sequence	c 211	11	100.0	450	6	CQ752687	Sequence
c 139	11	100.0	355	11	BV088311	BV088311 RPAMWSEQ	c 212	11	100.0	450	6	CQ752687	Sequence
c 140	11	100.0	355	11	BV097354	BV097354 RPAMWSEQ	c 213	11	100.0	453	11	G73255	AX331406 Sequence
c 141	11	100.0	359	6	CQ421637	CQ421637 Sequence	c 214	11	100.0	455	6	AX331406	Sequence
c 142	11	100.0	359	11	G73280	G73280 csnpcmb1-p	215	11	100.0	456	6	CQ052080	Sequence
c 143	11	100.0	360	6	AX311086	AX311086 Sequence	216	11	100.0	456	6	CQ067124	Sequence
c 144	11	100.0	365	6	CQ053216	CQ053216 Sequence	217	11	100.0	456	6	CQ094175	Sequence
c 145	11	100.0	365	6	CQ068342	CQ068342 Sequence	218	11	100.0	456	6	CQ132959	Sequence
c 146	11	100.0	365	6	CQ095417	Sequence	219	11	100.0	456	6	CQ200662	Sequence
c 147	11	100.0	365	6	CQ134165	Sequence	220	11	100.0	456	6	CQ216171	Sequence
c 148	11	100.0	365	6	CQ172672	Sequence	221	11	100.0	456	6	CQ254736	Sequence
c 149	11	100.0	365	6	CQ201855	Sequence	222	11	100.0	456	6	CQ328875	Sequence
c 150	11	100.0	365	6	CQ217418	Sequence	223	11	100.0	456	6	CQ328875	Sequence
c 151	11	100.0	365	6	CQ255979	Sequence	c 224	11	100.0	456	6	CQ515395	Sequence
c 152	11	100.0	365	6	CQ293072	Sequence	c 225	11	100.0	457	9	H006101811	AF016354 Homo sapi
c 153	11	100.0	365	6	CQ330045	Sequence	226	11	100.0	461	6	CQ684251	Sequence
c 154	11	100.0	368	11	G77571	G77571 S209P6309FE	227	11	100.0	462	6	CQ051431	Sequence
c 155	11	100.0	369	14	AV691968	AV691968 Hepatitis	228	11	100.0	462	6	CQ066481	Sequence
c 156	11	100.0	380	6	CQ702029	CQ702029 Sequence	229	11	100.0	462	6	CQ093530	Sequence
c 157	11	100.0	380	11	G35744	G35744 STS hl4a939	230	11	100.0	462	6	CQ132301	Sequence
c 158	11	100.0	384	11	G00761	G00761 fruit fly S	231	11	100.0	462	6	CQ170871	Sequence
159	11	100.0	386	6	AR502706	AR502706 Sequence	232	11	100.0	462	6	CQ200016	Sequence
160	11	100.0	386	6	AR517988	AR517988 Sequence	233	11	100.0	462	6	CQ215497	Sequence
c 161	11	100.0	388	11	G55155	G55155 SHGC-100209	234	11	100.0	462	6	CQ254093	Sequence
162	11	100.0	393	6	CQ467741	Sequence	235	11	100.0	462	6	CQ291104	Sequence
163	11	100.0	394	8	ATH527431	ATH527431 Arabidops	236	11	100.0	462	6	CQ328219	Sequence
164	11	100.0	396	6	AR391207	AR391207 Sequence	237	11	100.0	462	11	G69760	G69760 713510831FB
165	11	100.0	396	6	AR392912	AR392912 Sequence	238	11	100.0	462	11	G77109	G77109 S208P6375RD

C 239	11	100.0	465	11	G70367	G70367 713500831FV	312	11	100.0	535	11	G70300	G70300 713500831FB
C 240	11	100.0	467	6	CQ460001	CQ460001 Sequence	313	11	100.0	536	11	G69726	G69726 713500831FB
C 241	11	100.0	468	6	CQ049240	CQ049240 Sequence	314	11	100.0	536	11	G70403	G70403 713500831FV
C 242	11	100.0	468	6	CQ064261	CQ064261 Sequence	315	11	100.0	537	11	BV041016	BV041016 S212P6922
C 243	11	100.0	468	6	CQ091201	CQ091201 Sequence	C 316	11	100.0	538	3	BHU66671	U66671 Entamoeba h
C 244	11	100.0	468	6	CQ130039	CQ130039 Sequence	C 317	11	100.0	539	11	G81496	G81496 S208P6400PD
C 245	11	100.0	468	6	CQ168658	CQ168658 Sequence	C 318	11	100.0	541	9	AY027774	AY027774 Homo sapi
C 246	11	100.0	468	6	CQ197781	CQ197781 Sequence	319	11	100.0	542	11	G70254	G70254 713500831FS
C 247	11	100.0	468	6	CQ213223	CQ213223 Sequence	320	11	100.0	543	8	AF493077	AF493077 Phaneroch
C 248	11	100.0	468	6	CQ251802	CQ251802 Sequence	321	11	100.0	543	11	G69527	G69527 713500831FA
C 249	11	100.0	468	6	CQ288956	CQ288956 Sequence	322	11	100.0	543	11	G69732	G69732 713500831FB
C 250	11	100.0	468	6	CQ325962	CQ325962 Sequence	C 323	11	100.0	544	3	AF532043	AF532043 Physa acu
C 251	11	100.0	468	6	CQ702226	CQ702226 Sequence	324	11	100.0	545	6	CQ672262	CQ672262 Sequence
C 252	11	100.0	471	11	G70216	G70216 713500831FR	325	11	100.0	545	11	G69522	G69522 713500831FA
C 253	11	100.0	472	6	CQ418458	CQ418458 Sequence	C 326	11	100.0	545	11	G77971	G77971 S209P6159RC
C 254	11	100.0	472	6	CQ426228	CQ426228 Sequence	327	11	100.0	546	11	G81755	G81755 S210P6249FD
C 255	11	100.0	472	6	CQ681596	CQ681596 Sequence	328	11	100.0	548	11	G83271	G83271 S210P6121RG
C 256	11	100.0	472	9	S78684S2	S78685 Homo sapien	C 329	11	100.0	549	8	AF186632	AF186632 Pennisetu
C 257	11	100.0	474	6	CQ698653	CQ698653 Sequence	330	11	100.0	550	11	G69766	G69766 713500831FB
C 258	11	100.0	474	11	G71155	G71155 713510831FM	C 331	11	100.0	551	6	AR255909	AR255909 Sequence
C 259	11	100.0	475	6	AR414421	AR414421 Sequence	C 332	11	100.0	551	6	AX040589	AX040589 Sequence
C 260	11	100.0	475	6	AX971255	AX971255 Sequence	333	11	100.0	551	11	G69598	G69598 713510831FB
C 261	11	100.0	475	6	BD109974	BD109974 EST and e	334	11	100.0	552	6	AR395114	AR395114 Sequence
C 262	11	100.0	477	1	AV236466	AV236466 Anaplasma	C 335	11	100.0	552	11	G69999	G69999 713500831FN
C 263	11	100.0	477	6	AR547771	AR547771 Sequence	336	11	100.0	552	11	G70045	G70045 713500831FN
C 264	11	100.0	478	6	CQ054320	CQ054320 Sequence	C 337	11	100.0	553	1	U97483	U97483 Rickettsia
C 265	11	100.0	478	6	CQ073557	CQ073557 Sequence	338	11	100.0	554	6	AX241774	AX241774 Sequence
C 266	11	100.0	478	6	CQ104439	CQ104439 Sequence	339	11	100.0	554	11	G69968	G69968 713500831FN
C 267	11	100.0	478	6	CQ143158	CQ143158 Sequence	C 340	11	100.0	556	11	BV055859	BV055859 S212P6025
C 268	11	100.0	478	6	CQ178643	CQ178643 Sequence	C 341	11	100.0	559	11	BV187892	BV187892 sqm15569
C 269	11	100.0	478	6	CQ202992	CQ202992 Sequence	342	11	100.0	560	11	BV112139	BV112139 PZA01681
C 270	11	100.0	478	6	CQ226339	CQ226339 Sequence	343	11	100.0	561	6	CQ528465	CQ528465 Sequence
C 271	11	100.0	478	6	CQ264481	CQ264481 Sequence	C 344	11	100.0	563	1	VCH231075	AJ231075 Vibrio ch
C 272	11	100.0	478	6	CQ301576	CQ301576 Sequence	C 345	11	100.0	565	6	AX400375	AX400375 Sequence
C 273	11	100.0	478	6	CQ338791	CQ338791 Sequence	C 346	11	100.0	570	6	AR303079	AR303079 Sequence
C 274	11	100.0	480	9	F461712803	AF461714 Homo sapi	C 347	11	100.0	570	8	AF126818	AF126818 Ampelomyc
C 275	11	100.0	481	6	CQ052847	CQ052847 Sequence	348	11	100.0	575	6	CQ776485	CQ776485 Sequence
C 276	11	100.0	481	6	CQ067935	CQ067935 Sequence	349	11	100.0	576	6	CQ072596	CQ072596 Sequence
C 277	11	100.0	481	6	CQ094989	CQ094989 Sequence	350	11	100.0	576	6	CQ103407	CQ103407 Sequence
C 278	11	100.0	481	6	CQ216977	CQ216977 Sequence	351	11	100.0	576	6	CQ142241	CQ142241 Sequence
C 279	11	100.0	481	11	G69688	G69688 713500831FB	C 352	11	100.0	577	11	BV112148	BV112148 PZA01681
C 280	11	100.0	481	13	AX713443	AX713443 Unculture	C 353	11	100.0	579	11	BV112145	BV112145 PZA01681
C 281	11	100.0	485	11	BV005736	BV005736 BARC0002	C 354	11	100.0	580	6	AX387326	AX387326 Sequence
C 282	11	100.0	486	6	CQ479618	CQ479618 Sequence	355	11	100.0	582	11	BV112147	BV112147 PZA01681
C 283	11	100.0	487	11	G70293	G70293 713510831FB	356	11	100.0	582	11	BV112143	BV112143 PZA01681
C 284	11	100.0	487	11	G70686	G70686 713510831FB	C 357	11	100.0	583	11	BV112146	BV112146 PZA01681
C 285	11	100.0	489	6	CQ528155	CQ528155 Sequence	C 358	11	100.0	583	11	BV112135	BV112135 PZA01681
C 286	11	100.0	490	11	G69931	G69931 713510831FN	C 359	11	100.0	583	11	BV112141	BV112141 PZA01681
C 287	11	100.0	493	1	AF508017	AF508017 Helicobac	C 360	11	100.0	584	11	G87470	G87470 S208P6755FF
C 288	11	100.0	495	6	CQ524379	CQ524379 Sequence	361	11	100.0	585	11	BV112144	BV112144 PZA01681
C 289	11	100.0	498	1	AY112687	AY112687 Anaplasma	C 362	11	100.0	586	9	AY027772	AY027772 Homo sapi
C 290	11	100.0	505	6	AR424178	AR424178 Sequence	C 363	11	100.0	590	6	CQ225167	CQ225167 Sequence
C 291	11	100.0	505	6	AX984872	AX984872 Sequence	364	11	100.0	590	6	CQ337472	CQ337472 Sequence
C 292	11	100.0	505	6	BD119731	BD119731 EST and e	C 365	11	100.0	593	11	BV112140	BV112140 PZA01681
C 293	11	100.0	508	11	BV077085	BV077085 S212P6146	366	11	100.0	595	11	BV112138	BV112138 PZA01681
C 294	11	100.0	518	11	G70084	G70084 713500831FN	367	11	100.0	595	11	BV112136	BV112136 PZA01681
C 295	11	100.0	519	11	G69559	G69559 713510831FB	C 368	11	100.0	599	11	G99545	G99545 S208P6725RF
C 296	11	100.0	519	11	G69992	G69992 713510831FN	369	11	100.0	601	11	BV112133	BV112133 PZA01681
C 297	11	100.0	519	11	G70117	G70117 713500831FN	370	11	100.0	601	11	BV112142	BV112142 PZA01681
C 298	11	100.0	524	11	G99361	G99361 S208P6706FB	371	11	100.0	601	11	BV179796	BV179796 sqm10676
C 299	11	100.0	525	6	CQ519452	CQ519452 Sequence	372	11	100.0	602	11	BV055978	BV055978 S212P6167
C 300	11	100.0	528	6	CQ737175	CQ737175 Sequence	373	11	100.0	603	11	BV112134	BV112134 PZA01681
C 301	11	100.0	528	11	G69606	G69606 713500831FB	374	11	100.0	603	11	BV112137	BV112137 PZA01681
C 302	11	100.0	528	11	G69644	G69644 713510831FB	375	11	100.0	611	11	BV161559	BV161559 RPAMMSQ0
C 303	11	100.0	528	11	G70398	G70398 713510831FV	376	11	100.0	615	3	AY081769	AY081769 Bombyx mo
C 304	11	100.0	530	9	AY027773	AY027773 Homo sapi	377	11	100.0	618	14	HPCNS2PA	MS5971 Hepatitis C
C 305	11	100.0	530	11	G90298	G90298 S210P6050F6	C 378	11	100.0	623	6	BD193991	BD193991 Enterococ
C 306	11	100.0	531	6	AX361027	AX361027 Sequence	379	11	100.0				
C 307	11	100.0	531	6	AX377693	AX377693 Sequence	380	11	100.0				
C 308	11	100.0	531	11	BV209964	BV209964 ZEBF10 4	381	11	100.0				
C 309	11	100.0	532	8	AK102011	AK102011 Oryza sat	382	11	100.0				
C 310	11	100.0	534	11	G52650	G52650 SHGC-85705	383	11	100.0				
C 311	11	100.0	535	11	G69651	G69651 713500831FB	C 384	11	100.0				

C 385	11	100.0	627	6	AX387353 Sequence	AX387353 Sequence	C 458	11	100.0	795	3	AY451312 Echinomet
C 386	11	100.0	631	11	BV023223 S212P6044	BV023223 S212P6044	C 459	11	100.0	798	3	AY451311 Echinomet
C 387	11	100.0	634	6	AX387354 Sequence	AX387354 Sequence	C 460	11	100.0	799	5	AY509834 Scardinu
C 388	11	100.0	635	6	CQ523393 Sequence	CQ523393 Sequence	C 461	11	100.0	799	11	BV166430 KCMJ6_880
C 389	11	100.0	636	6	AX400546 Sequence	AX400546 Sequence	C 462	11	100.0	801	8	AX275459 Soltanum d
C 390	11	100.0	637	3	AF153749 Sepia off	AF153749 Sepia off	C 463	11	100.0	806	6	AX393325 Sequence
C 391	11	100.0	641	11	BV018433 S212P6035	BV018433 S212P6035	C 464	11	100.0	807	3	AY451275 Echinomet
C 392	11	100.0	654	11	G06154 human SFS W	G06154 human SFS W	C 465	11	100.0	810	3	AY451250 Echinomet
C 393	11	100.0	657	11	BV022841 S212P6115	BV022841 S212P6115	C 466	11	100.0	810	11	BV208788 RAB9B_254
C 394	11	100.0	660	9	HSRPL18AH	X80821 H.sapiens m	C 467	11	100.0	812	6	BD192944 207 human
C 395	11	100.0	660	11	BV078357 px-6c7 Fl	BV078357 px-6c7 Fl	C 468	11	100.0	812	6	CQ821940 Sequence
C 396	11	100.0	668	6	AX255881 Sequence	AX255881 Sequence	C 469	11	100.0	813	3	AY451274 Echinomet
C 397	11	100.0	678	6	AX395115 Sequence	AX395115 Sequence	C 470	11	100.0	813	6	BD148503 Primer fo
C 398	11	100.0	678	11	BV022592	BV022592	C 471	11	100.0	813	6	AX868441 Sequence
C 399	11	100.0	683	8	AF443179	AF443179 Nicotiana	C 472	11	100.0	814	14	AF004463 Venezuela
C 400	11	100.0	693	3	EMU39507	U39507 Echinometra	C 473	11	100.0	816	3	AY451307 Echinomet
C 401	11	100.0	699	3	EMU39508	U39508 Echinometra	C 474	11	100.0	816	3	AY451315 Echinomet
C 402	11	100.0	705	11	BV044499	BV044499 S212P6637	C 475	11	100.0	816	6	AR449375 Sequence
C 403	11	100.0	706	9	HSR339642	AJ339642 Homo sapi	C 476	11	100.0	819	3	AY451272 Echinomet
C 404	11	100.0	711	3	EMU39509	U39509 Echinometra	C 477	11	100.0	819	3	AY451273 Echinomet
C 405	11	100.0	711	3	EMU39511	U39511 Echinometra	C 478	11	100.0	822	3	AY451251 Echinomet
C 406	11	100.0	711	3	EMU39512	AY451283 Echinomet	C 479	11	100.0	822	3	AY451261 Echinomet
C 407	11	100.0	720	3	AX51283	AX51283 Echinomet	C 480	11	100.0	822	3	AY451309 Echinomet
408	11	100.0	722	6	AX525797	AX525797 Sequence	C 481	11	100.0	824	8	AY333925 Antirrhin
409	11	100.0	724	14	HCU37610	U37610 Hepatitis C	C 482	11	100.0	825	3	AY451262 Echinomet
410	11	100.0	724	14	HCU37611	U37611 Hepatitis C	C 483	11	100.0	825	3	AY451308 Echinomet
411	11	100.0	724	14	HCU37624	U37624 Hepatitis C	C 484	11	100.0	825	3	AY451310 Echinomet
412	11	100.0	724	14	HCU37625	U37625 Hepatitis C	C 485	11	100.0	826	3	AY451265 Echinomet
413	11	100.0	724	14	HCU37626	U37626 Hepatitis C	C 486	11	100.0	828	3	AY451243 Echinomet
414	11	100.0	724	14	HCU37627	U37627 Hepatitis C	C 487	11	100.0	828	3	AY451246 Echinomet
415	11	100.0	724	14	HCU37631	U37631 Hepatitis C	C 488	11	100.0	828	3	AY451247 Echinomet
C 416	11	100.0	726	3	EOU39502	U39502 Echinometra	C 489	11	100.0	828	3	AY451252 Echinomet
C 417	11	100.0	726	3	EOU39503	U39503 Echinometra	C 490	11	100.0	828	3	AY451253 Echinomet
C 418	11	100.0	729	3	EOU39506	U39506 Echinometra	C 491	11	100.0	828	3	AY451255 Echinomet
419	11	100.0	731	11	BV012435	BV012435 ORS 167 S	C 492	11	100.0	828	3	AY451256 Echinomet
420	11	100.0	733	11	BV122394	BV122394 PZA01695	C 493	11	100.0	828	3	AY451257 Echinomet
421	11	100.0	734	11	BV122397	BV122397 PZA01695	C 494	11	100.0	828	3	AY451258 Echinomet
422	11	100.0	735	11	BV122405	BV122405 PZA01695	C 495	11	100.0	828	3	AY451260 Echinomet
423	11	100.0	736	11	BV122393	BV122393 PZA01695	C 496	11	100.0	828	3	AY451263 Echinomet
424	11	100.0	736	11	BV122400	BV122400 PZA01695	C 497	11	100.0	828	3	AY451266 Echinomet
425	11	100.0	737	11	BV122403	BV122403 PZA01695	C 498	11	100.0	828	3	AY451267 Echinomet
426	11	100.0	737	11	BV122395	BV122395 PZA01695	C 499	11	100.0	828	3	AY451316 Echinomet
427	11	100.0	738	11	BV122402	BV122402 PZA01695	C 500	11	100.0	831	3	AY451269 Echinomet
428	11	100.0	738	11	BV122404	BV122404 PZA01695	C 501	11	100.0	831	3	AY451318 Echinomet
429	11	100.0	739	11	BV122391	BV122391 PZA01695	C 502	11	100.0	831	3	AY451319 Echinomet
430	11	100.0	739	11	BV122392	BV122392 PZA01695	C 503	11	100.0	831	3	AY451321 Echinomet
431	11	100.0	739	11	BV122399	BV122399 PZA01695	C 504	11	100.0	831	3	AY451322 Echinomet
432	11	100.0	740	11	BV122396	BV122396 PZA01695	C 505	11	100.0	834	3	AY451323 Echinomet
433	11	100.0	740	11	BV122398	BV122398 PZA01695	C 506	11	100.0	834	3	AY451242 Echinomet
434	11	100.0	740	11	BV122406	BV122406 PZA01695	C 507	11	100.0	834	3	AY451270 Echinomet
435	11	100.0	741	11	BV122401	BV122401 PZA01695	C 508	11	100.0	834	3	AY451271 Echinomet
436	11	100.0	750	6	AR454846	AR454846 Sequence	C 509	11	100.0	834	3	AY451286 Echinomet
C 437	11	100.0	750	6	AX427661	AX427661 Sequence	C 510	11	100.0	834	3	AY451289 Echinomet
C 438	11	100.0	753	3	ESU39514	U39514 Echinometra	C 511	11	100.0	834	3	AY451317 Echinomet
C 439	11	100.0	759	6	AX414092	AX414092 Sequence	C 512	11	100.0	837	3	AY451249 Echinomet
C 440	11	100.0	761	6	AR494922	AR494922 Sequence	C 513	11	100.0	837	3	AY451259 Echinomet
C 441	11	100.0	761	8	AF378056	AF378056 Sorghum b	C 514	11	100.0	837	3	AY451288 Echinomet
C 442	11	100.0	762	6	CQ740543	CQ740543 Sequence	C 515	11	100.0	837	3	AY451297 Echinomet
C 443	11	100.0	762	8	AF378039	AF378039 Lycopersi	C 516	11	100.0	837	3	AY451304 Echinomet
C 444	11	100.0	762	8	AF378039	AF378039 Lycopersi	C 517	11	100.0	837	3	AY451320 Echinomet
C 445	11	100.0	763	6	AR494926	AR494926 Sequence	C 518	11	100.0	840	3	AY451245 Echinomet
C 446	11	100.0	763	8	AF378060	AF378060 Sorghum b	C 519	11	100.0	840	3	AY451282 Echinomet
C 447	11	100.0	768	3	AY451284	AY451284 Echinomet	C 520	11	100.0	841	8	AB026440 Nicotiana
C 448	11	100.0	768	11	BV058545	BV058545 S212P6600	C 521	11	100.0	842	11	BV068299 S212P6051
449	11	100.0	771	6	BD149264	BD149264 Primer fo	C 522	11	100.0	843	3	AY451244 Echinomet
450	11	100.0	771	6	AX869202	AX869202 Sequence	C 523	11	100.0	843	3	AY451248 Echinomet
C 451	11	100.0	773	3	LIN275321	AJ275321 Leishmani	C 524	11	100.0	843	3	AY451254 Echinomet
C 452	11	100.0	786	6	CQ728376	CQ728376 Sequence	C 525	11	100.0	843	3	AY451279 Echinomet
C 453	11	100.0	787	6	AR354238	AR354238 Sequence	C 526	11	100.0	843	3	AY451292 Echinomet
C 454	11	100.0	787	6	AR535794	AR535794 Sequence	C 527	11	100.0	843	3	AY451293 Echinomet
455	11	100.0	787	10	L47300S11	L47309 Rattus norv	C 528	11	100.0	843	3	AY451305 Echinomet
456	11	100.0	789	8	AB010953	AB010953 Toronia f	C 529	11	100.0	843	3	AY451313 Echinomet
C 457	11	100.0	793	11	BV033512	BV033512 S212P6625	C 530	11	100.0	843	3	AY451314 Echinomet

C 531	11	100.0	843	6	CQ740805	CQ740805 Sequence	C 604	11	100.0	1053	6	AX489452	AX489452 Sequence
C 532	11	100.0	846	3	AY451268	AY451268 Echinomet	C 605	11	100.0	1059	6	AR123363	AR123363 Sequence
C 533	11	100.0	846	3	AY451281	AY451281 Echinomet	C 606	11	100.0	1065	6	CQ803816	CQ803816 Sequence
C 534	11	100.0	847	6	I44710	I44710 Sequence 20	C 607	11	100.0	1071	6	AX570144	AX570144 Sequence
C 535	11	100.0	847	6	I52116	I52116 Sequence 20	C 608	11	100.0	1072	5	CR353032	CR353032 Gallus ga
C 536	11	100.0	849	3	AY451264	AY451264 Echinomet	C 609	11	100.0	1074	6	I44702	I44702 Sequence 4
C 537	11	100.0	852	11	BV015079	BV015079 S212P6040	C 610	11	100.0	1074	6	I52108	I52108 Sequence 4
C 538	11	100.0	855	3	AY451278	AY451278 Echinomet	C 611	11	100.0	1074	6	AR479673	AR479673 Sequence
C 539	11	100.0	855	3	AY451280	AY451280 Echinomet	C 612	11	100.0	1076	6	I44700	I44700 Sequence 1
C 540	11	100.0	858	3	AY451290	AY451290 Echinomet	C 613	11	100.0	1076	6	I52106	I52106 Sequence 1
C 541	11	100.0	858	3	AY451291	AY451291 Echinomet	C 614	11	100.0	1076	6	AR364044	AR364044 Sequence
C 542	11	100.0	863	5	BR331637	BR331637 Gallus ga	C 615	11	100.0	1076	6	MZERIP	M71222 Z.mays ribo
C 543	11	100.0	863	5	BD206392	BD206392 Human nuc	C 616	11	100.0	1077	5	AY383548	AY383548 Pleurodel
C 544	11	100.0	863	6	AR400707	AR400707 Sequence	C 617	11	100.0	1083	6	AR395092	AR395092 Sequence
C 545	11	100.0	863	6	AX013597	AX013597 Sequence	C 618	11	100.0	1092	8	STENCHIT	X14133 Potato mRNA
C 546	11	100.0	865	14	MLVTRPD	Y07808 MLV-related	C 619	11	100.0	1092	14	AF014959	AF014959 Hepatitis
C 547	11	100.0	866	6	BD079677	BD079677 Cancer-as	C 620	11	100.0	1097	8	AF043248	AF043248 Solanum t
C 548	11	100.0	870	3	AY451294	AY451294 Echinomet	C 621	11	100.0	1098	5	CR408251	CR408251 Gallus ga
C 549	11	100.0	870	3	AY451295	AY451295 Echinomet	C 622	11	100.0	1100	8	STU02607	STU02607 Solanum tub
C 550	11	100.0	870	3	AY451296	AY451296 Echinomet	C 623	11	100.0	1102	6	AX003309	AX003309 Sequence
C 551	11	100.0	870	3	AY451298	AY451298 Echinomet	C 624	11	100.0	1105	6	I44701	I44701 Sequence 3
C 552	11	100.0	870	3	AY451300	AY451300 Echinomet	C 625	11	100.0	1105	6	I52107	I52107 Sequence 3
C 553	11	100.0	879	6	CO643964	CO643964 Sequence	C 626	11	100.0	1105	6	AR364045	AR364045 Sequence
C 554	11	100.0	880	6	BD060507	BD060507 Secreted	C 627	11	100.0	1108	8	AF043247	AF043247 Solanum t
C 555	11	100.0	882	3	AY451276	AY451276 Echinomet	C 628	11	100.0	1117	6	CQ722054	CQ722054 Sequence
C 556	11	100.0	882	3	AY451302	AY451302 Echinomet	C 629	11	100.0	1125	6	AR395398	AR395398 Sequence
C 557	11	100.0	882	5	BR303353	BR303353 Gallus ga	C 630	11	100.0	1130	14	HPCVPGP	D00757 Hepatitis C
C 558	11	100.0	882	6	AX608099	AX608099 Sequence	C 631	11	100.0	1140	4	AV170112	AV170112 Viverra t
C 559	11	100.0	885	3	AY451277	AY451277 Echinomet	C 632	11	100.0	1140	5	AY509833	AY509833 Scardinu
C 560	11	100.0	885	3	AY451303	AY451303 Echinomet	C 633	11	100.0	1140	5	AY509835	AY509835 Scardinu
C 561	11	100.0	888	3	AY451306	AY451306 Echinomet	C 634	11	100.0	1140	5	AY509836	AY509836 Scardinu
C 562	11	100.0	888	3	AY451285	AY451285 Echinomet	C 635	11	100.0	1140	5	AY509837	AY509837 Scardinu
C 563	11	100.0	907	8	STU02608	STU02608 Solanum tub	C 636	11	100.0	1140	5	AY509838	AY509838 Scardinu
C 564	11	100.0	909	6	AX427660	AX427660 Sequence	C 637	11	100.0	1140	5	AY509839	AY509839 Scardinu
C 565	11	100.0	910	6	E06891	E06891 DNA encodin	C 638	11	100.0	1140	5	AY509840	AY509840 Scardinu
C 566	11	100.0	913	3	AX522440	AX522440 Lepeophth	C 639	11	100.0	1140	5	AY509841	AY509841 Scardinu
C 567	11	100.0	920	6	AX277145	AX277145 Sequence	C 640	11	100.0	1140	5	AY509842	AY509842 Scardinu
C 568	11	100.0	924	1	SMU26731	SMU26731 Stenotropha	C 641	11	100.0	1140	5	AY509843	AY509843 Scardinu
C 569	11	100.0	924	8	AB026439	AB026439 Nicotiana	C 642	11	100.0	1140	5	AY509844	AY509844 Scardinu
C 570	11	100.0	944	6	AR123368	AR123368 Sequence	C 643	11	100.0	1140	5	AY509845	AY509845 Scardinu
C 571	11	100.0	951	8	AF197330	AF197330 Eucalyptu	C 644	11	100.0	1140	5	AY509846	AY509846 Scardinu
C 572	11	100.0	951	8	AF197334	AF197334 Eucalyptu	C 645	11	100.0	1140	5	AY509847	AY509847 Scardinu
C 573	11	100.0	959	8	ZMA300265	AFJ300265 Zea mays	C 646	11	100.0	1140	5	AY509848	AY509848 Scardinu
C 574	11	100.0	960	6	CQ414733	CQ414733 Sequence	C 647	11	100.0	1140	5	MISECTOB	Y10444 S.erythrop
C 575	11	100.0	963	8	MZERIP2A	I26305 Zea mays ri	C 648	11	100.0	1161	6	I44707	I44707 Sequence 14
C 576	11	100.0	978	6	I44705	I44705 Sequence 10	C 649	11	100.0	1161	6	I52113	I52113 Sequence 14
C 577	11	100.0	978	6	I52111	I52111 Sequence 10	C 650	11	100.0	1164	6	CQ805740	CQ805740 Sequence
C 578	11	100.0	983	8	AF233881	AF233881 Zea mays	C 651	11	100.0	1167	8	AK061061	AK061061 Oryza sat
C 579	11	100.0	985	6	I44704	I44704 Sequence 8	C 652	11	100.0	1175	8	AF178951	AF178951 Zea mays
C 580	11	100.0	985	6	I52110	I52110 Sequence 8	C 653	11	100.0	1185	6	AR506487	AR506487 Sequence
C 581	11	100.0	985	9	BC004308	BC004308 Homo sapi	C 654	11	100.0	1192	10	BC019368	BC019368 Mus muscu
C 582	11	100.0	986	6	AR509830	AR509830 Sequence	C 655	11	100.0	1195	8	AY079331	AY079331 Arabidops
C 583	11	100.0	986	6	AR509830	AR509830 Sequence	C 656	11	100.0	1195	3	CEL487543	CEL487543 Caenorhab
C 584	11	100.0	987	6	HSN340461	AJ340461 Homo sapi	C 657	11	100.0	1207	6	AR004337	AR004337 Sequence
C 585	11	100.0	987	6	AR123360	AR123360 Sequence 12	C 658	11	100.0	1207	6	AR004338	AR004338 Sequence
C 586	11	100.0	987	6	I52112	I52112 Sequence 12	C 659	11	100.0	1207	6	AR006828	AR006828 Sequence
C 587	11	100.0	987	6	AR364047	AR364047 Sequence	C 660	11	100.0	1207	4	AF548433	AF548433 Tachylos
C 588	11	100.0	1001	6	AX081566	AX081566 Sequence	C 661	11	100.0	1218	4	AF548433	AF548433 Tachylos
C 589	11	100.0	1001	6	AX374747	AX374747 Sequence	C 662	11	100.0	1219	6	AR194503	AR194503 Sequence
C 590	11	100.0	1002	6	AX003310	AX003310 Sequence	C 663	11	100.0	1219	6	AR221954	AR221954 Sequence
C 591	11	100.0	1002	6	AX003311	AX003311 Sequence	C 664	11	100.0	1219	6	BD082634	BD082634 Methods a
C 592	11	100.0	1012	8	AK070231	AK070231 Oryza sat	C 665	11	100.0	1219	6	BD082649	BD082649 Methods a
C 593	11	100.0	1015	9	BC071939	BC071939 Homo sapi	C 666	11	100.0	1219	6	BD092928	BD092928 Methods a
C 594	11	100.0	1022	6	AX597891	AX597891 Sequence	C 667	11	100.0	1227	8	AY089181	AY089181 Arabidops
C 595	11	100.0	1023	10	RNU77633	U77633 Rattus norv	C 668	11	100.0	1236	8	AF209109	AF209109 Gnetum ul
C 596	11	100.0	1028	6	AK364046	AK364046 Sequence	C 669	11	100.0	1244	6	AR123372	AR123372 Sequence
C 597	11	100.0	1029	6	I44703	I44703 Sequence 6	C 670	11	100.0	1245	6	AR003853	AR003853 Sequence
C 598	11	100.0	1029	6	I52109	I52109 Sequence 6	C 671	11	100.0	1246	8	D89206	D89206 Schizosacch
C 599	11	100.0	1037	3	AY321151	AY321151 Aiptasia	C 672	11	100.0	1248	6	AR550904	AR550904 Sequence
C 600	11	100.0	1039	8	MZERIP2A	M33926 Zea mays ri	C 673	11	100.0	1248	8	AY706156	AY706156 Fragaria
C 601	11	100.0	1049	6	CQ716726	CQ716726 Sequence	C 674	11	100.0	1254	8	AF197617	AF197617 Gnetum gn
C 602	11	100.0	1049	9	AB036693	AB036693 Homo sapi	C 675	11	100.0	1263	5	BR31396	BR31396 Gallus ga
C 603	11	100.0	1053	6	AR123366	AR123366 Sequence	C 676	11	100.0	1263	6	AR378743	AR378743 Sequence

677	11	100.0	1263	9	AK000397	AK000397 Homo sapi	750	11	100.0	1431	6	AE319274	AR319274 Sequence
678	11	100.0	1275	6	AX654279	AX654279 Sequence	c 751	11	100.0	1431	8	BT012031	BT012031 Arabidops
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VERSION	AX003312.1 GI:9927129
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	DNA
	linear
	22 bp
	PAT 24-AUG-2000

ALIGNMENTS


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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS
TITLE
JOURNAL
Angulo-Mora,J.F. and Mauffrey,P.
Sequences coding for kin17 protein and their applications
Patent: WO 929845-A 5 17-JUN-1999;
ANGULO MORA JAIME FRANCISCO (FR); COMMISSARIAT ENERGIE ATOMIQUE
(FR)
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Location/Qualifiers
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RESULT 5
BD095189/c
LOCUS
DEFINITION
Novel polypeptide, novel DNA, novel antibody, and novel genetic
modified animal.
ACCESSION
BD095189
VERSION
BD095189.1 GI:22640777
KEYWORDS
WO 0138529-A/7.
SOURCE
synthetic construct
ORGANISM
other sequences; artificial sequences.
1 (bases 1 to 23)
REFERENCE
AUTHORS
Shiraishi,N., Sekine,S., Nabeshima,Y., Fujimori,T. and Ito,S.
TITLE
Novel polypeptide, novel DNA, novel antibody, and novel genetic
modified animal
JOURNAL
Patent: WO 0138529-A 7 31-MAY-2001;
KYOWA HAKKO KOGYO CO LTD,NORHIKO SHIRAISHI,SUSUMU SEKINE,YOICHI
NABESHIMA, TOSHIHIKO FUJIMORI,SHINJI ITO
COMMENT
OS Artificial Sequence
PN WO 0138529-A/7
PD 31-MAY-2001
PF 17-NOV-2000 WO 2000JP008121
PR 19-NOV-1999 JP 99P 329649
PI NORHIKO SHIRAISHI,SUSUMU SEKINE,YOICHI NABESHIMA,TOSHIHIKO
PI FUJIMORI,
PI SHINJI ITO
PC C12N15/12,C07K14/47,C07K16/18,A61K38/17,A61P43/00,G01N33/53,
PC C12N15/B5,
PC C12N1/21,C12P21/02,C12Q1/68,A01K67/027,C12Q1/02 CC
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RESULT 6
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DEFINITION
Sequence 7 from Patent WO0233106.
ACCESSION
AX427666
VERSION
AX427666.1 GI:21537785
KEYWORDS
synthetic construct
SOURCE
synthetic construct
ORGANISM
other sequences; artificial sequences.
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REFERENCE
AUTHORS
Neelam,A., Atkinson,H.J., Mcpherson,M.J. and Thomas,C.J.R.
TITLE
Plant cell death system
JOURNAL
Patent: WO 0233106-A 7 25-APR-2002;
CAMBRIDGE ADVANCED TECH (GB)
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RESULT 7
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DEFINITION
Sequence 7919 from Patent WO0157270.
ACCESSION
CQ057099
VERSION
CQ057099.1 GI:41031605
KEYWORDS
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SOURCE
Homo sapiens
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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REFERENCE
AUTHORS
Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
TITLE
Human genome-derived single exon nucleic acid probes useful for
analysis of gene expression in human breast and hbl 100 cells
JOURNAL
Patent: WO 0157270-A 7919 09-AUG-2001;
Aecomica, Inc. (US)
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RESULT 8
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LOCUS

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DEFINITION Sequence 12162 from Patent WO0157278.
ACCESSION CQ076362
VERSION CQ076362.1 GI:41046231
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
TITLE Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
JOURNAL Human genome-derived single exon nucleic acid probes useful for
ANALYSIS analysis of gene expression in human hela cells or other human
PATENT: WO 0157278-A 12162 09-AUG-2001;
Aeomica, Inc. (US)
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Db 34 CTTTGGCACTA 44

RESULT 9
CQ107351
LOCUS
DEFINITION Sequence 16210 from Patent WO0157272.
ACCESSION CQ107351
VERSION CQ107351.1 GI:41076404
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
TITLE Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
JOURNAL Human genome-derived single exon nucleic acid probes useful for
ANALYSIS analysis of gene expression in human placenta
PATENT: WO 0157272-A 16210 09-AUG-2001;
Aeomica, Inc. (US)
FEATURES Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 8.8e+03;
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Db 34 CTTTGGCACTA 44

RESULT 10
CQ146017
LOCUS
DEFINITION Sequence 16062 from Patent WO0157273.
ACCESSION CQ146017
VERSION CQ146017.1 GI:41153367
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
TITLE Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
JOURNAL Human genome-derived single exon nucleic acid probes useful for
ANALYSIS analysis of gene expression in human bone marrow
PATENT: WO 0157276-A 16039 09-AUG-2001;
Aeomica, Inc. (US)
FEATURES Location/Qualifiers
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Db 34 CTTTGGCACTA 44

RESULT 11
CQ205816
LOCUS
DEFINITION Sequence 8093 from Patent WO0157271.
ACCESSION CQ205816
VERSION CQ205816.1 GI:41191920
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
TITLE Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
JOURNAL Human genome-derived single exon nucleic acid probes useful for
ANALYSIS analysis of gene expression in human breast and Bt 474 cells
PATENT: WO 0157271-A 8093 09-AUG-2001;
Aeomica, Inc. (US)
FEATURES Location/Qualifiers
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Db 34 CTTTGGCACTA 44

RESULT 12
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LOCUS
DEFINITION Sequence 16062 from Patent WO0157273.
ACCESSION CQ229223
VERSION CQ229223
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
TITLE Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
JOURNAL Human genome-derived single exon nucleic acid probes useful for
ANALYSIS analysis of gene expression in human breast and Bt 474 cells
PATENT: WO 0157271-A 8093 09-AUG-2001;
Aeomica, Inc. (US)
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Db 34 CTTTGGCACTA 44
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ACCESSION CQ229223
VERSION CQ229223.1 GI:41212441
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
AUTHORS HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE ANALYSIS OF GENE EXPRESSION IN HUMAN ADULT LIVER<130> PB 0004 WO
3<150> US 60/180,312<151> 04 February 2000 (04.02.00)<150> US
60/207,456<151> 26 May 2000 (26.05.00)<150> US 09/632,366<151> 03
August 2000 (03.08.00)<150> GB 24263.6<151> 03 October 2000
(03.10.00)<150> US 60/236,359<151> 27 September 2000
(27.09.00)<150> US 60/234,687<151> 21 September 2000
(21.09.00)<150> US 09/608,408<151> 30 June 2000 (30.06.00)<170>
Molecular Dynamics Sequence Listing Engine
JOURNAL Patent: WO 0157273-A 16062 09-AUG-2001;
Aeomica, Inc. (US)
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Db 34 CTTTGGCACTA 44

RESULT 13
LOCUS CQ267352
DEFINITION Sequence 15613 from Patent WO0157277.
ACCESSION CQ267352
VERSION CQ267352.1 GI:41239956
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
AUTHORS HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE Analysis of gene expression in human fetal liver
JOURNAL Patent: WO 0157277-A 15613 09-AUG-2001;
Aeomica, Inc. (US)
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Db 34 CTTTGGCACTA 44

ACCESSION CQ229223
VERSION CQ229223.1 GI:41212441
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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REFERENCE Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
AUTHORS HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE ANALYSIS OF GENE EXPRESSION IN HUMAN ADULT LIVER<130> PB 0004 WO
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60/207,456<151> 26 May 2000 (26.05.00)<150> US 09/632,366<151> 03
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(03.10.00)<150> US 60/236,359<151> 27 September 2000
(27.09.00)<150> US 60/234,687<151> 21 September 2000
(21.09.00)<150> US 09/608,408<151> 30 June 2000 (30.06.00)<170>
Molecular Dynamics Sequence Listing Engine
JOURNAL Patent: WO 0157273-A 16062 09-AUG-2001;
Aeomica, Inc. (US)
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Db 34 CTTTGGCACTA 44

RESULT 15
LOCUS CQ341641
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ACCESSION CQ341641
VERSION CQ341641.1 GI:41290712
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
AUTHORS HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE Analysis of gene expression in human brain
JOURNAL Patent: WO 0157275-A 15735 09-AUG-2001;
Aeomica, Inc. (US)
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Best Local Similarity 100.0%; Pred. No. 8.8e+03;
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Db 34 CTTTGGCACTA 44

RESULT 14
LOCUS CQ304373
DEFINITION Sequence 15478 from Patent WO0186003.
ACCESSION CQ304373
VERSION CQ304373.1 GI:41264950
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
AUTHORS HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE Analysis of gene expression in human lung
JOURNAL Patent: WO 0186003-A 15478 15-NOV-2001;
Aeomica, Inc. (US)
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Best Local Similarity 100.0%; Pred. No. 8.8e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CTTTGGCACTA 11
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Db 34 CTTTGGCACTA 44

RESULT 15
LOCUS CQ341641
DEFINITION Sequence 15735 from Patent WO0157275.
ACCESSION CQ341641
VERSION CQ341641.1 GI:41290712
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
AUTHORS HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE Analysis of gene expression in human brain
JOURNAL Patent: WO 0157275-A 15735 09-AUG-2001;
Aeomica, Inc. (US)
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AL163247.2, EVALUE 4.00e-11"
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Query Match 100.0%; Score 11; DB 6; Length 77;
Best Local Similarity 100.0%; Pred. No. 8.8e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 34 CTTTGGCACTA 44
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RESULT 16
AX910296
LOCUS AX910296 100 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 26159 from Patent EP1033401.
ACCESSION AX910296
VERSION AX910296.1 GI:40066376
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE Dumas Milne Edwards, J.B., Duclert, A. and Giordano, J.Y.
AUTHORS Expressed sequence tags and encoded human proteins
TITLE Patent: EP 1033401-A 26159 06-SEP-2000;
JOURNAL Genset (FR)
FEATURES
source Location/Qualifiers
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/db_xref="taxon:9606"
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Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 81 CTTTGGCACTA 91
RESULT 17
BD045829
LOCUS BD045829 100 bp DNA linear PAT 27-AUG-2002
DEFINITION Sequence tag and encoded human protein.
ACCESSION BD045829
VERSION BD045829.1 GI:22587571
KEYWORDS JP 2001269182-A/22075.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 100)
REFERENCE Edwards, J.B.D.M., Duclair, B. and Jordan, J.Y.
AUTHORS Sequence tag and encoded human protein
TITLE Patent: JP 2001269182-A 22075 02-OCT-2001;
JOURNAL GENSET
COMMENT QS Homo sapiens (human)
PN JP 2001269182-A/22075
PD 02-OCT-2001
PF 24-FEB-2000 JP 2000118773
PR 26-FEB-1999 US 60/122487
PI JEAN BAPTISTE DUMAS MILNE EDWARDS, EIMERIC DUCLAIR, JEAN YVES
PC C12N15/09, C07K14/435, C07K16/18, C12N1/15, C12N1/19, C12N1/21, PC
C12N5/10,
PC C12P21/02, C12P21/08, C12Q1/68//G06F17/30, C12N15/00, C12N5/00, PC
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FH Key Location/Qualifiers.
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RESULT 18
AX325267
LOCUS AX325267 121 bp DNA linear PAT 02-SEP-2002
DEFINITION Sequence 1405 from Patent WO0192512.
ACCESSION AX325267
VERSION AX325267.1 GI:18096023
KEYWORDS
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1
REFERENCE Kmiec, E.B., Gamper, H.B., Rice, M.C. and Kim, J.
AUTHORS Targeted chromosomal genomic alterations in plants using modified
TITLE single stranded oligonucleotides
JOURNAL Patent: WO 0192512-A 1405 06-DEC-2001;
UNIVERSITY OF DELAWARE (US)
FEATURES
source Location/Qualifiers
1..121
/organism="Oryza sativa"
/mol_type="unassigned DNA"
/db_xref="taxon:4530"
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Query Match 100.0%; Score 11; DB 6; Length 121;
Best Local Similarity 100.0%; Pred. No. 8.6e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CTTTGGCACTA 11
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Db 23 CTTTGGCACTA 33
RESULT 19
AX325268
LOCUS AX325268 121 bp DNA linear PAT 02-SEP-2002
DEFINITION Sequence 1406 from Patent WO0192512.
ACCESSION AX325268
VERSION AX325268.1 GI:18096024
KEYWORDS
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1
REFERENCE Kmiec, E.B., Gamper, H.B., Rice, M.C. and Kim, J.
AUTHORS Targeted chromosomal genomic alterations in plants using modified
TITLE single stranded oligonucleotides
JOURNAL Patent: WO 0192512-A 1406 06-DEC-2001;
UNIVERSITY OF DELAWARE (US)
FEATURES
source Location/Qualifiers
1..121
/organism="Oryza sativa"
/mol_type="unassigned DNA"
/db_xref="taxon:4530"
ORIGIN
Query Match 100.0%; Score 11; DB 6; Length 121;
Best Local Similarity 100.0%; Pred. No. 8.6e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CTTTGGCACTA 11
|||||
Db 99 CTTTGGCACTA 89

RESULT 20	G00343	129 bp	DNA	linear	STS 28-SEP-1998
LOCUS	G00343				
DEFINITION	BSWS785 Eric D. Green Homo sapiens STS genomic, sequence tagged site.				
ACCESSION	G00343				
VERSION	G00343.1	GI:485201			
KEYWORDS	STS.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS	1 (bases 1 to 129) Bouffard,G.G., Iyer,L.M., Idol,J.R., Braden,V.V., Cunningham,A.F., Weintraub,L.A., Mohr-Tidwell,R.M., Peluso,D.C., Fulton,R.S., Leckie,M.P. and Green,E.D.				
TITLE	A collection of 1814 human chromosome 7-specific STSs				
JOURNAL	Genome Res.	7 (1),	59-64	(1997)	
MEDLINE	97189344				
PUBMED	9037602				
REFERENCE	2 (bases 1 to 129)				
AUTHORS	Green,E.D.				
TITLE	Human chromosome 7 STSs (1997)				
JOURNAL	Unpublished	(1997)			
COMMENT	GDB: GDB:1317228 Contact: Eric D. Green Genome Technology Branch National Human Genome Research Institute/NIH 49 Convent Dr., MSC4431, Bldg. 49, Rm. 2A08, Bethesda, MD 20892 Tel: 3014020201 Fax: 3014024735 Email: egreen@nhgri.nih.gov Primer A: TGCACCTATTCGACATG Primer B: AGCCAGTTTATGTCATAG STS size: 67 PCR Profile: Preoak: 0 degrees C for 0.00 minute(s) Denaturation: 92 degrees C for 1.00 minute(s) Annealing: 60 degrees C for 2.00 minute(s) Polymerization: 72 degrees C for 2.00 minute(s) PCR Cycles: 35 Thermal Cycler: PerkinElmer TC Protocol: Template: 30-100 ng Primer: each 1 uM dNTPs: each 200 uM Taq Polymerase: 0.05 units/ul Total Vol: 5 ul				
Buffer:	MgCl2: 2.5 mM KCl: 50 mM Tris-HCl: 10 mM pH: 8.3				

The sequence for this STS was derived from a single read. For additional information about the NHGRI chromosome 7 mapping project, see <http://www.nhgri.nih.gov/DIR/STB/CHR7>. Also see Genomics 11:548-64 (1991) [NUID=92128937].

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    Location/Qualifiers
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        /organism="Homo sapiens"
        /mol_type="genomic DNA"
        /db_xref="taxon:9606"
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      52..118
        primer_bind
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        complement(101..118)
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Best Local Similarity 100.0%; Pred. No. 8.6e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  CTTTGGCACTA 11
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DB      93  CTTTGGCACTA 103

RESULT 21
BX284306
LOCUS   BX284306                149 bp      DNA          linear      STS 12-JUN-2003
DEFINITION
Arabidopsis thaliana transposon insertion STS SM_3.23750, sequence
tagged site.
ACCESSION
BX284306                BX284306
VERSION
STX: STS, sequence tagged site.
KEYWORDS
SOURCE
ORGANISM
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eustosids II; Brassicales; Brassicaceae; Arabidopsids.

REFERENCE
1
AUTHORS
Clarke,J.H., Bowles,B., Carter,J., Hart,D., McCullagh,B.,
Murphy,G., Langham,S., LeGrys,C., Jones,J.D.G. and Bevan,M.
JOURNAL
Unpublished
REFERENCE
2 (bases 1 to 149)
AUTHORS
Clarke,J.H.
TITLE
Direct Submission
JOURNAL
Submitted (03-MAR-2003) Clarke J.H., John Innes Centre, Colney
Lane, Norwich, NR4 7UJ, UK
COMMENT
AT denotes an activation tag dissociation transposon within a
single line, ET an enhancer trap dissociation transposon, GT a gene
trap dissociation transposon, MT a mis-expression enhancer trap
dissociation transposon, SM a defective suppressor mutator
transposon. _3 denotes a sequence derived from the 3'end of the
transposon, _5 denotes a sequence derived from the 5'end of the
transposon BBRC GARNET, ATIS project
On-line seed stock requests: http://nasc.nott.ac.uk/ NASC stock
code: DEAD.

FEATURES
            Location/Qualifiers
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                 /organism="Arabidopsis thaliana"
                 /mol_type="Genomic DNA"
                 /variety="Columbia-0 NASC stock code N1092"
                 /db_xref="taxon:3702"
                 /clone="AC007505"
                 /note="Derived from superpool 7.17 NASC code N40312"
STX            1..149
               /standard_name="SM_3.23750"

ORIGIN
Query Match          100.0%; Score 11; DB 11; Length 149;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  CTTTGGCACTA 11
      |||||
DB      124 CTTTGGCACTA 134

RESULT 22
CQ659646/c
LOCUS   CQ659646                150 bp      DNA          linear      PAT 03-FEB-2004
DEFINITION
Sequence 4572 from Patent WO02070737.
ACCESSION
CQ659646
VERSION
CQ659646.1 GI:42128603
KEYWORDS
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS
Liew,C.C., Marshall,W.E. and Zhang,H.

```

TITLE Compositions and methods relating to osteoarthritis
JOURNAL Patent: WO 02070737-A 4572 12-SEP-2002;
Chondrogene Inc. (CA)
FEATURES
source
Location/Qualifiers
1. 150
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 100.0%; Score 11; DB 6; Length 150;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CTTTGGCACTA 11
|||||
Db 139 CTTTGGCACTA 129
RESULT 23
CQ058212/c
LOCUS 153 bp DNA linear PAT 19-JAN-2004
DEFINITION Sequence 9032 from Patent WO0157270.
ACCESSION CQ058212
VERSION CQ058212.1 GI:41032718
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
AUTHORS Human genome-derived single exon nucleic acid probes useful for
analysis of gene expression in human breast and hbl 100 cells
TITLE Patent: WO 0157270-A 9032 09-AUG-2001;
JOURNAL Patent: WO 0157270-A 9032 09-AUG-2001;
Aeomica, Inc. (US)
FEATURES
source
Location/Qualifiers
1. 153
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="MAP TO AL035633.15-EXPRESSED IN HBL100, SIGNAL =
2-NT HIT: AF263306.1, EVALUE 4.00e-81-EST HUMAN HIT:
AV746139.1, EVALUE 5.20e-01-SWISSPROT HIT: P98160, EVALUE
3.90e+00"
ORIGIN
Query Match 100.0%; Score 11; DB 6; Length 153;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CTTTGGCACTA 11
|||||
Db 99 CTTTGGCACTA 89
RESULT 24
CQ077548/c
LOCUS 153 bp DNA linear PAT 20-JAN-2004
DEFINITION Sequence 13348 from Patent WO0157278.
ACCESSION CQ077548
VERSION CQ077548.1 GI:41047417
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
AUTHORS Human genome-derived single exon nucleic acid probes useful for
analysis of gene expression in human hela cells or other human
cervical epithelial cells
TITLE Patent: WO 0157278-A 13348 09-AUG-2001;
JOURNAL

FEATURES
source
Location/Qualifiers
Aeomica, Inc. (US)
1. 153
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="MAP TO AL035633.15-EXPRESSED IN HELA, SIGNAL =
2.5-NT HIT: AF263306.1, EVALUE 4.00e-81-EST HUMAN HIT:
AV746139.1, EVALUE 5.20e-01-SWISSPROT HIT: P98160, EVALUE
3.90e+00"
ORIGIN
Query Match 100.0%; Score 11; DB 6; Length 153;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CTTTGGCACTA 11
|||||
Db 99 CTTTGGCACTA 89
RESULT 25
CQ108562/c
LOCUS 153 bp DNA linear PAT 21-JAN-2004
DEFINITION Sequence 17421 from Patent WO0157272.
ACCESSION CQ108562
VERSION CQ108562.1 GI:41077615
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
AUTHORS Human genome-derived single exon nucleic acid probes useful for
analysis of gene expression in human placenta
TITLE Patent: WO 0157272-A 17421 09-AUG-2001;
JOURNAL Patent: WO 0157272-A 17421 09-AUG-2001;
Aeomica, Inc. (US)
FEATURES
source
Location/Qualifiers
1. 153
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/db_xref="taxon:9606"
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AV746139.1, EVALUE 5.20e-01-SWISSPROT HIT: P98160, EVALUE
3.90e+00"
ORIGIN
Query Match 100.0%; Score 11; DB 6; Length 153;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CTTTGGCACTA 11
|||||
Db 99 CTTTGGCACTA 89
RESULT 26
CQ147196/c
LOCUS 153 bp DNA linear PAT 21-JAN-2004
DEFINITION Sequence 17218 from Patent WO0157276.
ACCESSION CQ147196
VERSION CQ147196.1 GI:41154546
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
AUTHORS Human genome-derived single exon nucleic acid probes useful for
analysis of gene expression in human bone marrow
TITLE

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JOURNAL Patent: WO 0157276-A 17218 09-AUG-2001;
FEATURES Location/Qualifiers
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1..153
/organism="Homo sapiens"
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AV746139.1, EVALUE 5.20e-01-SWISSPROT HIT: P98160, EVALUE
3.90e+00"

ORIGIN
Query Match 100.0%; Score 11; DB 6; Length 153;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTGGCACTA 11
|||||
Db 99 CTTTGGCACTA 89

RESULT 27
CQ182574/c Q182574 153 bp DNA linear PAT 21-JAN-2004
LOCUS
DEFINITION Sequence 13970 from Patent WO0157274.
ACCESSION CQ182574
VERSION CQ182574.1 GI:41177360
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
AUTHORS Human genome-derived single exon nucleic acid probes useful for
analysis of gene expression in human heart
TITLE JOURNAL Patent: WO 0157274-A 13970 09-AUG-2001;
FEATURES Location/Qualifiers
source
1..153
/organism="Homo sapiens"
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AV746139.1, EVALUE 5.20e-01-SWISSPROT HIT: P98160, EVALUE
3.90e+00"

ORIGIN
Query Match 100.0%; Score 11; DB 6; Length 153;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTGGCACTA 11
|||||
Db 99 CTTTGGCACTA 89

RESULT 28
CQ206983/c Q206983 153 bp DNA linear PAT 21-JAN-2004
LOCUS
DEFINITION Sequence 9260 from Patent WO0157271.
ACCESSION CQ206983
VERSION CQ206983.1 GI:41193087
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
AUTHORS Human genome-derived single exon nucleic acid probes useful for
analysis of gene expression in human breast and bt 474 cells
TITLE JOURNAL Patent: WO 0157271-A 9260 09-AUG-2001;
FEATURES Location/Qualifiers
source
1..153
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/notice="MAP TO AL035633.15-EXPRESSED IN ADULT LIVER, SIGNAL
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AV746139.1, EVALUE 5.20e-01-SWISSPROT HIT: P98160, EVALUE
3.90e+00"

ORIGIN
Query Match 100.0%; Score 11; DB 6; Length 153;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTGGCACTA 11
|||||
Db 99 CTTTGGCACTA 89

RESULT 29
CQ230434/c Q230434 153 bp DNA linear PAT 21-JAN-2004
LOCUS
DEFINITION Sequence 17273 from Patent WO0157273.
ACCESSION CQ230434
VERSION CQ230434.1 GI:41213652
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
AUTHORS HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
ANALYSIS OF GENE EXPRESSION IN HUMAN ADULT LIVER<130> PB 0004 WO
3<150> US 60/180,312<151> 04 February 2000 (04.02.00)<150> US
60/207,456<151> 26 May 2000 (26.05.00)<150> US 09/632,366<151> 03
August 2000 (03.08.00)<150> GB 24263.6<151> 03 October 2000
(03.10.00)<150> US 60/236,359<151> 27 September 2000
(27.09.00)<150> US 60/234,687<151> 21 September 2000
(21.09.00)<150> US 09/608,408<151> 30 June 2000 (30.06.00)<170>
Molecular Dynamics Sequence Listing Engine
TITLE JOURNAL Patent: WO 0157273-A 17273 09-AUG-2001;
FEATURES Location/Qualifiers
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/db_xref="taxon:9606"
/notice="MAP TO AL035633.15-EXPRESSED IN ADULT LIVER, SIGNAL
= 1.8-NT HIT: AF263306.1, EVALUE 4.00e-81-EST HUMAN HIT:
AV746139.1, EVALUE 5.20e-01-SWISSPROT HIT: P98160, EVALUE
3.90e+00"

ORIGIN
Query Match 100.0%; Score 11; DB 6; Length 153;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTGGCACTA 11
|||||
Db 99 CTTTGGCACTA 89

RESULT 30
CQ268567/c Q268567 153 bp DNA linear PAT 23-JAN-2004
LOCUS
DEFINITION Sequence 16828 from Patent WO0157277.
ACCESSION CQ268567
VERSION CQ268567.1 GI:41241171
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KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
REFERENCE   1
AUTHORS     Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
TITLE       Human genome-derived single exon nucleic acid probes useful for
            analysis of gene expression in human fecal liver
JOURNAL     Patent: WO 0157277-A 16828 09-AUG-2001;
            Aeomica, Inc. (US)
FEATURES    Location/Qualifiers
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            /mol_type="unassigned DNA"
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            /note="MAP TO AL035633.15-EXPRESSED IN PETAL LIVER, SIGNAL
            = 2.4-NT HIT: AF263306.1, EVALUE 4.00e-81-EST HUMAN HIT:
            AV746139.1, EVALUE 5.20e-01-SWISSPROT HIT: P98160, EVALUE
            3.90e+00"

ORIGIN
Query Match      100.0%; Score 11; DB 6; Length 153;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11
   |||||
Db 99 CTTTGGCACTA 89

RESULT 31
CQ305599/c
LOCUS       CQ305599          153 bp    DNA          linear    PAT 23-JAN-2004
DEFINITION Sequence 16704 from Patent WO0186003.
ACCESSION  CQ305599
VERSION    CQ305599.1 GI:41266176
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE   1
AUTHORS     Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
TITLE       Human genome-derived single exon nucleic acid probes useful for
            analysis of gene expression in human lung
JOURNAL     Patent: WO 0186003-A 16704 15-NOV-2001;
            Aeomica, Inc. (US)
FEATURES    Location/Qualifiers
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            1..153
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
            /note="MAP TO AL035633.15-EXPRESSED IN LUNG, SIGNAL =
            2.6-NT HIT: AF263306.1, EVALUE 4.00e-81-EST HUMAN HIT:
            AV746139.1, EVALUE 5.20e-01-SWISSPROT HIT: P98160, EVALUE
            3.90e+00"

ORIGIN
Query Match      100.0%; Score 11; DB 6; Length 153;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11
   |||||
Db 99 CTTTGGCACTA 89

RESULT 32
CQ342787/c
LOCUS       CQ342787          153 bp    DNA          linear    PAT 23-JAN-2004
DEFINITION Sequence 16881 from Patent WO0157275.
ACCESSION  CQ342787

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VERSION      CQ342787.1 GI:41291858
KEYWORDS     .
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
REFERENCE    1
AUTHORS      Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
TITLE        Human genome-derived single exon nucleic acid probes useful for
            analysis of gene expression in human brain
JOURNAL      Patent: WO 0157275-A 16881 09-AUG-2001;
            Aeomica, Inc. (US)
FEATURES     Location/Qualifiers
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            1..153
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            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
            /note="MAP TO AL035633.15-EXPRESSED IN BRAIN, SIGNAL =
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            AV746139.1, EVALUE 5.20e-01-SWISSPROT HIT: P98160, EVALUE
            3.90e+00"

ORIGIN
Query Match      100.0%; Score 11; DB 6; Length 153;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11
   |||||
Db 99 CTTTGGCACTA 89

RESULT 33
ATH553769
LOCUS       ATH553769          198 bp    DNA          linear    PLN 29-MAR-2003
DEFINITION Arabidopsis thaliana T-DNA flanking sequence, left border, clone
            368C09.
ACCESSION  AJ553769
VERSION    AJ553769.1 GI:29370234
KEYWORDS   left border; T-DNA flanking sequence.
SOURCE     Arabidopsis thaliana (thale cress)
ORGANISM   Arabidopsis thaliana
REFERENCE   1
AUTHORS     Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F.,
            Chauvin,S., Bechtold,N., Cruaud,C., Derose,R., Pelletier,G.,
            Lepiniec,L., Caboche,M. and Lecharny,A.
TITLE       T-DNA integration into the Arabidopsis genome depends on sequences
            of pre-insertion sites
JOURNAL     EMBO Rep. 3 (12), 1152-1157 (2002)
MEDLINE    22363535
PUBMED     12446565
REFERENCE   2 (bases 1 to 198)
AUTHORS     Balzergue,S.
TITLE       Direct Submission
JOURNAL     Submitted (21-NOV-2002) Balzergue S., UMRGV, INRA/CNRS, 2 rue
            Gaston Cremieux, 91057 Evry cedex, FRANCE
COMMENT     PCR was performed on DNA from transformants of Arabidopsis thaliana
            plants from INRA (Versailles). The DNA fragment (s) resulting from
            the PCR were directly sequenced from the left or the right border
            to determine the genomic sequence flanking the insertion. T-DNA
            derived sequences were removed. Information to order the
            corresponding mutant line and a link to a database providing a
            graphical display of the insertion site are available at
            http://dbgap.versailles.inra.fr/publiclines/. This sequence has
            been generated in the framework of the French plant genomics
            program 'Genoplante' (http://www.genoplante.com and
            http://genoplante-info.infobiogen.fr/).
            Location/Qualifiers
            1..198
            /organism="Arabidopsis thaliana"

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/mol_type="genomic DNA"
/cultivar="Wassillewskija"
/db_xref="taxon:3702"
/clone="368C09"
/clone.lib="Arabidopsis thaliana T-DNA insertion lines"
misc_feature 1..198
note="T-DNA flanking sequence
left border"

ORIGIN
Query Match 100.0%; Score 11; DB 8; Length 198;
Best Local Similarity 100.0%; Pred. No. 8.4e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11
|||||
Db 33 CTTTGGCACTA 43

RESULT 34
BV201964 201 bp DNA linear STS 10-JUN-2004
LOCUS sqm207837 Human DNA (Sequenom) Homo sapiens STS genomic, sequence
tagged site.
DEFINITION BV201964
ACCESSION BV201964.1 GI:48170922
VERSION BV201964
KEYWORDS STS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 201)
AUTHORS Nelson,R.M., Marnellos,G., Kammerer,S., Hoyal,C.R., Shi,M.M.,
Cantor,C.R. and Braun,A.
TITLE Large-Scale Validation of Single Nucleotide Polymorphisms in Gene
Regions
JOURNAL Genome Res. (2004) In press
COMMENT Contact: Andreas Braun
Pharmaceuticals division
Sequenom, Inc.
3595 John Hopkins Court, San Diego, CA 92121, USA
Tel: 18582029018
Fax: 18582029020
Email: abraun@sequenom.com
Primer A: No primer sequence submitted
Primer B: No primer sequence submitted
STS size: 201.
Location/Qualifiers
source 1..201
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone.lib="Human DNA (Sequenom)"
<1..>201

STS
ORIGIN
Query Match 100.0%; Score 11; DB 11; Length 201;
Best Local Similarity 100.0%; Pred. No. 8.4e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11
|||||
Db 9 CTTTGGCACTA 19

RESULT 35
AX618370/c AX618370 204 bp DNA linear PAT 20-FEB-2003
LOCUS Sequence 1333 from Patent WO2094868.
DEFINITION AX618370
ACCESSION AX618370
VERSION AX618370.1 GI:28448504
KEYWORDS
```

```
Staphylococcus aureus
Staphylococcus aureus
Bacteria; Firmicutes; Bacillales; Staphylococcus.
REFERENCE 1
AUTHORS Maaignani,V.C., Mora,M.C. and Scarselli,M.C.
TITLE Staphylococcus aureus proteins and nucleic acids
JOURNAL Patent: WO 02094868-A 1333 28-NOV-2002;
Chiron Spa (IT)
FEATURES
Location/Qualifiers
source 1..204
/organism="Staphylococcus aureus"
/mol_type="unassigned DNA"
/db_xref="taxon:1280"

ORIGIN
Query Match 100.0%; Score 11; DB 6; Length 204;
Best Local Similarity 100.0%; Pred. No. 8.4e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11
|||||
Db 109 CTTTGGCACTA 99

RESULT 36
AR553184/c AR553184 207 bp DNA linear PAT 08-OCT-2004
LOCUS Sequence 8315 from patent US 6747137.
DEFINITION AR553184
ACCESSION AR553184
VERSION AR553184.1 GI:53946359
KEYWORDS SOURCE
Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 207)
AUTHORS Weinscock,K.G. and Bush,D.
TITLE Nucleic acid sequences relating to Candida albicans for diagnostics
and therapeutics
JOURNAL Patent: US 6747137-A 8315 08-JUN-2004;
FEATURES Location/Qualifiers
source 1..207
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 100.0%; Score 11; DB 6; Length 207;
Best Local Similarity 100.0%; Pred. No. 8.4e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11
|||||
Db 178 CTTTGGCACTA 168

RESULT 37
ATH526781/c ATH526781 226 bp DNA linear PLN 29-MAR-2003
LOCUS Arabidopsis thaliana T-DNA flanking sequence, left border, clone
126D03.
DEFINITION ATH526781
ACCESSION AJ526781.1 GI:26795041
VERSION AJ526781.1
KEYWORDS left border; T-DNA flanking sequence.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE 1
AUTHORS Brunaud,V., Balzerque,S., Dubreucq,B., Aubourg,S., Samson,F.,
Chauvin,S., Bechtold,N., Cruaud,C., Derose,R., Pelletier,G.,
Lepiniec,L., Caboche,M. and Lecharny,A.
TITLE T-DNA integration into the Arabidopsis genome depends on sequences
of pre-insertion sites
```

JOURNAL EMBO Rep. 3 (12), 1152-1157 (2002)
 MEDLINE 22363535
 PUBMED 12446565
 REFERENCE 2 (bases 1 to 226)
 AUTHORS Balzerque, S.
 TITLE Direct Submission
 JOURNAL Submitted (21-NOV-2002) Balzerque S., UMRGV, INRA/CNRS, 2 rue
 Gaston Cremieux, 91057 Evry cedex, FRANCE
 COMMENT PCR was performed on DNA from transformants of Arabidopsis thaliana
 plants from INRA (Versailles). The DNA fragment (g) resulting from
 the PCR were directly sequenced from the left or the right border
 to determine the genomic sequence flanking the insertion. T-DNA
 derived sequences were removed. Information to order the
 corresponding mutant line and a link to a database providing a
 graphical display of the insertion site are available at
<http://dbsgap.versailles.inra.fr/publiclines/>. This sequence has
 been generated in the framework of the French plant genomics
 program 'Genoplante' (<http://www.genoplante.com> and
<http://genoplante-info.infobiogen.fr>).

FEATURES
 source
 1..226
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /cultivar="Wassillewskija"
 /db_xref="taxon:3702"
 /clone="126D03"
 /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
 misc_feature
 1..226
 /note="T-DNA flanking sequence
 left border"

ORIGIN
 Query Match 100.0%; Score 11; DB 8; Length 226;
 Best Local Similarity 100.0%; Pred. No. 8.4e+03;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11
 |||||
 Db 57 CTTTGGCACTA 47

RESULT 38
 BV084044 232 bp DNA linear STS 30-SEP-2003
 LOCUS sc1275_p3 Ky21 Zea mays Ky21 Zea mays STS genomic, sequence tagged
 DEFINITION site.
 ACCESSION BV084044
 VERSION BV084044.1 GI:37055701
 KEYWORDS STS.
 SOURCE Zea mays
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 REFERENCE 1 (bases 1 to 232)
 AUTHORS McMullen, M.D., Vroh Bi, I., Schroeder, S.S. and Gaut, B.S.
 TITLE MPZ-UCI Joint SNP Discovery
 JOURNAL Unpublished (2003)
 COMMENT Contact: Brandon S. Gaut
 Dept. Ecology and Evolutionary Biology
 U.C. Irvine
 321 Steinhaus Hall, Irvine, CA 92697-2525, USA
 Tel: (949) 824-2564
 Fax: (949) 824-2181
 Email: bgaut@uci.edu
 Primer A: ATCTACCAATGCCCTCATATTT
 Primer B: GTTGTAGCAGTACAGCCAGTTCA
 Protocol:
 PCR amplification of genomic DNA
 Template: 50 ng
 Primer: each 0.5 uM
 dNTPs: each 200 uM

Tag Polymerase: RedTaq (Sigma)
 Total Vol: 10 ul
 Amplicon sequencing
 ABI protocol - using d-Rhodamine terminator cycle
 sequencing ready reaction with ampliTaq DNA polymerase FS
 Sequence ran on ABI 3700 sequencer.

Buffer:
 Genomic DNA amplification
 RedTaq (Sigma)
 Sequencing buffer
 d-Rhodamine kit (ABI)

PHRED/PHRAP Quality Scores 40 40 56 71 71 75 80 80 69 65 63 61 53
 57 72 71 71 71 62 61 76 82 85 90 90 78 74 74 72 61 62 59 64 64
 55 56 56 62 61 55 52 57 63 66 55 50 50 50 50 57 61 65 55 56 59
 52 50 50 55 55 59 70 85 81 85 51 40 40 4.

FEATURES
 Location/Qualifiers
 1..232
 /organism="Zea mays"
 /mol_type="genomic DNA"
 /cultivar="Ky21"
 /db_xref="taxon:4577"
 /clone_lib="Zea mays Ky21"
 /dev stage="seedling"
 /note="Organ: leaf; genomic DNA from inbred line"
 <1..232

STS
 ORIGIN
 Query Match 100.0%; Score 11; DB 11; Length 232;
 Best Local Similarity 100.0%; Pred. No. 8.4e+03;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11
 |||||
 Db 53 CTTTGGCACTA 63

RESULT 39
 BX467061 234 bp DNA linear STS 10-JUN-2003
 LOCUS Arabidopsis thaliana transposon insertion STS SM_3.38432, sequence
 DEFINITION tagged site.
 ACCESSION BX467061
 VERSION BX467061.1 GI:30141627
 KEYWORDS STS; STS, sequence tagged site.
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 REFERENCE 1
 AUTHORS Clarke, J.H., Bowles, B., Carter, J., Hart, D., McCullagh, B.,
 Murphy, G., Langham, S., LeGrys, C., Jones, J.D.G. and Bevan, M.
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 234)
 AUTHORS Clarke, J.H.
 TITLE Direct Submission
 JOURNAL Submitted (25-APR-2003) Clarke J.H., John Innes Centre, Colney
 Lane, Norwich, NR4 7UJ, UK
 COMMENT AT denotes an activation tag dissociation transposon within a
 single line, ET an enhancer trap dissociation transposon, Gr a gene
 trap dissociation transposon, MT a mis-expression enhancer trap
 dissociation transposon, SM a defective suppressor mutator
 transposon. _3 denotes a sequence derived from the 3' end of the
 transposon. _5 denotes a sequence derived from the 5' end of the
 transposon. BBSR GARNet, ARIS project
 On-line seed stock requests: <http://nasc.nott.ac.uk/> NASC stock
 code: N125143.

FEATURES
 Location/Qualifiers
 1..234
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"

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/variety="Columbia-0 NASC stock code N1092"
/db_xref="taxon:3702"
/clone="AC007505"
/note="Derived from superpool 16.15 NASC code N40710"
1..234
/standard_name="SM_3.38432"

STIS
ORIGIN
Query Match 100.0%; Score 11; DB 11; Length 234;
Best Local Similarity 100.0%; Pred. No. 8.4e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11
|||||
Db 84 CTTTGGCACTA 94

RESULT 40
BX467053 245 bp DNA linear STS 10-JUN-2003
LOCUS Arabidopsis thaliana transposon insertion STS SM_3.38431, sequence
DEFINITION tagged site.
ACCESSION BX467053
VERSION BX467053.1 GI:30141619
KEYWORDS STS; STS, sequence tagged site.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
1
REFERENCE
AUTHORS Clarke,J.H., Bowles,B., Carter,J., Hart,D., McCullagh,B.,
Murphy,G., Langham,S., LeGrys,C., Jones,J.D.G. and Bevan,M.
JOURNAL Unpublished
REFERENCE
AUTHORS Clarke,J.H.
TITLE Direct Submision
JOURNAL Submitted (25-APR-2003) Clarke J.H., John Innes Centre, Colney
Lane, Norwich, NR4 7UJ, UK
COMMENT AT denotes an activation tag dissociation transposon within a
trap dissociation transposon, Mt a mis-expression enhancer trap
dissociation transposon, SM a defective suppressor mutator
transposon. 3 denotes a sequence derived from the 3'end of the
transposon, 5 denotes a sequence derived from the 5'end of the
transposon. BEBRC GARNET, ATIS project
On-line seed stock requests: http://nasc.nott.ac.uk/ NASC stock
code: N125142.
Location/Qualifiers
1..245
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/variety="Columbia-0 NASC stock code N1092"
/db_xref="taxon:3702"
/clone="AC007505"
/note="Derived from superpool 16.15 NASC code N40710"
1..245
/standard_name="SM_3.38431"

STIS
ORIGIN
Query Match 100.0%; Score 11; DB 11; Length 245;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11
|||||
Db 84 CTTTGGCACTA 94

RESULT 41
CQ450823/c 246 bp DNA linear PAT 30-JAN-2004
LOCUS CQ450823
DEFINITION Sequence 16583 from Patent WO0192523.

```

```

ACCESSION CQ450823
VERSION CQ450823.1 GI:41419642
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE
AUTHORS Shimkets,R.A. and Leach,M.D.
TITLE Human polynucleotides and polypeptides encoded thereby
JOURNAL Patent: WO 0192523-A 16583 06-DEC-2001;
Curagen Corporation (US)
FEATURES
source
1..246
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 100.0%; Score 11; DB 6; Length 246;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11
|||||
Db 24 CTTTGGCACTA 14

RESULT 42
BV084038 250 bp DNA linear STS 30-SEP-2003
LOCUS sc1275_p3 CML333 Zea mays CML333 Zea mays STS genomic, sequence
DEFINITION tagged site.
ACCESSION BV084038
VERSION BV084038.1 GI:37055695
KEYWORDS Zea mays
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE
AUTHORS 1 (bases 1 to 250)
McMullen,M.D., Vroh Bi,I., Schroeder,S.S. and Gaut,B.S.
TITLE MP2-UCI Joint SNP Discovery
JOURNAL Unpublished (2003)
COMMENT
Contact: Brandon S. Gaut
Dept. Ecology and Evolutionary Biology
U.C. Irvine
321 Steinhaus Hall, Irvine, CA 92697-2525, USA
Tel: (949) 824-2564
Fax: (949) 824-2181
Email: bgaut@uci.edu
Primer A: ATCCTACCAATGCCCTCATATTT
Primer B: GTTGTAGCAGTACAGCCAGTTCA
Protocol:
PCR amplification of genomic DNA
Template: 50 ng
Primer: each 0.5 uM
dNTPs: each 200 uM
Tag Polymerase: Redtaq (Sigma)
Total Vol: 10 ul
Amplicon sequencing
ABI protocol - using d-Rhodamine terminator cycle
sequencing ready reaction with amplitaq DNA polymerase FS
Sequence ran on ABI 3700 sequencer.

Buffer:
Genomic DNA amplification
Redtaq (Sigma)
Sequencing buffer
d-Rhodamine kit (ABI)

```

PHRED/PHRAP Quality Scores 40 60 64 58 53 54 49 49 54 53 58 64 53
53 57 59 61 59 73 66 65 62 62 76 69 77 75 78 75 70 64 62 60 71 71
75 75 56 56 56 56 56 39 34 34 34 34 7 7 37 37 39 58 67 64 59
55 61 64 59 59 55 50 52 52 60 59 66 60 64 62 60 64 60 55 59
65 72 80.

FEATURES

source

Location/Qualifiers

1. .250
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="CML333"
/db_xref="taxon:4577"
/clone_lib="Zea mays CML333"
/dev_stage="seedling"
/note="Organ: leaf; genomic DNA from inbred line"
<1..>250

STS

ORIGIN

Query Match 100.0%; Score 11; DB 11; Length 250;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11

Db 71 CTTTGGCACTA 81

RESULT 43

BV084041

LOCUS

DEFINITION BV084041 250 bp DNA linear STS 30-SEP-2003
tagged site.

ACCESSION BV084041

VERSION BV084041.1

KEYWORDS GI:37055698

SOURCE Zea mays

ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 250)

AUTHORS McMullen,M.D., Vroh Bi,I., Schroeder,S.S. and Gaut,B.S.

TITLE MPZ-UCI Joint SNP Discovery

JOURNAL Unpublished (2003)

COMMENT

Contact: Brandon S. Gaut

Dept. Ecology and Evolutionary Biology

U.C. Irvine

321 Steinhaus Hall, Irvine, CA 92697-2525, USA

Tel: (949) 824-2564

Fax: (949) 824-2181

Email: bgaut@uci.edu

Primer A: ATCCTACCAATGCCCTCATATTT

Primer B: GTTGTAGCAGTACAGCCAGTTCA

Protocol:

PCR amplification of genomic DNA

Template: 50 ng

Primer: each 0.5 uM

dNTPs: each 200 uM

Taq Polymerase: RedTaq (Sigma)

Total Vol: 10 ul

Amplicon sequencing

ABI protocol - using d-Rhodamine terminator cycle

sequencing ready reaction with amplitaq DNA polymerase FS

Sequence ran on ABI 3700 sequencer.

Buffer:

Genomic DNA amplification

RedTaq (Sigma)

Sequencing buffer

d-Rhodamine kit (ABI)

PHRED/PHRAP Quality Scores 40 69 69 59 52 49 53 46 44 44 50 56 52
52 56 58 63 60 67 58 57 57 60 53 57 54 52 58 53 56 64 66 65 73

FEATURES

source

Location/Qualifiers

1. .250
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="I114H"
/db_xref="taxon:4577"
/clone_lib="Zea mays I114H"
/dev_stage="seedling"
/note="Organ: leaf; genomic DNA from inbred line"
<1..>250

STS

ORIGIN

Query Match 100.0%; Score 11; DB 11; Length 250;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11

Db 71 CTTTGGCACTA 81

RESULT 44

BV084045

LOCUS

DEFINITION BV084045 250 bp DNA linear STS 30-SEP-2003
tagged site.

ACCESSION BV084045

VERSION BV084045.1

KEYWORDS GI:37055702

SOURCE Zea mays

ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 250)

AUTHORS McMullen,M.D., Vroh Bi,I., Schroeder,S.S. and Gaut,B.S.

TITLE MPZ-UCI Joint SNP Discovery

JOURNAL Unpublished (2003)

COMMENT

Contact: Brandon S. Gaut

Dept. Ecology and Evolutionary Biology

U.C. Irvine

321 Steinhaus Hall, Irvine, CA 92697-2525, USA

Tel: (949) 824-2564

Fax: (949) 824-2181

Email: bgaut@uci.edu

Primer A: ATCCTACCAATGCCCTCATATTT

Primer B: GTTGTAGCAGTACAGCCAGTTCA

Protocol:

PCR amplification of genomic DNA

Template: 50 ng

Primer: each 0.5 uM

dNTPs: each 200 uM

Taq Polymerase: RedTaq (Sigma)

Total Vol: 10 ul

Amplicon sequencing

ABI protocol - using d-Rhodamine terminator cycle

sequencing ready reaction with amplitaq DNA polymerase FS

Sequence ran on ABI 3700 sequencer.

Buffer:

Genomic DNA amplification

RedTaq (Sigma)

Sequencing buffer

d-Rhodamine kit (ABI)

PHRED/PHRAP Quality Scores 40 69 73 61 48 48 39 41 42 47 54 59 52
52 34 34 26 26 26 26 45 51 66 66 75 76 80 69 65 60 55 60 68
75 74 74 56 56 56 56 35 35 35 35 9 9 51 51 45 69 74 72 76
69 68 63 66 68 58 55 55 55 55 71 73 74 66 73 76 55 59 55 60 60

FEATURES

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/mmap="16"
primer_bind 10..159
primer_bind 10..30
primer_bind complement(140..159)
ORIGIN
Query Match 100.0%; Score 11; DB 11; Length 250;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CTTTGGCACTA 11
Db 31 CTTTGGCACTA 41

RESULT 47
LOCUS CQ675738/c 251 bp DNA linear PAT 03-FEB-2004
DEFINITION Sequence 20664 from Patent WO02070737.
ACCESSION CQ675738
VERSION CQ675738.1 GI:42179569
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Liew, C.C., Marshall, W.E. and Zhang, H.
TITLES Compositions and methods relating to osteoarthritis
JOURNAL Patent: WO 02070737-A 20664 12-SEP-2002;
Chondrogene Inc. (CA)
FEATURES
source 1..251
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 100.0%; Score 11; DB 6; Length 251;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CTTTGGCACTA 11
Db 194 CTTTGGCACTA 184

RESULT 48
LOCUS BV084034 251 bp DNA linear STS 30-SEP-2003
DEFINITION sc1275_p3 NC350 Zea mays NC350 Zea mays STS genomic, sequence
tagged site.
ACCESSION BV084034
VERSION BV084034.1 GI:37055691
KEYWORDS STS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE
AUTHORS 1 (bases 1 to 251)
TITLES (bases 1 to 251)
JOURNAL MPZ-UCI Joint SNP Discovery
COMMENT Unpublished (2003)
Contact: Brandon S. Gaut
Dept. Ecology and Evolutionary Biology
U.C. Irvine
321 Steinhaus Hall, Irvine, CA 92697-2525, USA
Tel: (949) 824-2564
Fax: (949) 824-2181
Email: bgaut@uci.edu
Primer A: ATCCTACCAATGCCCTCATATTT
Primer B: GTTGTAGCAGTACAGCCAGTTCA
Protocol:

Primer B: GTTGTAGCAGTACAGCCAGTTCA
Protocol:
PCR amplification of genomic DNA
Template: 50 ng each 0.5 uM
Primer: each 200 uM
dNTPs: each 200 uM
Taq Polymerase: RedTaq (Sigma)
Total Vol: 10 ul
Amplicon sequencing
ABI protocol - using d-Rhodamine terminator cycle
sequencing ready reaction with amplitaq DNA polymerase FS
Sequence ran on ABI 3700 sequencer.

Buffer:
Genomic DNA amplification
RedTaq (Sigma)
Sequencing buffer
d-Rhodamine kit (ABI)

PHRED/PHRAP Quality Scores 40 62 69 56 49 49 49 50 50 55 60 52
49 57 34 34 35 44 44 44 51 56 56 56 51 74 70 71 71 69 71 71
72 73 71 71 73 73 71 73 88 90 85 74 69 75 58 57 57 62 58 54 59 63
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60 60 66 74.
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Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CTTTGGCACTA 11
Db 72 CTTTGGCACTA 82

RESULT 49
LOCUS BV084035 251 bp DNA linear STS 30-SEP-2003
DEFINITION sc1275_p3 Kul3 Zea mays Kul3 Zea mays STS genomic, sequence tagged
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ACCESSION BV084035
VERSION BV084035.1 GI:37055692
KEYWORDS STS.
SOURCE Zea mays
ORGANISM Zea mays
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE
AUTHORS 1 (bases 1 to 251)
TITLES (bases 1 to 251)
JOURNAL MPZ-UCI Joint SNP Discovery
COMMENT Unpublished (2003)
Contact: Brandon S. Gaut
Dept. Ecology and Evolutionary Biology
U.C. Irvine
321 Steinhaus Hall, Irvine, CA 92697-2525, USA
Tel: (949) 824-2564
Fax: (949) 824-2181
Email: bgaut@uci.edu
Primer A: ATCCTACCAATGCCCTCATATTT
Primer B: GTTGTAGCAGTACAGCCAGTTCA
Protocol:

```

```

PCR amplification of genomic DNA
Template:      50 ng
Primer:       each 0.5 uM
dNTPs:        each 200 uM
Taq Polymerase: RedTaq (Sigma)
Total Vol:    10 ul
Amplicon sequencing
ABI protocol - using d-Rhodamine terminator cycle
sequencing ready reaction with ampliTag DNA polymerase FS
Sequence ran on ABI 3700 sequencer.

Buffer:
Genomic DNA amplification
RedTaq (Sigma)
Sequencing buffer
d-Rhodamine kit (ABI)

PHRED/PHRAP Quality Scores 40 55 59 54 49 49 53 53 50 50 55 59 54
54 39 39 25 25 25 51 51 56 71 71 77 73 72 67 70 66 66 71
71 71 71 71 73 81 73 76 66 66 66 66 60 60 60 66 60 66 70
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FEATURES
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RESULT 50
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DEFINITION sc1275_p3 Kull1 Zea mays Kull1 Zea mays STS genomic, sequence
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ACCESSION BV084036
VERSION   BV084036.1 GI:37055693
KEYWORDS STS.
SOURCE    Zea mays
ORGANISM  Zea mays
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE  1 (bases 1 to 251)
AUTHORS   McMullen,M.D., Vroh Bi,I., Schroeder,S.S. and Gaut,B.S.
TITLE     MPZ-UCI Joint SNP Discovery
JOURNAL   Unpublished (2003)
COMMENT   Contact: Brandon S. Gaut
          Dept. Ecology and Evolutionary Biology
          U.C. Irvine
          321 Steinhaus Hall, Irvine, CA 92697-2525, USA
          Tel: (949) 824-2564
          Fax: (949) 824-2181
          Email: bgaut@uci.edu
          Primer A: ATCCTACCAATGCCCTCATATTT
          Primer B: GTTGTAGCAGTACAGCCAGTTCA
          Protocol:
          PCR amplification of genomic DNA
          Template:      50 ng

```

```

Primer:       each 0.5 uM
dNTPs:        each 200 uM
Taq Polymerase: RedTaq (Sigma)
Total Vol:    10 ul
Amplicon sequencing
ABI protocol - using d-Rhodamine terminator cycle
sequencing ready reaction with ampliTag DNA polymerase FS
Sequence ran on ABI 3700 sequencer.

Buffer:
Genomic DNA amplification
RedTaq (Sigma)
Sequencing buffer
d-Rhodamine kit (ABI)

PHRED/PHRAP Quality Scores 40 66 59 60 51 52 41 46 44 52 54 52 47
47 55 66 62 62 64 68 68 78 81 71 71 75 86 74 61 65 60 56 58 63
77 76 76 74 77 76 79 74 82 63 67 67 67 65 72 72 68 68 57 61 63
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FEATURES
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STS
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Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CTTTGGCACTA 11
        |||||
Db      72 CTTTGGCACTA 82

Search completed: March 12, 2005, 10:28:49
Job time : 1462 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 12, 2005, 07:00:47 ; Search time 235 Seconds
(without alignments)
277.094 Million cell updates/sec

Title: US-10-070-588A-112

Perfect score: 11

Sequence: 1 ctttggcacta 11

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 4390206 seqs, 2959870667 residues

Word size : 0

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : N_Geneseq_16Dec04.*

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3: Geneseqn2000s.*

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5: Geneseqn2001bs.*

6: Geneseqn2002as.*

7: Geneseqn2002bs.*

8: Geneseqn2003as.*

9: Geneseqn2003bs.*

10: Geneseqn2003cs.*

11: Geneseqn2003ds.*

12: Geneseqn2004as.*

13: Geneseqn2004bs.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 1	11	100.0	11	AA02843	AA02843 Human pre
C 2	11	100.0	11	AA02842	AA02842 Human pre
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C 4	11	100.0	17	ACD57843	ACD57843 HCV DNAY
C 5	11	100.0	17	ACD57844	ACD57844 HCV DNAY
C 6	11	100.0	17	ACD64826	ACD64826 HCV minus
C 7	11	100.0	17	AD183295	AD183295 HCV DNAY
C 8	11	100.0	17	AD186768	AD186768 HCV DNAY
C 9	11	100.0	17	AD186767	AD186767 HCV DNAY
C 10	11	100.0	17	AD183296	AD183296 HCV DNAY
C 11	11	100.0	18	AAH23171	AAH23171 Nitric ox
C 12	11	100.0	22	AAH85553	AAH85553 PCR prime
C 13	11	100.0	23	AAH24199	AAH24199 PCR prime
C 14	11	100.0	33	AAH76792	AAH76792 Human bro
C 15	11	100.0	47	AAH38062	AAH38062 Maize pro
C 16	11	100.0	77	AA122229	AA122229 Probe #12
C 17	11	100.0	77	ABA67308	ABA67308 Human foe
C 18	11	100.0	77	AA147524	AA147524 Probe #16
C 19	11	100.0	77	ABA49398	ABA49398 Human bre
C 20	11	100.0	77	AAK41482	AAK41482 Human bon

21	11	100.0	77	4	AAK15744	AAK15744 Human bra
22	11	100.0	77	4	ABS41072	ABS41072 Human liv
23	11	100.0	77	5	AAI07928	AAI07928 Probe #79
24	11	100.0	77	6	ABS15487	ABS15487 Human gen
25	11	100.0	100	3	AAK22084	AAK22084 Human sec
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27	11	100.0	121	6	ABK26045	ABK26045 Amino aci
28	11	100.0	121	12	ADN44736	ADN44736 Mutant ce
29	11	100.0	121	12	ADN44737	ADN44737 Mutant ce
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C 31	11	100.0	153	4	ABA68523	ABA68523 Human foe
C 32	11	100.0	153	4	AAI48735	AAI48735 Probe #17
C 33	11	100.0	153	4	ABA50565	ABA50565 Human bre
C 34	11	100.0	153	4	ABA35504	ABA35504 Probe #13
C 35	11	100.0	153	4	AAK42661	AAK42661 Human bon
C 36	11	100.0	153	4	AAK16890	AAK16890 Human bra
C 37	11	100.0	153	4	ABS42283	ABS42283 Human liv
C 38	11	100.0	153	5	AAI09041	AAI09041 Probe #90
C 39	11	100.0	153	6	ABS16713	ABS16713 Human gen
C 40	11	100.0	204	8	ACF72987	ACF72987 Staphyloc
41	11	100.0	213	6	ABS68966	ABS68966 Novel mur
C 42	11	100.0	240	6	ABL71901	ABL71901 Corn tass
43	11	100.0	245	5	ABA11368	ABA11368 Human nar
C 44	11	100.0	246	6	ABN24053	ABN24053 Human ORF
C 45	11	100.0	255	5	AAH81973	AAH81973 Rat diffe
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C 47	11	100.0	273	6	ABQ67322	ABQ67322 Listeria
48	11	100.0	276	3	AAK23036	AAK23036 Human sec
49	11	100.0	284	4	AAI23068	AAI23068 Human bre
C 50	11	100.0	286	4	AA560629	AA560629 Human can
C 51	11	100.0	290	4	AAK58491	AAK58491 Human imm
C 52	11	100.0	293	4	AA560256	AA560256 Human can
53	11	100.0	294	8	ACA37530	ACA37530 Prokaryot
C 54	11	100.0	297	6	ABL85556	ABL85556 Human ova
C 55	11	100.0	301	2	AAQ27769	AAQ27769 Heat-resi
56	11	100.0	303	4	AAH24197	AAH24197 Mouse age
C 57	11	100.0	308	6	ABQ56040	ABQ56040 Human ova
58	11	100.0	309	4	AAI23110	AAI23110 Probe #13
59	11	100.0	309	4	ABA68199	ABA68199 Human foe
60	11	100.0	309	4	AAI48413	AAI48413 Probe #17
61	11	100.0	309	4	ABA50256	ABA50256 Human bre
62	11	100.0	309	4	ABA35210	ABA35210 Probe #13
63	11	100.0	309	4	AAK42333	AAK42333 Human bon
64	11	100.0	309	4	AAK16579	AAK16579 Human bra
65	11	100.0	309	4	ABS41948	ABS41948 Human liv
66	11	100.0	309	5	AAI08760	AAI08760 Probe #87
67	11	100.0	309	6	ABS16392	ABS16392 Human gen
C 68	11	100.0	314	4	AA560943	AA560943 Human can
C 69	11	100.0	321	10	ADF00678	ADF00678 Bacterial
70	11	100.0	325	12	ACH90211	ACH90211 Human gen
C 71	11	100.0	329	4	AAH50678	AAH50678 Human tum
72	11	100.0	332	4	AA524505	AA524505 Human ova
73	11	100.0	333	6	ABN25437	ABN25437 Human ORP
74	11	100.0	341	3	AAK03627	AAK03627 Human sec
75	11	100.0	342	5	AAH83113	AAH83113 Human ova
76	11	100.0	353	3	ADF56998	ADF56998 Urogenita
C 77	11	100.0	355	5	ABV17449	ABV17449 Human pro
C 78	11	100.0	357	10	ABZ40917	ABZ40917 N. gonorr
79	11	100.0	359	4	AAI14206	AAI14206 Human bre
80	11	100.0	360	6	ABN77089	ABN77089 Human ORF
C 81	11	100.0	365	4	AAI14209	AAI14209 Probe #41
C 82	11	100.0	365	4	ABA55935	ABA55935 Human foe
C 83	11	100.0	365	4	AAI35590	AAI35590 Probe #42
C 84	11	100.0	365	4	ABA45437	ABA45437 Human bre
C 85	11	100.0	365	4	ABA25602	ABA25602 Probe #40
C 86	11	100.0	365	4	AAK29630	AAK29630 Human bon
C 87	11	100.0	365	4	AAK04148	AAK04148 Human bra
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C 89	11	100.0	365	5	AAI04045	AAI04045 Probe #40
C 90	11	100.0	365	6	ABS04186	ABS04186 Human gen
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93	11	100.0	376	3	ADF57075	ADF57075 Urogenita

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95	11	100.0	378	ADB09447	Adb09447 Alloiococ	C 168	11	100.0	478	4	ABA64437	ABA64437 Human foe
96	11	100.0	382	AAH35668	Aah35668 Human col	C 169	11	100.0	478	4	AAI44612	AAI44612 Probe #13
97	11	100.0	393	ABL87541	AbI87541 Human ova	C 170	11	100.0	478	4	ABA46574	ABA46574 Human bra
98	11	100.0	396	AAF94839	Aaf94839 Human ova	C 171	11	100.0	478	4	ABA31573	ABA31573 Probe #10
99	11	100.0	396	ABL48789	AbI48789 Ovarian c	C 172	11	100.0	478	4	AAK38623	AAK38623 Human bon
100	11	100.0	396	ABT03106	Abt03106 Human ova	C 173	11	100.0	478	4	AAK12894	AAK12894 Human bra
101	11	100.0	396	ADM10699	Adm10699 Human ova	C 174	11	100.0	478	4	ABS38188	ABS38188 Human liv
102	11	100.0	396	ADJ11029	Adj11029 Represent	C 175	11	100.0	478	5	AAI05149	AAI05149 Probe #51
103	11	100.0	396	ADM43290	Adm43290 Human ova	C 176	11	100.0	478	6	ABS12690	ABS12690 Human gen
104	11	100.0	404	AAK61967	Aak61967 Human inm	C 177	11	100.0	478	9	ACH47793	ACH47793 Human inf
105	11	100.0	412	ACH30318	Ach30318 Human tes	C 178	11	100.0	478	10	ADBE2223	ADBE2223 Arabidops
106	11	100.0	422	ABX35329	Abx35329 Bovine ES	C 179	11	100.0	479	9	ACH35102	ACH35102 Human end
107	11	100.0	423	AAI13892	Aai13892 Probe #38	C 180	11	100.0	479	10	ACD93599	ACD93599 Human col
108	11	100.0	423	ABA55600	AbA55600 Human foe	C 181	11	100.0	481	4	AAI13802	AAI13802 Probe #37
109	11	100.0	423	AAI35254	Aai35254 Probe #39	C 182	11	100.0	481	4	AAI35162	AAI35162 Probe #38
110	11	100.0	423	ABA45119	AbA45119 Human bre	C 183	11	100.0	481	4	ABS28826	ABS28826 Human liv
111	11	100.0	423	ABA25297	AbA25297 Probe #37	C 184	11	100.0	481	5	AAI03676	AAI03676 Probe #36
112	11	100.0	423	AAK29293	Aak29293 Human bon	C 185	11	100.0	484	9	ACH35805	ACH35805 Human end
113	11	100.0	423	AAK03827	Aak03827 Human bra	C 186	11	100.0	486	5	ABV11494	ABV11494 Human pro
114	11	100.0	423	ABS28919	AbS28919 Human liv	C 187	11	100.0	487	4	AAI01690	AAI01690 Human rep
115	11	100.0	423	AAI03756	Aai03756 Probe #37	C 188	11	100.0	489	5	ABV60003	ABV60003 Human pro
116	11	100.0	423	AAO02900	Aao02900 DNA encod	C 189	11	100.0	493	12	ADO55078	ADO55078 Gene #175
117	11	100.0	423	ABS03855	AbS03855 Human gen	C 190	11	100.0	495	4	AAV53839	AAV53839 Helicobac
118	11	100.0	425	ADP95751	Adp95751 Cotton ex	C 191	11	100.0	495	5	ABV56227	ABV56227 Human pro
119	11	100.0	434	ABX53729	Abx53729 Bovine ES	C 192	11	100.0	495	12	ADO34558	ADO34558 Human SLI
120	11	100.0	438	ACI21273	ACI21273 DNA clone	C 193	11	100.0	497	8	ABZ52714	ABZ52714 Aspergill
121	11	100.0	443	ADF57455	AdF57455 Urogenita	C 194	11	100.0	499	8	ABZ52947	ABZ52947 Aspergill
122	11	100.0	444	AAD38058	Aad38058 Maize rib	C 195	11	100.0	502	4	AAI34729	AAI34729 Human mus
123	11	100.0	444	ADO63122	Ado63122 Transcrip	C 196	11	100.0	502	8	ABX57717	ABX57717 cDNA enco
124	11	100.0	445	ABV37976	Abv37976 Human pro	C 197	11	100.0	502	12	ADJ27444	ADJ27444 Human mus
125	11	100.0	446	ABV32639	Abv32639 Human pro	C 198	11	100.0	506	9	ACL21285	ACL21285 DNA clone
126	11	100.0	448	ABL80271	AbI80271 Human ova	C 199	11	100.0	511	3	AAV98705	AAV98705 Human col
127	11	100.0	451	ADR26621	Adr26621 Breast ca	C 200	11	100.0	511	12	ACH67989	ACH67989 Human gen
128	11	100.0	455	ABL63578	AbI63578 Breast ca	C 201	11	100.0	518	10	ADBE1299	ADBE1299 Arabidops
129	11	100.0	456	AAI12991	Aai12991 Probe #29	C 202	11	100.0	519	6	ABV98170	ABV98170 Human pan
130	11	100.0	456	ABA54692	AbA54692 Human foe	C 203	11	100.0	525	5	ABV51300	ABV51300 Human pro
131	11	100.0	456	AAI34348	Aai34348 Probe #30	C 204	11	100.0	525	10	ADD49609	ADD49609 Human lun
132	11	100.0	456	ABA44244	AbA44244 Human bre	C 205	11	100.0	530	11	ADT97846	ADT97846 Colton can
133	11	100.0	456	AAK28424	Aak28424 Human bon	C 206	11	100.0	531	4	AAK71000	AAK71000 Human inm
134	11	100.0	456	AAK02978	Aak02978 Human bra	C 207	11	100.0	531	6	ABL55589	ABL55589 HCV bait
135	11	100.0	456	ABS28020	AbS28020 Human liv	C 208	11	100.0	532	13	ACN61789	ACN61789 Cotton gy
136	11	100.0	456	AAI02909	Aai02909 Probe #29	C 209	11	100.0	550	11	ADT95733	ADT95733 Colton can
137	11	100.0	456	ABV47243	Abv47243 Human pro	C 210	11	100.0	551	2	AZ22865	Az22865 Rice phos
138	11	100.0	456	ABS02932	AbS02932 Human gen	C 211	11	100.0	551	12	ACH76511	ACH76511 Human gen
139	11	100.0	457	AAI02856	Aai02856 Human rep	C 212	11	100.0	552	10	ADH83244	ADH83244 Enterococ
140	11	100.0	457	ACF71181	AcF71181 Photorthab	C 213	11	100.0	554	4	AAH31949	AAH31949 Human olf
141	11	100.0	460	ABX45697	Abx45697 Bovine ES	C 214	11	100.0	556	6	ABT10525	ABT10525 Human bre
142	11	100.0	460	ACN90123	ACN90123 Breast ca	C 215	11	100.0	560	13	ADQ58471	ADQ58471 Novel can
143	11	100.0	462	AAI12348	Aai12348 Probe #22	C 216	11	100.0	561	5	ABV60313	ABV60313 Human pro
144	11	100.0	462	ABA54049	AbA54049 Human foe	C 217	11	100.0	561	6	ABQ57829	ABQ57829 Human col
145	11	100.0	462	AAI33703	Aai33703 Probe #23	C 218	11	100.0	564	4	AAI05701	AAI05701 Human rep
146	11	100.0	462	ABA43598	AbA43598 Human bre	C 219	11	100.0	564	13	ACN60377	ACN60377 Cotton gy
147	11	100.0	462	ABA23801	AbA23801 Probe #22	C 220	11	100.0	565	6	ABK62144	ABK62144 Rat seque
148	11	100.0	462	AAK27766	Aak27766 Human bon	C 221	11	100.0	565	10	ADB55123	ADB55123 Toxicity-
149	11	100.0	462	AAK02322	Aak02322 Human bra	C 222	11	100.0	565	10	ADB49652	ADB49652 Primary r
150	11	100.0	462	ABS27346	AbS27346 Human liv	C 223	11	100.0	565	10	ADBA9652	ADBA9652 Human gen
151	11	100.0	462	AAI02260	Aai02260 Probe #22	C 224	11	100.0	566	2	AAI19858	AAI19858 Human gen
152	11	100.0	462	ABS02218	AbS02218 Human gen	C 225	11	100.0	569	9	ACL21280	ACL21280 DNA clone
153	11	100.0	467	ABL79801	AbI79801 Human ova	C 226	11	100.0	570	9	ACA62943	ACA62943 A. quisequ
154	11	100.0	468	AAI10128	Aai10128 Probe #61	C 227	11	100.0	571	9	ACL21295	ACL21295 DNA clone
155	11	100.0	468	ABA51758	AbA51758 Human foe	C 228	11	100.0	573	3	AAF09475	AAF09475 Fusarium
156	11	100.0	468	AAI31374	Aai31374 Probe #60	C 229	11	100.0	573	12	ADM32020	ADM32020 Vaccinia
157	11	100.0	468	ABA21586	AbA21586 Probe #52	C 230	11	100.0	573	12	ADM32021	ADM32021 Vaccinia
158	11	100.0	468	AAK25504	Aak25504 Human bon	C 231	11	100.0	573	12	ADM32022	ADM32022 Vaccinia
159	11	100.0	468	AAK00065	Aak00065 Human bra	C 232	11	100.0	573	12	ADM32019	ADM32019 Vaccinia
160	11	100.0	468	ABS25072	AbS25072 Human liv	C 233	11	100.0	574	13	ACN60436	ACN60436 Cotton gy
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162	11	100.0	468	ABS00070	AbS00070 Human gen	C 235	11	100.0	575	12	ADJ74919	ADJ74919 Marker ge
163	11	100.0	471	ABT10410	Abt10410 Human bre	C 236	11	100.0	575	12	ADM32031	ADM32031 Vaccinia
164	11	100.0	472	AAI18795	Aai18795 Human bre	C 237	11	100.0	575	12	ADM32025	ADM32025 Vaccinia
165	11	100.0	472	AAI10311	Aai10311 Human bre	C 238	11	100.0	575	12	ADM32026	ADM32026 Vaccinia
166	11	100.0	476	ADG37466	Adg37466 Aspergill	C 239	11	100.0	575	12	ADM32027	ADM32027 Vaccinia

c 240	11	100.0	575	12	ADM32033	Adm32033 Vaccinia	c 313	11	100.0	776	4	AAK62718	AAK62718 Human imm
c 241	11	100.0	575	12	ADM32034	Adm32034 Vaccinia	c 314	11	100.0	787	2	AAV74667	AAV74667 Staphyloc
c 242	11	100.0	575	12	ADM32032	Adm32032 Vaccinia	c 315	11	100.0	806	6	ABL92116	ABL92116 Human Tum
c 243	11	100.0	575	12	ADM32030	Adm32030 Vaccinia	c 316	11	100.0	806	10	ADE96293	ADE96293 Human uri
c 244	11	100.0	576	4	AAI18463	AAI18463 Probe #83	c 317	11	100.0	806	10	ABX72041	ABX72041 DNA encod
c 245	11	100.0	576	4	ABA63468	ABA63468 Human toe	c 318	11	100.0	812	2	AAV84439	AAV84439 Human sec
c 246	11	100.0	576	4	AAI43580	AAI43580 Probe #12	c 319	11	100.0	812	4	ABA83222	ABA83222 Human.sec
c 247	11	100.0	576	4	ABA30666	ABA30666 Probe #91	c 320	11	100.0	812	9	ACH04723	ACH04723 Novel Hum
c 248	11	100.0	576	4	AAK37706	AAK37706 Human bon	c 321	11	100.0	813	9	ACD44533	ACD44533 Human cDN
c 249	11	100.0	576	4	AAK12001	AAK12001 Human bra	c 322	11	100.0	813	4	AAH06511	AAH06511 Human cDN
c 250	11	100.0	576	4	ABS37356	ABS37356 Human liv	c 323	11	100.0	816	12	ADL02353	ADL02353 DNA encod
c 251	11	100.0	576	6	ABS11697	ABS11697 Human gen	c 324	11	100.0	824	6	ABN98948	ABN98948 Arabidops
c 252	11	100.0	577	9	ACL21287	ACL21287 DNA clone	c 325	11	100.0	847	2	AAAT7761	AAAT7761 RIP fusio
c 253	11	100.0	579	3	AAAC56133	AAAC56133 Eucalyptu	c 326	11	100.0	847	2	AAAT79869	AAAT79869 Pro-ribo
c 254	11	100.0	579	12	ADM32024	Adm32024 Vaccinia	c 327	11	100.0	864	3	AAAC39809	AAAC39809 Arabidops
c 255	11	100.0	580	6	ABN62287	ABN62287 Human can	c 328	11	100.0	866	2	AAAX39943	AAAX39943 Gastric c
c 256	11	100.0	584	9	ACL21279	ACL21279 DNA clone	c 329	11	100.0	879	6	ABN66504	ABN66504 Streptoco
c 257	11	100.0	584	9	ACL21284	ACL21284 DNA clone	c 330	11	100.0	880	2	AAV88389	AAV88389 EST clone
c 258	11	100.0	585	11	ADT95500	Adt95500 Colon can	c 331	11	100.0	882	10	ADE96298	ADE96298 Human uri
c 259	11	100.0	585	12	ADM32023	Adm32023 Vaccinia	c 332	11	100.0	891	8	ACA33009	ACA33009 Prokaryot
c 260	11	100.0	588	3	AAAC32679	AAC32679 Arabidops	c 333	11	100.0	892	11	ACN84258	ACN84258 Breast ca
c 261	11	100.0	589	3	ACA48522	ACA48522 Arabidops	c 334	11	100.0	894	4	AAAS53121	AAAS53121 Enterococ
c 262	11	100.0	590	4	AAK11575	AAK11575 Human bra	c 335	11	100.0	909	6	AAAD38056	AAAD38056 Maize pro
c 263	11	100.0	590	4	ABS37016	ABS37016 Human liv	c 336	11	100.0	910	2	AAQS58815	AAQS58815 NANBH vir
c 264	11	100.0	594	12	ADM32029	Adm32029 Vaccinia	c 337	11	100.0	910	12	ADJ81661	ADJ81661 Non-A-non
c 265	11	100.0	595	9	ACL21278	ACL21278 DNA clone	c 338	11	100.0	920	4	AAAS32972	AAAS32972 DNA encod
c 266	11	100.0	597	6	ABQ58934	ABQ58934 Human col	c 339	11	100.0	937	2	AAAT13899	AAAT13899 HCV E2 an
c 267	11	100.0	598	9	ACL21297	ACL21297 DNA clone	c 340	11	100.0	944	2	AAAX78475	AAAX78475 Maize RIP
c 268	11	100.0	600	12	ACH66952	ACH66952 Human gen	c 341	11	100.0	960	5	ADL63592	ADL63592 Human ova
c 269	11	100.0	605	10	ADC56801	ADC56801 Mouse cha	c 342	11	100.0	966	4	AAH78733	AAH78733 Human HSK
c 270	11	100.0	608	9	ACL21303	ACL21303 DNA clone	c 343	11	100.0	966	4	AAAL35410	AAAL35410 Human mus
c 271	11	100.0	611	6	ABQ57631	ABQ57631 Human col	c 344	11	100.0	966	8	ABX58398	ABX58398 cDNA enco
c 272	11	100.0	616	10	ADB57338	ADB57338 Toxicity-	c 345	11	100.0	966	12	ADJ28125	ADJ28125 Human mus
c 273	11	100.0	621	11	ADT95306	Adt95306 Colon can	c 346	11	100.0	969	8	ACA29512	ACA29512 Prokaryot
c 274	11	100.0	623	2	AAAX13322	AAAX13322 Enterococ	c 347	11	100.0	978	2	AAQ20478	AAQ20478 Maize RIP
c 275	11	100.0	623	6	ABS99317	ABS99317 Enterococ	c 348	11	100.0	978	2	AAAT77756	AAAT77756 RIP fusio
c 276	11	100.0	623	8	ACA28837	ACA28837 Prokaryot	c 349	11	100.0	978	2	AAAT79864	AAAT79864 Truncated
c 277	11	100.0	625	9	ACL21293	ACL21293 DNA clone	c 350	11	100.0	984	2	AAAT79863	AAAT79863 Single ch
c 278	11	100.0	625	9	ACL21286	ACL21286 DNA clone	c 351	11	100.0	985	2	AAAT77755	AAAT77755 RIP fusio
c 279	11	100.0	627	6	ABN62314	ABN62314 Human can	c 352	11	100.0	986	2	AAAT77757	AAAT77757 RIP fusio
c 280	11	100.0	629	13	ACN45781	ACN45781 Cotton pr	c 353	11	100.0	986	2	AAAT79865	AAAT79865 Truncated
c 281	11	100.0	634	6	ABN62315	ABN62315 Human can	c 354	11	100.0	987	2	AAQ20479	AAQ20479 Maize RIP
c 282	11	100.0	635	5	ABV55241	ABV55241 Human pro	c 355	11	100.0	987	2	AAAX78467	AAAX78467 Maize KRI
c 283	11	100.0	636	5	AAAS67558	AAAS67558 DNA encod	c 356	11	100.0	993	8	ACA52689	ACA52689 Prokaryot
c 284	11	100.0	636	6	ABK62315	ABK62315 Rat sequ	c 357	11	100.0	1001	4	AAF91445	AAF91445 Haemophil
c 285	11	100.0	636	12	ADP71597	ADP71597 Renal tox	c 358	11	100.0	1001	6	ABK37825	ABK37825 DNA sequ
c 286	11	100.0	641	9	ACL21294	ACL21294 DNA clone	c 359	11	100.0	1002	2	AAAX85552	AAAX85552 Probe der
c 287	11	100.0	643	13	ACN46467	ACN46467 Cotton pr	c 360	11	100.0	1002	2	AAAX85551	AAAX85551 cDNA of a
c 288	11	100.0	648	12	ACH91604	ACH91604 Human gen	c 361	11	100.0	1029	2	AAAT77754	AAAT77754 RIP fusio
c 289	11	100.0	652	3	AAF15615	AAF15615 Human pro	c 362	11	100.0	1032	12	ADL81763	ADL81763 P. aerugi
c 290	11	100.0	652	4	AAF72780	AAF72780 Human pro	c 363	11	100.0	1029	2	AAAT79862	AAAT79862 Maize gin
c 291	11	100.0	654	2	AAH87388	AAH87388 Human sin	c 364	11	100.0	1049	12	ADI34872	ADI34872 Human RAB
c 292	11	100.0	668	4	AAAS56408	AAAS56408 Human cDN	c 365	11	100.0	1050	5	AAAS91757	AAAS91757 DNA encod
c 293	11	100.0	669	11	ACN81228	ACN81228 Breast ca	c 366	11	100.0	1053	2	AAAX78473	AAAX78473 Maize RIP
c 294	11	100.0	677	3	AAA63869	AAA63869 cDNA sequ	c 367	11	100.0	1053	6	ABZ32465	ABZ32465 Candida a
c 295	11	100.0	678	9	ACL21282	ACL21282 DNA clone	c 368	11	100.0	1059	2	AAAX78470	AAAX78470 Maize RIP
c 296	11	100.0	678	10	ADH83245	ADH83245 Enterococ	c 369	11	100.0	1065	12	ADN72332	ADN72332 Thale cre
c 297	11	100.0	697	9	ACL21288	ACL21288 DNA clone	c 370	11	100.0	1071	10	ABX07389	ABX07389 S. pneumo
c 298	11	100.0	722	6	ABT09231	ABT09231 Phase-1 R	c 371	11	100.0	1074	2	AAAT79873	AAAT79873 Maize rib
c 299	11	100.0	722	12	ADH22909	ADH22909 Partial D	c 372	11	100.0	1076	2	AAQ20476	AAQ20476 Maize pro
c 300	11	100.0	741	4	AAAS31370	AAAS31370 Human cDN	c 373	11	100.0	1076	2	AAAT77753	AAAT77753 proRIP co
c 301	11	100.0	741	5	ABA13461	ABA13461 Human ner	c 374	11	100.0	1076	2	AAAT79861	AAAT79861 Maize pro
c 302	11	100.0	741	6	ABQ66694	ABQ66694 Human pol	c 375	11	100.0	1083	10	ADH83222	ADH83222 Enterococ
c 303	11	100.0	741	10	ADC10716	ADC10716 Human cDN	c 376	11	100.0	1083	10	ADCF67543	ADCF67543 Photothab
c 304	11	100.0	750	6	ABK49386	ABK49386 Hepatitis	c 377	11	100.0	1083	13	ADTA43657	ADTA43657 Bacterial
c 305	11	100.0	750	6	AAD38057	AAD38057 Maize pro	c 378	11	100.0	1099	3	AAA96894	AAA96894 Nucleotid
c 306	11	100.0	756	10	ACF67928	ACF67928 Photothab	c 379	11	100.0	1102	2	AAAX85550	AAAX85550 cDNA of a
c 307	11	100.0	759	6	ABQ68270	ABQ68270 Listeria	c 380	11	100.0	1105	2	AAQ20477	AAQ20477 Maize pro
c 308	11	100.0	759	3	ADD33618	ADD33618 Mouse mit	c 381	11	100.0	1105	2	AAAT79872	AAAT79872 Maize pro
c 309	11	100.0	760	3	AAAC36981	AAAC36981 Arabidops	c 382	11	100.0	1111	4	AAAS27054	AAAS27054 cDNA enco
c 310	11	100.0	766	13	ADR64606	ADR64606 Cotton cD	c 383	11	100.0	1111	10	ADB93232	ADB93232 Human cDN
c 311	11	100.0	771	4	AAH07272	AAH07272 Human cDN	c 384	11	100.0	1113	10	ADR91780	ADR91780 Novel S.
c 312	11	100.0	775	10	ADD33621	ADD33621 Mouse mit	c 385	11	100.0	1114	4	AAAS27473	AAAS27473 cDNA enco

C 386	11	100.0	1114	10	ADB93651	Adh93651 Human cDN
C 387	11	100.0	1125	10	ADH83528	Adh83528 Enterococ
C 388	11	100.0	1132	13	AQ87663	Aq87663 Human tum
C 389	11	100.0	1132	13	ACN39543	Acn39543 Tumour-as
C 390	11	100.0	1161	2	AAQ20480	Aaq20480 Maize RIP
C 391	11	100.0	1161	2	AAT77758	Aat77758 RIP fusio
C 392	11	100.0	1161	2	AAT79866	Aat79866 Pro-ribo
C 393	11	100.0	1164	12	ADN74256	Adn74256 Thale cre
C 394	11	100.0	1167	12	ADN04795	Adn04795 Antipsori
C 395	11	100.0	1167	13	ADP55197	Adp55197 Human PRO
C 396	11	100.0	1167	13	ADR66261	Adr66261 Human pro
C 397	11	100.0	1167	13	ADR66603	Adr66603 Human pro
C 398	11	100.0	1167	13	ADR66186	Adr66186 Human pro
C 399	11	100.0	1174	4	AAK74329	Aak74329 Human imm
C 400	11	100.0	1174	4	AAK66156	Aak66156 Human imm
C 401	11	100.0	1174	4	AAK66159	Aak66159 Human imm
C 402	11	100.0	1174	4	AAK74228	Aak74228 Human imm
C 403	11	100.0	1174	4	AAK74327	Aak74327 Human imm
C 404	11	100.0	1174	4	AAK66155	Aak66155 Human imm
C 405	11	100.0	1174	5	ABA18478	Abal8478 Human ner
C 406	11	100.0	1174	5	ABA18480	Abal8480 Human ner
C 407	11	100.0	1174	5	ABA18479	Abal8479 Human ner
C 408	11	100.0	1204	10	ADE96294	Ade96294 Human uri
C 409	11	100.0	1207	2	AAQ40332	Aaq40332 Sequence
C 410	11	100.0	1207	2	AAQ40331	Aaq40331 Sequence
C 411	11	100.0	1216	5	AH76788	Aah76788 Human bro
C 412	11	100.0	1219	2	AAV53637	Aav53637 Contig 26
C 413	11	100.0	1219	2	AAV53352	Aav53352 DNA encod
C 414	11	100.0	1219	2	AAV00904	Aax00904 Human des
C 415	11	100.0	1219	2	AAV82636	Aav82636 Contig 26
C 416	11	100.0	1219	3	AAA14588	Aaa14588 Nucleotid
C 417	11	100.0	1219	3	AAA09447	Aaa09447 Human con
C 418	11	100.0	1219	3	AAH49933	Aah49933 Human del
C 419	11	100.0	1219	6	ABS76707	Abs76707 Human del
C 420	11	100.0	1219	6	ABS71820	Abs71820 Human del
C 421	11	100.0	1226	3	AAAC55011	Aac55011 Arabidops
C 422	11	100.0	1227	3	AAAC32944	Aac32944 Arabidops
C 423	11	100.0	1233	6	ABN98266	Abn98266 Arabidops
C 424	11	100.0	1244	2	AAH78479	Aah78479 Maize RIP
C 425	11	100.0	1245	2	AAQ97306	Aaq97306 Pancreati
C 426	11	100.0	1245	2	AAV40687	Aav40687 Human pan
C 427	11	100.0	1262	12	ADQ23233	Adq23233 Human sof
C 428	11	100.0	1263	10	ADF03464	Adf03464 Bacteri
C 429	11	100.0	1266	12	ADJ10451	Adj10451 DNA of th
C 430	11	100.0	1275	8	ADA70826	Ada70826 Rice gene
C 431	11	100.0	1290	3	AAH48859	Aah48859 Arabidops
C 432	11	100.0	1293	10	ACF68660	Acf68660 Photornab
C 433	11	100.0	1296	2	AAH85549	Aax85549 cDNA of a
C 434	11	100.0	1296	4	ABL11827	Abi11827 Drosophil
C 435	11	100.0	1296	9	ADB07547	Adb07547 Alloiooc
C 436	11	100.0	1299	8	ACA39022	Ac39022 Prokaryot
C 437	11	100.0	1320	8	ACA28053	Ac28053 Prokaryot
C 438	11	100.0	1337	3	AAH48518	Aah48518 Arabidops
C 439	11	100.0	1355	3	AAZ98183	Aaz98183 Human sig
C 440	11	100.0	1357	5	ABV30252	Abv30252 Human pro
C 441	11	100.0	1365	10	ACF04840	Acf04840 Wheat hom
C 442	11	100.0	1375	13	ADR25080	Adr25080 Breast ca
C 443	11	100.0	1389	12	ADL02819	Adl02819 DNA encod
C 444	11	100.0	1390	2	AAH85570	Aax85570 cDNA of a
C 445	11	100.0	1392	8	ACA18507	Ac18507 Prokaryot
C 446	11	100.0	1395	4	AAH52913	Aax52913 Enterococ
C 447	11	100.0	1397	3	AAH41116	Aac41116 Arabidops
C 448	11	100.0	1398	2	AAH74973	Aav74973 Staphyloc
C 449	11	100.0	1401	4	AAH51360	Aas51360 Enterococ
C 450	11	100.0	1422	2	AAQ20481	Aaq20481 Maize RIP
C 451	11	100.0	1422	2	AAH77759	Aat77759 RIP fusio
C 452	11	100.0	1422	2	AAH79867	Aat79867 Pro-ribo
C 453	11	100.0	1431	9	ADA30537	Ada30537 DNA encod
C 454	11	100.0	1434	8	ACA46117	Aca46117 Prokaryot
C 455	11	100.0	1443	6	ABZ78274	Abz78274 A. niger
C 456	11	100.0	1443	6	ABZ78237	Abz78237 A. niger
C 457	11	100.0	1443	6	ABA90327	Ab90327 Human pol
C 458	11	100.0	1458	2	AAQ79936	Aaq79936 Murine Ki
C 459	11	100.0	1510	6	AAH17397	Aas17397 cDNA enco
C 460	11	100.0	1515	8	ACA38885	Ac38885 Prokaryot
C 461	11	100.0	1537	3	AAH36394	Aac36394 Arabidops
C 462	11	100.0	1569	13	ADQ94299	Aq94299 Arabidops
C 463	11	100.0	1575	3	AAH35960	Aac35960 Arabidops
C 464	11	100.0	1587	12	ADL03010	Adl03010 DNA encod
C 465	11	100.0	1596	8	ACA39158	Ac39158 Prokaryot
C 466	11	100.0	1611	12	ADL04211	Adl04211 DNA encod
C 467	11	100.0	1656	13	ACN38176	Acn38176 Tumour-as
C 468	11	100.0	1663	3	AAH78055	Aac78055 Human can
C 469	11	100.0	1683	2	AAQ20482	Aaq20482 Maize RIP
C 470	11	100.0	1683	2	AAT77760	Aat77760 RIP fusio
C 471	11	100.0	1683	2	AAT79868	Aat79868 Pro-ribo
C 472	11	100.0	1690	13	ADR26149	Adr26149 Breast ca
C 473	11	100.0	1695	2	AAT77762	Aat77762 RIP fusio
C 474	11	100.0	1695	2	AAT79870	Aat79870 Pro-ribo
C 475	11	100.0	1696	5	ADM19525	Adm19525 Novel hum
C 476	11	100.0	1698	11	ADM03470	Adm03470 Human cDN
C 477	11	100.0	1706	2	AAQ28232	Aaq28232 DNA encod
C 478	11	100.0	1713	4	AAK90386	Aak90386 Human dig
C 479	11	100.0	1713	4	AAK90385	Aak90385 Human dig
C 480	11	100.0	1713	5	AAH39943	Aas39943 Genomic s
C 481	11	100.0	1713	5	AAH39940	Aas39940 Genomic s
C 482	11	100.0	1713	6	ABK12470	Abk12470 Sperm rec
C 483	11	100.0	1713	9	ADB32900	Adb32900 Human nov
C 484	11	100.0	1713	9	ADB32903	Adb32903 Human nov
C 485	11	100.0	1721	11	ADM03308	Adm03308 Human cDN
C 486	11	100.0	1722	2	AAT77763	Aat77763 RIP fusio
C 487	11	100.0	1722	2	AAT79871	Aat79871 Pro-ribo
C 488	11	100.0	1740	12	ADO55217	Ado55217 Human bla
C 489	11	100.0	1748	2	AAH08944	Aax08944 Fragment
C 490	11	100.0	1752	6	ABZ13769	Abz13769 Arabidops
C 491	11	100.0	1752	6	ABA90328	Ab90328 Human pol
C 492	11	100.0	1752	8	ACF72988	Acf72988 Staphyloc
C 493	11	100.0	1752	13	ACN37607	Acn37607 Tumour-as
C 494	11	100.0	1766	10	ADG32798	Adg32798 Human DNA
C 495	11	100.0	1766	12	ADP03057	Adp03057 Human hou
C 496	11	100.0	1766	13	ADQ84544	Adq84544 Human tum
C 497	11	100.0	1766	13	ACN39866	Acn39866 Tumour-as
C 498	11	100.0	1766	13	ADS88555	Ads88555 Human hou
C 499	11	100.0	1775	13	ADS47680	Ads47680 Bacteri
C 500	11	100.0	1775	13	ADS47681	Ads47681 Bacteri
C 501	11	100.0	1787	8	ACC62281	Acc62281 Human NOV
C 502	11	100.0	1791	3	AAH76102	Aac76102 Human ORF
C 503	11	100.0	1791	6	ABK73785	Abk73785 Bacillus
C 504	11	100.0	1799	2	AAQ97798	Aaq97798 Clone pre
C 505	11	100.0	1808	3	AAH50417	Aac50417 Arabidops
C 506	11	100.0	1810	12	ADQ64635	Adq64635 Novel hum
C 507	11	100.0	1811	3	AAH34909	Aac34909 Arabidops
C 508	11	100.0	1819	12	ADL83303	Adl83303 Human PRO
C 509	11	100.0	1825	4	ABL23579	Ab123579 Drosophil
C 510	11	100.0	1826	2	AAH08945	Aax08945 Fragment
C 511	11	100.0	1826	10	ADB75369	Adb75369 Prostate
C 512	11	100.0	1826	10	ADB31337	Adb31337 Bicalutam
C 513	11	100.0	1826	13	ADN25537	Adn25537 Breast ca
C 514	11	100.0	1826	13	ACN41058	Acn41058 Tumour-as
C 515	11	100.0	1826	13	ADP23323	Adp23323 PRO polyp
C 516	11	100.0	1828	12	ADQ84185	Adq84185 Human tum
C 517	11	100.0	1832	4	AAF27705	Aaf27705 Human tra
C 518	11	100.0	1833	5	ADM19262	Adm19262 Novel hum
C 519	11	100.0	1845	12	ADJ10455	Adj10455 DNA of th
C 520	11	100.0	1850	10	ADL13026	Adl13026 A. gossyp
C 521	11	100.0	1851	4	ABL10591	Ab110591 Drosophil
C 522	11	100.0	1862	4	AAF32779	Aaf32779 Human sec
C 523	11	100.0	1866	5	AAH50309	Aas50309 DNA encod
C 524	11	100.0	1879	4	ABL21007	Ab121007 Drosophil
C 525	11	100.0	1879	5	AAH17209	Aad17209 Drosophil
C 526	11	100.0	1886	6	AAH51671	Aal51671 Signal pe
C 527	11	100.0	1909	4	AAH86368	Aaf86368 Murine Mi
C 528	11	100.0	1922	10	ADC51631	Adc51631 Babesia g
C 529	11	100.0	1926	4	AAH72755	Aaf72755 Human pro
C 530	11	100.0	1926	10	ADF75254	Adf75254 Thale cre
C 531	11	100.0	1934	2	AAT42302	Aat42302 Maize rib

532	11	100.0	1937	12	ADQ97591	Adq97591 Mouse can	c 605	11	100.0	2396	10	ACF58208	Acf58208 B. antrac
533	11	100.0	1938	12	ADJ10453	Adj10453 DNA of th	c 606	11	100.0	2430	4	AAc86015	Aac86015 Wax type
534	11	100.0	1943	5	ADL63188	Adl63188 Human ova	c 607	11	100.0	2455	2	AAv26363	Aav26363 Moraxella
535	11	100.0	1946	4	ABL03079	Ab103079 Drosophil	c 608	11	100.0	2463	12	ADJ40189	Adj40189 Plant cDN
536	11	100.0	1950	6	ABZ78217	Abz78217 A. niger	c 609	11	100.0	2470	10	ADJ40213	Adj40213 Leukaemia
537	11	100.0	1951	2	AAQ94449	Aaq94449 Bacterial	c 610	11	100.0	2483	10	ADJ40213	Adj40213 Leukaemia
538	11	100.0	1951	2	AAQ94507	Aaq94507 Transferr	c 611	11	100.0	2491	6	ABQ60924	Abq60924 Human RNA
539	11	100.0	1951	2	AAZ89171	Aaz89171 H. influe	c 612	11	100.0	2498	4	AAK82449	Aak82449 Human imm
540	11	100.0	1951	2	AAV21443	Aav21443 H. influe	c 613	11	100.0	2505	6	ABK89930	Abk89930 cDNA enco
541	11	100.0	1951	3	AAZ91005	Aaz91005 H. influe	c 614	11	100.0	2507	4	ABL24860	Ab124860 Drosophil
542	11	100.0	1953	10	ADD46838	Add46838 Rat gene	c 615	11	100.0	2517	12	ADJ10457	Adj10457 DNA of th
543	11	100.0	1953	10	ADE56291	Ade56291 Rat gene	c 616	11	100.0	2517	12	ADJ10457	Adj10457 DNA of th
544	11	100.0	1954	2	AAQ94450	Aaq94450 Bacterial	c 617	11	100.0	2520	2	AAQ77884	Aaq77884 Neural th
545	11	100.0	1954	5	AAZ83755	Aaz83755 DNA enco	c 618	11	100.0	2520	2	AAQ77884	Aaq77884 Neural th
546	11	100.0	1955	2	AAZ89172	Aaz89172 H. influe	c 619	11	100.0	2520	2	AAQ77884	Aaq77884 Neural th
547	11	100.0	1955	2	AAZ89172	Aaz89172 H. influe	c 620	11	100.0	2520	2	AAQ77884	Aaq77884 Neural th
548	11	100.0	1955	2	AAZ89172	Aaz89172 H. influe	c 621	11	100.0	2520	2	AAQ77884	Aaq77884 Neural th
549	11	100.0	1955	3	AAZ91006	Aaz91006 H. influe	c 622	11	100.0	2522	4	AAZ31061	Aaz31061 Rat GFRal
550	11	100.0	1974	2	AAQ94448	Aaq94448 Bacterial	c 623	11	100.0	2545	3	AAZ51266	Aaz51266 Human RNA
551	11	100.0	1974	2	AAQ94506	Aaq94506 Transferr	c 624	11	100.0	2554	12	ADM18433	Adm18433 Human chr
552	11	100.0	1974	2	AAZ89170	Aaz89170 H. influe	c 625	11	100.0	2562	3	AAA26725	Aaa26725 Candida a
553	11	100.0	1974	2	AAZ89170	Aaz89170 H. influe	c 626	11	100.0	2562	3	AAA26725	Aaa26725 Candida a
554	11	100.0	1974	3	AAZ91004	Aaz91004 H. influe	c 627	11	100.0	2582	4	AAH18575	Aah18575 Human cDN
555	11	100.0	1993	2	AAQ94447	Aaq94447 Bacterial	c 628	11	100.0	2585	10	ADE96297	Ade96297 Human uri
556	11	100.0	1993	2	AAQ94505	Aaq94505 Transferr	c 629	11	100.0	2595	5	AAH12711	Aah12711 Rat bombe
557	11	100.0	1993	2	AAZ89169	Aaz89169 H. influe	c 630	11	100.0	2598	10	ADC77668	Adc77668 Human 619
558	11	100.0	1993	2	AAZ21441	Aaz21441 H. influe	c 631	11	100.0	2598	13	ADQ89145	Adq89145 Human uro
559	11	100.0	1993	3	AAZ91003	Aaz91003 H. influe	c 632	11	100.0	2620	6	ABQ99343	Abq99343 Human cod
560	11	100.0	2000	6	ABZ16599	Abz16599 Arabidops	c 633	11	100.0	2629	4	AAZ26026	Aaz26026 Human cDN
561	11	100.0	2000	8	ADA73076	Ada73076 Rice gene	c 634	11	100.0	2629	8	ABX73367	Abx73367 Human nov
562	11	100.0	2000	8	ADA71457	Ada71457 Rice gene	c 635	11	100.0	2635	10	ADE40460	Ade40460 Human ser
563	11	100.0	2000	8	ADA71457	Ada71457 Rice gene	c 636	11	100.0	2635	10	ACA56660	Aca56660 Human eig
564	11	100.0	2000	8	ADA71877	Ada71877 Rice gene	c 637	11	100.0	2635	12	ADI56456	Adi56456 Human pol
565	11	100.0	2000	8	ADA73137	Ada73137 Rice gene	c 638	11	100.0	2638	6	ABQ99586	Abq99586 Human cod
566	11	100.0	2000	12	ADJ41213	Adj41213 Plant cDN	c 639	11	100.0	2642	10	ADG32924	Adg32924 Human DNA
567	11	100.0	2007	4	ABL07189	Ab107189 Drosophil	c 640	11	100.0	2664	9	ADA29066	Ada29066 DNA enco
568	11	100.0	2007	12	ADK16488	Adk16488 Nanoarcha	c 641	11	100.0	2700	12	ADP28448	Adp28448 Human sec
569	11	100.0	2055	13	ADP56553	Adp56553 Human PRO	c 642	11	100.0	2700	12	ADP28447	Adp28447 Human sec
570	11	100.0	2058	10	ADL62904	Adl62904 Human apo	c 643	11	100.0	2701	5	AAZ67720	Aaz67720 DNA enco
571	11	100.0	2058	13	ADP24029	Adp24029 PRO poly	c 644	11	100.0	2713	4	AAK85252	Aak85252 Human imm
572	11	100.0	2070	12	ADL16362	Adl16362 PB116 ve	c 645	11	100.0	2722	3	AAZ59922	Aaz59922 Human sec
573	11	100.0	2112	5	AAZ65041	Aaz65041 DNA enco	c 646	11	100.0	2754	3	AAZ45843	Aaz45843 Arabidops
574	11	100.0	2114	2	AAQ51236	Aaq51236 Plant NAD	c 647	11	100.0	2754	6	ABZ13981	Abz13981 Arabidops
575	11	100.0	2120	12	ADP04480	Adp04480 Sea squir	c 648	11	100.0	2754	8	ADA68022	Ada68022 Arabidops
576	11	100.0	2121	10	ADB62617	Adb62617 Human cDN	c 649	11	100.0	2754	12	ADN72372	Adn72372 Thale cre
577	11	100.0	2128	4	ABL24013	Ab124013 Drosophil	c 650	11	100.0	2773	6	ABS51339	Abs51339 cDNA enco
578	11	100.0	2159	5	ABV24585	Abv24585 Human pro	c 651	11	100.0	2785	4	AAH14593	Aah14593 Human cDN
579	11	100.0	2163	4	ABA89338	Ab89338 Escherich	c 652	11	100.0	2790	10	ACF70024	Acf70024 Photornab
580	11	100.0	2169	10	ADB63370	Adb63370 Human cDN	c 653	11	100.0	2803	12	ADI16283	Adi16283 Human nuc
581	11	100.0	2178	12	ADM29100	Adm29100 HCV and h	c 654	11	100.0	2820	11	ADM03100	Adm03100 Human cDN
582	11	100.0	2181	11	ADM03741	Adm03741 Human cDN	c 655	11	100.0	2830	4	AAH17837	Aah17837 Human cDN
583	11	100.0	2187	8	ACA64722	Ac64722 Staphyloc	c 656	11	100.0	2839	4	AAH16448	Aah16448 Human cDN
584	11	100.0	2187	9	ADA30229	Ada30229 DNA enco	c 657	11	100.0	2842	10	ADE96296	Ade96296 Human uri
585	11	100.0	2187	10	ADF43361	Adf43361 Staphyloc	c 658	11	100.0	2853	8	ACA23231	Ac23231 Prokaryot
586	11	100.0	2190	8	ACA46308	Ac46308 Prokaryot	c 659	11	100.0	2856	11	ABD11591	Abd11591 Pseudomon
587	11	100.0	2208	8	ACF72480	Acf72480 Staphyloc	c 660	11	100.0	2892	4	AAK85236	Aak85236 Human imm
588	11	100.0	2211	4	AAZ54911	Aaz54911 Staphyloc	c 661	11	100.0	2892	4	AAK85235	Aak85235 Human imm
589	11	100.0	2274	11	ADM02241	Adm02241 Human cDN	c 662	11	100.0	2897	4	AAH14555	Aah14555 Human cDN
590	11	100.0	2287	11	ADI30779	Adi30779 Human cDN	c 663	11	100.0	2904	3	AAZ46114	Aaz46114 Arabidops
591	11	100.0	2288	10	ADE96295	Ade96295 Human uri	c 664	11	100.0	2938	5	ADL45797	Adl45797 Human ova
592	11	100.0	2292	8	ABZ24969	Abz24969 Zinc fing	c 665	11	100.0	2943	2	AAV40704	Aav40704 Spo-rel c
593	11	100.0	2307	12	ADQ90469	Adq90469 E. faeciu	c 666	11	100.0	2966	10	ADD47288	Add47288 Rat gene
594	11	100.0	2307	12	ADQ64657	Adq64657 Novel hum	c 667	11	100.0	2966	10	ADE58151	Ade58151 Rat gene
595	11	100.0	2337	12	ADL16340	Adl16340 Bacillus	c 668	11	100.0	2976	6	ABN70173	Abn70173 Streptoco
596	11	100.0	2363	10	ADL46352	Adl46352 Human gen	c 669	11	100.0	2979	8	ACA50693	Ac50693 Prokaryot
597	11	100.0	2371	2	AAQ24477	Aaq24477 Heat-resi	c 670	11	100.0	2979	12	ADJ40051	Adj40051 Plant cDN
598	11	100.0	2372	4	ABL21686	Ab121686 Drosophil	c 671	11	100.0	3027	4	AAZ31210	Aaz31210 Human cDN
599	11	100.0	2379	8	ACA37067	Ac37067 Prokaryot	c 672	11	100.0	3027	6	ABQ66534	Abq66534 Human pol
600	11	100.0	2388	2	AAV84554	Aav84554 Human sec	c 673	11	100.0	3027	10	ADC10556	Adc10556 Human cDN
601	11	100.0	2388	4	ABA83337	Ab83337 Human sec	c 674	11	100.0	3035	4	AAH16041	Aah16041 Human cDN
602	11	100.0	2388	9	ACH04838	Ach04838 Novel hum	c 675	11	100.0	3035	10	ADB75284	Adb75284 Prostata
603	11	100.0	2388	9	ACD44648	Ac444648 Human cDN	c 676	11	100.0	3039	11	ACN43859	Acn43859 Human mRN
604	11	100.0	2393	13	ADS50918	Ads50918 Bacterial	c 677	11	100.0	3060	6	ABN59744	Abn59744 Novel hum

678	11	100.0	3070	4	ABL05830	Abi05830 Drosophil	c 751	11	100.0	4328	5	AAS42504	Aas42504 Human cDN
679	11	100.0	3078	8	ADD46798	Add46798 Human gen	c 752	11	100.0	4336	4	ABL11826	Abi11826 Drosophil
680	11	100.0	3088	10	ADS31020	Ads31020 Human gen	c 753	11	100.0	4423	10	AAL50321	Aal50321 Murine iG
c 681	11	100.0	3094	13	ADR08274	Adr08274 Full leng	c 754	11	100.0	4447	3	AAA90951	Aaa90951 B. lactof
c 682	11	100.0	3106	4	AH72702	Aah72702 Human cer	c 755	11	100.0	4447	3	AAA90934	Aaa90934 B. lactof
c 683	11	100.0	3106	5	ADL63236	Adl63236 Human ova	c 756	11	100.0	4447	6	ABL49734	Abi49734 Brevibact
c 684	11	100.0	3106	11	ACN91634	Acn91634 Breast ca	c 757	11	100.0	4447	6	ABL49733	Abi49733 Brevibact
c 685	11	100.0	3134	4	ABL09496	Abi09496 Drosophil	c 758	11	100.0	4447	6	ABL22583	Abi22583 B. lactof
c 686	11	100.0	3135	6	ABQ60937	Abq60937 RAB9-like	c 759	11	100.0	4447	6	AAD22582	Aad22582 B. lactof
c 687	11	100.0	3135	12	ADF43052	Adf43052 Human K1o	c 760	11	100.0	4447	10	ADB66212	Adb66212 B. lactof
c 688	11	100.0	3151	4	AH14644	Aah14644 Human cDN	c 761	11	100.0	4450	8	ABT17806	Abt17806 Aspergill
c 689	11	100.0	3152	12	ADO35874	Ado35874 Novel mou	c 762	11	100.0	4505	5	ABV19620	Abv19620 Aspergill
c 690	11	100.0	3175	6	ABZ35351	Abz35351 Human gen	c 763	11	100.0	4531	5	ABV25119	Abv25119 Human pro
c 691	11	100.0	3287	2	AAK13297	Aax13297 Enterococ	c 764	11	100.0	4580	8	ABX71048	Abx71048 Novel hum
c 692	11	100.0	3287	6	ABE99092	Abse99092 Enterococ	c 765	11	100.0	4659	13	ADR07337	Adr07337 Full leng
c 693	11	100.0	3294	2	AAQ70179	Aaq70179 Sequence	c 766	11	100.0	4661	12	ADN05217	Adn05217 Antipsori
c 694	11	100.0	3355	12	ADG31195	Adg31195 Novel mou	c 767	11	100.0	4682	8	ABX71047	Abx71047 Novel hum
c 695	11	100.0	3398	5	AAS73705	Aas73705 DNA encod	c 768	11	100.0	4699	2	AAQ94442	Aaq94442 Bacteri
c 696	11	100.0	3460	2	AAV39131	Aav39131 Polypepti	c 769	11	100.0	4699	2	AAQ94442	Aaq94442 Bacteri
c 697	11	100.0	3460	4	AH233959	Aah233959 Human K1o	c 770	11	100.0	4699	2	AAZ49500	Aaz49500 Transferr
c 698	11	100.0	3471	4	ABL22276	Abi22276 Drosophil	c 771	11	100.0	4699	2	AAZ89156	Aaz89156 H. influe
c 699	11	100.0	3495	4	AAS06755	Aas06755 Polynucle	c 772	11	100.0	4699	2	AAV21428	Aav21428 H. influe
c 700	11	100.0	3498	8	ACA44451	Aca44451 Prokaryot	c 773	11	100.0	4821	2	AAZ90998	Aaz90998 H. influe
c 701	11	100.0	3506	6	AAI64198	Aai64198 Rat CRF2a	c 774	11	100.0	4920	6	ABQ70975	Abq70975 Listeria
c 702	11	100.0	3506	12	ADQ62971	Adq62971 Novel hum	c 775	11	100.0	4924	10	ADC30190	Adc30190 Human nov
c 703	11	100.0	3522	10	ADF03508	Adf03508 Bacteri	c 776	11	100.0	5002	13	ADT05461	Adt05461 Haemophil
c 704	11	100.0	3540	13	ADR08224	Adr08224 Full leng	c 777	11	100.0	5009	2	AAQ94444	Aaq94444 Bacteri
c 705	11	100.0	3570	10	ADC35141	Adc35141 Human bre	c 778	11	100.0	5009	2	AAZ49502	Aaz49502 Transferr
c 706	11	100.0	3585	3	AAA35157	Aaa35157 Human ade	c 779	11	100.0	5009	2	AAZ89158	Aaz89158 H. influe
c 707	11	100.0	3585	3	AAF21279	Aaf21279 Human low	c 780	11	100.0	5009	2	AAV21430	Aav21430 H. influe
c 708	11	100.0	3585	6	ABA94920	Abas94920 Human ecN	c 781	11	100.0	5009	3	AAZ91000	Aaz91000 H. influe
c 709	11	100.0	3585	10	ABZ96973	Abz96973 Human nuc	c 782	11	100.0	5011	10	ADD31993	Add31993 Rat corti
c 710	11	100.0	3585	11	ABD20822	Abd20822 Human pul	c 783	11	100.0	5033	2	AAQ94443	Aaq94443 Bacteri
c 711	11	100.0	3586	4	ABH23153	Abh23153 Nitric ox	c 784	11	100.0	5033	2	AAZ49501	Aaz49501 Transferr
c 712	11	100.0	3631	12	ADL72876	Adl72876 Anthrax v	c 785	11	100.0	5033	2	AAZ89157	Aaz89157 H. influe
c 713	11	100.0	3738	4	ABL01852	Abi01852 Drosophil	c 786	11	100.0	5033	2	AAV21429	Aav21429 H. influe
c 714	11	100.0	3748	12	ADQ22398	Adq22398 Human sof	c 787	11	100.0	5033	3	AAZ90999	Aaz90999 H. influe
c 715	11	100.0	3776	12	ADO36012	Ado36012 Novel mou	c 788	11	100.0	5070	4	ABL18819	Abi18819 Drosophil
c 716	11	100.0	3786	12	ADI34873	Adi34873 Human RAB	c 789	11	100.0	5099	2	AAQ94445	Aaq94445 Bacteri
c 717	11	100.0	3872	2	AAK39630	Aax39630 Breast ca	c 790	11	100.0	5099	2	AAZ49503	Aaz49503 Transferr
c 718	11	100.0	3874	4	AAK71182	Aak71182 Human imm	c 791	11	100.0	5099	2	AAZ89159	Aaz89159 H. influe
c 719	11	100.0	3945	12	ADF72084	Adf72084 Mouse KPC	c 792	11	100.0	5099	2	AAV21431	Aav21431 H. influe
c 720	11	100.0	3964	4	ABL10590	Abi10590 Drosophil	c 793	11	100.0	5099	3	AAZ91001	Aaz91001 H. influe
c 721	11	100.0	3988	5	ABR17723	Abra17723 Human ner	c 794	11	100.0	5112	5	AAH81790	Aah81790 Human dif
c 722	11	100.0	4029	6	ABL69187	Abi69187 Prostata	c 795	11	100.0	5125	2	AAQ47196	Aaq47196 Plasmid p
c 723	11	100.0	4029	6	ABL69745	Abi69745 Prostata	c 796	11	100.0	5144	2	AAQ94446	Aaq94446 Bacteri
c 724	11	100.0	4029	6	ABN95785	Abn95785 Gene #228	c 797	11	100.0	5144	2	AAZ49504	Aaz49504 Transferr
c 725	11	100.0	4035	8	ABX34739	Abx34739 Human mdd	c 798	11	100.0	5144	2	AAZ89168	Aaz89168 H. influe
c 726	11	100.0	4044	2	AAQ85096	Aaq85096 Region up	c 799	11	100.0	5144	2	AAV21440	Aav21440 H. influe
c 727	11	100.0	4044	2	AAZ70214	Aaz70214 S. cyphim	c 800	11	100.0	5144	3	AAZ91002	Aaz91002 H. influe
c 728	11	100.0	4045	2	AAK37251	Aax37251 Human 3-O	c 801	11	100.0	5224	4	ABL25720	Abi25720 Drosophil
c 729	11	100.0	4054	4	ABL23578	Abi23578 Drosophil	c 802	11	100.0	5323	2	AAQ47195	Aaq47195 Plasmid p
c 730	11	100.0	4058	4	ABL03757	Abi03757 Drosophil	c 803	11	100.0	5379	8	ABT19761	Abt19761 Aspergill
c 731	11	100.0	4089	10	ADD14759	Add14759 Human src	c 804	11	100.0	5397	8	ABL29757	Abi29757 Drosophil
c 732	11	100.0	4089	10	ADF81641	Adf81641 Leukaemia	c 805	11	100.0	5402	5	AAZ93666	Aaz93666 DNA encod
c 733	11	100.0	4089	13	ADR52786	Adr52786 Drug ther	c 806	11	100.0	5402	6	AAK83447	Aak83447 Human cDN
c 734	11	100.0	4119	4	AAI06664	Aai06664 Human rep	c 807	11	100.0	5402	8	ACC43649	Acc43649 Nucleotid
c 735	11	100.0	4119	4	AAH08003	Aah08003 Human ova	c 808	11	100.0	5402	8	AAZ50462	Aaz50462 KIAA0317
c 736	11	100.0	4132	6	ADP30558	Adp30558 Human kin	c 809	11	100.0	5402	10	ADF59746	Adf59746 Human con
c 737	11	100.0	4146	13	ADR14140	Adr14140 Human NF-	c 810	11	100.0	5403	12	ADO00893	Ado00893 Human hom
c 738	11	100.0	4202	5	ABR19239	Abra19239 Human ner	c 811	11	100.0	5403	12	ADO07699	Ado07699 Human pol
c 739	11	100.0	4214	4	ABL20859	Abi20859 Drosophil	c 812	11	100.0	5458	13	ADP54222	Adp54222 Human PRO
c 740	11	100.0	4214	5	ABV24766	Abv24766 Human pro	c 813	11	100.0	5475	10	ADF00552	Adf00552 Bacteri
c 741	11	100.0	4236	4	ABL07188	Abi07188 Drosophil	c 814	11	100.0	5513	6	ABN87479	Abn87479 Human dev
c 742	11	100.0	4254	5	ABX71276	Abx71276 Human bra	c 815	11	100.0	5533	12	ADO19175	Ado19175 Human PRO
c 743	11	100.0	4254	12	ADN05923	Adn05923 Antipsori	c 816	11	100.0	5544	2	AAV74421	Aav74421 Staphyloc
c 744	11	100.0	4259	4	ABL03078	Abi03078 Drosophil	c 817	11	100.0	5580	4	ABL12322	Abi12322 Drosophil
c 745	11	100.0	4290	10	ADF90750	Adf90750 Human hep	c 818	11	100.0	5637	13	ACN40745	Acn40745 Tumour-as
c 746	11	100.0	4292	10	ADF74205	Adf74205 Human nov	c 819	11	100.0	5640	13	ADP54397	Adp54397 Human PRO
c 747	11	100.0	4298	3	AZ48248	Aaz48248 Human oxi	c 820	11	100.0	5668	13	ADQ82885	Adq82885 Human KIA
c 748	11	100.0	4298	10	ADJ56287	Adj56287 Fruit fly	c 821	11	100.0	5760	8	ABX63067	Abx63067 Human cDN
c 749	11	100.0	4305	11	ADM86782	Adm86782 Human cDN	c 822	11	100.0	5762	6	AAZ94920	Aaz94920 Human DNA
c 750	11	100.0	4307	3	AAZ86947	Aaz86947 Inositolp	c 823	11	100.0	5762	6	ABS62765	Abs62765 Prostate

824	11	100.0	5816	6	ABQ61202	Abq61202 Human pro	897	11	100.0	9587	13	ADR82189	Adr82189 Hepatitis
825	11	100.0	5832	6	ABQ71069	Abq71069 listeria	898	11	100.0	9595	2	AAX24843	Aax24843 Infectiou
826	11	100.0	5918	6	ABL61773	Abi61773 Colon ade	899	11	100.0	9595	2	AAX23492	Aax23492 Infectiou
827	11	100.0	5918	6	ABN95264	Abn95264 Gene #176	900	11	100.0	9595	4	AAC86939	Aac86939 Nucleotid
828	11	100.0	5931	8	ACD05847	Acd05847 Novel hum	901	11	100.0	9595	12	ADO36222	Ado36222 Hepatitis
829	11	100.0	5961	4	AAI06666	Aai06666 Human rep	902	11	100.0	9595	12	ADO79396	Ado79396 Hepatitis
830	11	100.0	5961	4	ABA08005	Abao8005 Human ova	903	11	100.0	9599	2	AAX24833	Aax24833 Infectiou
C 831	11	100.0	6001	12	ADM47847	Adm47847 Polynucle	904	11	100.0	9599	2	AAX24832	Aax24832 Infectiou
C 832	11	100.0	6057	4	ABL06146	Abi06146 Drosophil	905	11	100.0	9599	2	AAX24832	Aax24832 Infectiou
C 833	11	100.0	6072	4	ABL13102	Abi13102 Drosophil	906	11	100.0	9599	4	AAC86938	Aac86938 Nucleotid
C 834	11	100.0	6156	2	AAV03517	Aav03517 Human tra	907	11	100.0	9599	12	ADJ56743	Adj56743 Hepatitis
C 835	11	100.0	6156	6	ABR98056	Abk98056 DNA encod	908	11	100.0	9599	12	ADJ64255	Adj64255 Hepatitis
C 836	11	100.0	6156	6	ABR98056	Abk98056 DNA encod	909	11	100.0	9605	6	ABR91431	Abk91431 Hepatitis
C 837	11	100.0	6156	8	ABZ71960	Abz71960 Human cdn	910	11	100.0	9605	6	ABR91431	Abk91431 Hepatitis
C 838	11	100.0	6156	12	ADQ95897	Adq95897 T cell ac	911	11	100.0	9605	6	ABR91429	Abk91429 Hepatitis
C 839	11	100.0	6156	13	ADR25673	Adr25673 Breast ca	912	11	100.0	9605	6	ABR91432	Abk91432 Hepatitis
C 840	11	100.0	6314	10	ADL16199	Adl16199 Rat prote	913	11	100.0	9605	6	ABR91411	Abk91411 Hepatitis
C 841	11	100.0	6314	13	ADQ87404	Adq87404 Human tum	914	11	100.0	9605	6	ABR91430	Abk91430 Hepatitis
C 842	11	100.0	6349	4	ABU20858	Abi20858 Drosophil	915	11	100.0	9605	6	ABR91428	Abk91428 Hepatitis
C 843	11	100.0	6402	12	ADQ24795	Adq24795 Human sof	916	11	100.0	9605	6	ABR91425	Abk91425 Hepatitis
C 844	11	100.0	6417	12	ADN73990	Adn73990 Thale cre	917	11	100.0	9605	6	ABR91426	Abk91426 Hepatitis
C 845	11	100.0	6566	10	ADN09723	Adn09723 Novel DNA	918	11	100.0	9605	6	ABR91433	Abk91433 Hepatitis
C 846	11	100.0	6746	4	ABL03756	Abi03756 Drosophil	919	11	100.0	9605	6	ADJ25332	Adj25332 Hepatitis
C 847	11	100.0	6807	13	ADR88342	Adr88342 Aspergill	920	11	100.0	9608	6	ABR91427	Abk91427 Hepatitis
C 848	11	100.0	7029	4	ABL29756	Abi29756 Drosophil	921	11	100.0	9622	10	AAI54424	Aai54424 Hepatitis
C 849	11	100.0	7106	2	AAQ47193	Aaq47193 Plasmid p	922	11	100.0	9646	6	ABK87285	Abk87285 CDNA enco
C 850	11	100.0	7106	2	AAQ97494	Aaq97494 pHCV167 s	923	11	100.0	9646	6	ABK87285	Abk87285 CDNA enco
C 851	11	100.0	7178	12	ADL72979	Adl72979 Hepatitis	924	11	100.0	9646	8	ACA62466	ACA62466 HCV H77 C
C 852	11	100.0	7298	2	AAQ47192	Aaq47192 Plasmid p	C 925	11	100.0	9652	4	ABU18818	Abi18818 Drosophil
C 853	11	100.0	7298	8	ADL41556	Adl41556 Human sec	926	11	100.0	9734	13	ACN41639	Acn41639 Human dia
C 854	11	100.0	7328	10	ADJ38117	Adj38117 CDNA clon	927	11	100.0	9824	6	ABK51688	Abk51688 Human nuc
C 855	11	100.0	7328	10	ADA57687	Ada57687 BAC fragm	928	11	100.0	9824	9	ADB84030	Adb84030 Human NUR
C 856	11	100.0	7347	13	ADT05467	Adt05467 Haemophil	929	11	100.0	9824	9	ADB83988	Adb83988 Human NUR
C 857	11	100.0	7551	12	ADL72981	Adl72981 Hepatitis	930	11	100.0	9872	4	ABK65239	Abk65239 Human imm
C 858	11	100.0	7530	13	ADR84221	Adr84221 Aspergill	C 931	11	100.0	9872	8	ABZ73976	Abz73976 Secreted
C 859	11	100.0	7715	4	ABL21006	Abi21006 Drosophil	C 932	11	100.0	9872	10	ABT16916	Abt16916 Human sec
C 860	11	100.0	7754	12	ADL72977	Adl72977 Hepatitis	C 933	11	100.0	9872	10	ABZ67557	Abz67557 Human sec
C 861	11	100.0	7943	4	ABK83418	Abk83418 Human imm	934	11	100.0	9878	8	AAK65238	AAk65238 Human imm
C 862	11	100.0	8454	4	ABL24012	Abi24012 Drosophil	C 935	11	100.0	9878	8	ABZ73977	Abz73977 Secreted
C 863	11	100.0	8460	12	ADN11771	Adn11771 Hepatitis	C 936	11	100.0	9878	10	ABT16917	Abt16917 Human sec
C 864	11	100.0	8500	6	ABA93871	Abg93871 E. Coli/c	C 937	11	100.0	9878	10	ABZ67558	Abz67558 Human sec
C 865	11	100.0	8688	3	AAQ24748	Aaq24748 Arabidops	938	11	100.0	10061	13	ACN41638	Acn41638 Human dia
C 866	11	100.0	8688	6	ABZ13943	Abz13943 Arabidops	C 939	11	100.0	10231	5	ABA20864	AbA20864 Human ner
C 867	11	100.0	8730	4	AAK78558	AAk78558 Human imm	C 940	11	100.0	10231	8	ADA15555	Ada15555 Human sec
C 868	11	100.0	8730	4	AAK84610	AAk84610 Human imm	C 941	11	100.0	10231	10	ADD38116	Add38116 CDNA clon
C 869	11	100.0	8810	10	ABZ79879	Abz79879 Human nuc	C 942	11	100.0	10231	10	ADA57686	Ada57686 BAC fragm
C 870	11	100.0	9035	6	ABR89430	AbR89430 Human tum	943	11	100.0	10256	10	ADJ63706	Adj63706 Human gen
C 871	11	100.0	9229	8	ABX34821	Abx34821 Human mdd	944	11	100.0	10256	10	ADJ63702	Adj63702 Human gen
C 872	11	100.0	9365	6	AAQ25518	Aaq25518 Hepatitis	945	11	100.0	10256	10	ADJ63714	Adj63714 Human gen
C 873	11	100.0	9370	2	AAQ75165	Aaq75165 AF-4 tran	946	11	100.0	10256	10	ADJ63710	Adj63710 Human gen
C 874	11	100.0	9390	6	ABK83836	Abk83836 Human cdn	947	11	100.0	10803	10	ADD67945	Add67945 Modified
C 875	11	100.0	9390	9	ACF04208	Act04208 Human AF4	948	11	100.0	10803	10	ABX10617	Abx10617 MKO-2 nuc
C 876	11	100.0	9390	9	ACF04206	Act04206 Human AF4	949	11	100.0	10883	9	ADB84042	Adb84042 Human NUR
C 877	11	100.0	9390	10	ADB75439	Adb75439 Prostate	C 950	11	100.0	11042	4	ABL17026	AbL17026 Drosophil
C 878	11	100.0	9390	10	ADK67001	Adk67001 Gene #91	951	11	100.0	11062	6	AAA98965	Aaa98965 Hepatitis
C 879	11	100.0	9390	12	ADQ87230	Adq87230 Human tum	952	11	100.0	11076	3	AAA98965	Aaa98965 Hepatitis
C 880	11	100.0	9390	13	ADR25359	Adr25359 Breast ca	953	11	100.0	11570	3	AAA95905	Aaa95905 Human KIX
C 881	11	100.0	9390	13	ADR66749	Adr66749 Human pro	954	11	100.0	11570	12	ADK52482	Adk52482 Human kal
C 882	11	100.0	9390	13	ADR665817	Adr665817 Human pro	955	11	100.0	11570	13	ADR72623	Adr72623 Human ren
C 883	11	100.0	9391	2	AAQ75164	Aaq75164 AF-4 tran	956	11	100.0	11570	13	ADR72875	Adr72875 Human ova
C 884	11	100.0	9401	2	AAQ411882	Aaq411882 Hepatitis	957	11	100.0	11674	3	AAZ36210	Aaz36210 Nucleotid
C 885	11	100.0	9402	2	AAQ411345	Aaq411345 Human hep	958	11	100.0	12119	4	AAK86936	Aak86936 Nucleotid
C 886	11	100.0	9405	2	AAQ40426	Aaq40426 Full-leng	959	11	100.0	12277	8	ABZ223912	Abz223912 Human 30S
C 887	11	100.0	9416	2	AAQ22871	Aaq22871 NANBV Hut	C 960	11	100.0	12413	4	ABU17040	AbU17040 Drosophil
C 888	11	100.0	9416	2	AAQ22871	Aaq22871 NANBV Hut	961	11	100.0	12744	6	ABS78893	AbS78893 E. coli C
C 889	11	100.0	9416	6	ABK87300	Abk87300 cDNA enco	962	11	100.0	12744	10	ADH80460	Adh80460 Escherich
C 890	11	100.0	9416	6	ABK87300	Abk87300 cDNA enco	C 963	11	100.0	12822	4	ABL17012	AbL17012 Drosophil
C 891	11	100.0	9416	8	ACA62483	ACA62483 HCV-H CDN	C 964	11	100.0	12822	4	ABL02550	AbL02550 Drosophil
C 892	11	100.0	9416	10	AAQ60865	Aaq60865 Hepatitis	C 965	11	100.0	12980	2	AAV59364	Aav59364 Hepatitis
C 893	11	100.0	9518	5	AAQ03778	Aaq03778 Hepatitis	966	11	100.0	12980	6	ACA62469	ACA62469 DNA encod
C 894	11	100.0	9518	5	AAQ03808	Aaq03808 Hepatitis	967	11	100.0	12980	8	ACA62469	ACA62469 DNA encod
C 895	11	100.0	9546	5	ABA19240	AbA19240 Human ner	968	11	100.0	13198	3	AAZ36211	Aaz36211 Nucleotid
C 896	11	100.0	9554	5	ABA19241	AbA19241 Human ner	969	11	100.0	13860	8	ACA44867	ACA44867 Prokaryot

c 970 11 100.0 13865 2 AAX13137
 c 971 11 100.0 13865 6 AAS98932
 c 972 11 100.0 14105 4 ABL29585
 c 973 11 100.0 14707 6 AAL53529
 c 974 11 100.0 15188 4 ABL25090
 c 975 11 100.0 15565 4 AAK80612
 c 976 11 100.0 15613 4 AAL37160
 c 977 11 100.0 15613 8 ABX60148
 c 978 11 100.0 15613 12 ADJ30898
 c 979 11 100.0 16256 10 ADC86818
 c 980 11 100.0 16222 3 AAZ36212
 c 981 11 100.0 16738 4 AAK70864
 c 982 11 100.0 17072 12 ADQ18719
 c 983 11 100.0 17212 4 ABL11550
 c 984 11 100.0 17269 4 ABL29584
 c 985 11 100.0 18564 4 AAK65368
 c 986 11 100.0 18564 8 ABZ74461
 c 987 11 100.0 18564 8 ADA98881
 c 988 11 100.0 19332 2 AAT46159
 c 989 11 100.0 21045 4 AAS26721
 c 990 11 100.0 21045 8 ABX74070
 c 991 11 100.0 21295 10 ADE54120
 c 992 11 100.0 22109 13 ABD33209
 c 993 11 100.0 22419 11 ACN44908
 c 994 11 100.0 22874 4 ABL04654
 c 995 11 100.0 23852 12 ADQ97840
 c 996 11 100.0 25032 9 ADA02495
 c 997 11 100.0 25032 10 ADB72233
 c 998 11 100.0 25032 10 ADE82935
 c 999 11 100.0 25032 10 ADE95743
 c1000 11 100.0 25772 4 AAK81332

ALIGNMENTS

RESULT 1
 AAS02843/c
 ID AAS02843 standard; DNA; 11 BP.
 XX
 AC AAS02843;
 XX
 DT 29-AUG-2001 (first entry)
 XX
 DE Human pregnane X receptor (hPXR) gene, PCR primer #113.
 XX
 DE Human; pregnane X receptor; hPXR; PCR primer; diagnostic; cancer;
 KW Human; pregnane X receptor; hPXR; PCR primer; diagnostic; cancer;
 KW therapeutic; chemotherapy; gene therapy; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200120026-A2.
 XX
 XX 22-MAR-2001.
 XX
 PF 08-SEP-2000; 2000WO-EP008827.
 XX
 PR 10-SEP-1999; 99EP-00118120.
 XX
 PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
 XX
 PI Wojnowski L, Hustert E;
 XX
 DR WPI; 2001-273428/28.
 XX
 PT Novel variant of the human pregnane X receptor gene, associated with
 PT insufficient metabolism and/or sensitivity to drugs, is useful for
 PT diagnosing and treating diseases with drugs that are modulators of their
 PT gene product.
 XX
 PS Claim 1; Page 45; 108pp; English.
 XX
 PR 10-SEP-1999; 99EP-00118120.
 XX
 PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
 XX
 PI Wojnowski L, Hustert E;
 XX
 DR WPI; 2001-273428/28.
 XX
 PT Novel variant of the human pregnane X receptor gene, associated with
 PT insufficient metabolism and/or sensitivity to drugs, is useful for
 PT diagnosing and treating diseases with drugs that are modulators of their
 PT gene product.
 XX
 PS Claim 1; Page 45; 108pp; English.
 XX
 CC AAS02731-AAS02909 represent human pregnane X receptor (hPXR) coding

CC sequences and PCR primers of the invention. The human pregnane X receptor
 CC sequences are used to make antibodies, or a substance capable of binding
 CC specifically to the gene product of hPXR gene, for diagnosing and
 CC treating various diseases, such as cancer, with drugs that are
 CC substrates, inhibitors or modulators of the hPXR gene product. The
 CC proteins can be used to identify and obtain products and drugs for
 CC treatment of diseases which are amenable to chemotherapy. The nucleic
 CC acids can be used in gene therapy for the treatment or prevention of
 CC disorders associated with hPXR expression
 XX
 SQ Sequence 11 BP; 4 A; 2 C; 3 G; 2 T; 0 U; 0 Other;
 Query Match 100.0%; Score 11; DB 5; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.9e+03;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CTTTGGCACTA 11
 Db 11 CTTTGGCACTA 1
 RESULT 2
 AAS02842
 ID AAS02842 standard; DNA; 11 BP.
 XX
 AC AAS02842;
 XX
 DT 29-AUG-2001 (first entry)
 XX
 DE Human pregnane X receptor (hPXR) gene, PCR primer #112.
 XX
 DE Human; pregnane X receptor; hPXR; PCR primer; diagnostic; cancer;
 KW therapeutic; chemotherapy; gene therapy; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200120026-A2.
 XX
 XX 22-MAR-2001.
 XX
 PF 08-SEP-2000; 2000WO-EP008827.
 XX
 PR 10-SEP-1999; 99EP-00118120.
 XX
 PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
 XX
 PI Wojnowski L, Hustert E;
 XX
 DR WPI; 2001-273428/28.
 XX
 PT Novel variant of the human pregnane X receptor gene, associated with
 PT insufficient metabolism and/or sensitivity to drugs, is useful for
 PT diagnosing and treating diseases with drugs that are modulators of their
 PT gene product.
 XX
 PS Claim 1; Page 45; 108pp; English.
 XX
 PR 10-SEP-1999; 99EP-00118120.
 XX
 PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
 XX
 PI Wojnowski L, Hustert E;
 XX
 DR WPI; 2001-273428/28.
 XX
 PT Novel variant of the human pregnane X receptor gene, associated with
 PT insufficient metabolism and/or sensitivity to drugs, is useful for
 PT diagnosing and treating diseases with drugs that are modulators of their
 PT gene product.
 XX
 PS Claim 1; Page 45; 108pp; English.
 XX
 CC AAS02731-AAS02909 represent human pregnane X receptor (hPXR) coding

Query Match 100.0%; Score 11; DB 5; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.9e+03;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 SQ Sequence 11 BP; 2 A; 3 C; 2 G; 4 T; 0 U; 0 Other;

QY 1 CTTTGGCACTA 11
 DB 1 CTTTGGCACTA 11

RESULT 3
 ACD64825/c
 ID ACD64825 standard; RNA; 17 BP.
 XX
 AC ACD64825;
 XX
 DT 30-SEP-2003 (first entry)
 XX
 DE HCV minus strand DNazyme substrate sequence #1736.
 XX
 KW Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
 KW RNA stability; RNA expression; RNA synthesis; antisense;
 KW enzymatic nucleic acid; hammerhead ribozyme; DNazyme; inozyme; zinzyme;
 KW amberyne; G-cleaver ribozyme; decoy molecule; aptamer;
 KW HBV reverse transcriptase; Enhancer I region; viral replication;
 KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;
 KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
 KW virucide; antiinflammatory; substrate; ss.
 XX
 OS Hepatitis C virus.
 XX
 PN WO200281494-A1.
 XX
 PD 17-OCT-2002.
 XX
 PF 26-MAR-2002; 2002WO-US009187.
 XX
 PR 26-MAR-2001; 2001US-00817879.
 PR 08-JUN-2001; 2001US-00877478.
 PR 08-JUN-2001; 2001US-0296876P.
 PR 24-OCT-2001; 2001US-0335059P.
 PR 05-DEC-2001; 2001US-0337055P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MACE/) MACEJAK D.
 PA (MCSW/) MCSWIGGEN J.
 PA (MORR/) MORRISSEY D.
 PA (PAVC/) PAVCO P.
 PA (LEEP/) LEE P.
 PA (DRAP/) DRAPER K.
 PA (ROBE/) ROBERTS E.
 XX
 PI Blatt L, Macejak D, Mcswiggen J, Morrissey J, Pavco P, Lee P;
 PI Draper K, Roberts E;
 XX
 DR WPI; 2003-229207/22.
 XX
 PT Novel compound useful for treating cirrhosis, liver failure,
 PT hepatocellular carcinoma, or condition associated with hepatitis C virus
 PT infection.
 XX
 PS Claim 1; Page 306; 387pp; English.
 XX
 CC The present invention relates to nucleic acid molecules which modulate
 CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
 CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
 CC and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,
 CC inozymes, zinzymes, amberyne, and G-cleaver ribozymes. Also disclosed
 CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse
 CC transcriptase and/or HBV reverse transcriptase primer sequences, as well
 CC as oligonucleotides that specifically bind the Enhancer I region of HBV
 CC DNA. The nucleic acids may be used to modulate the expression of HBV
 CC genes and HBV viral replication. Also disclosed is a method for screening
 CC compounds and/or potential therapies directed against HBV, and compounds
 CC that modulate the expression and/or replication of HCV. The compounds and
 CC methods of the invention are useful for the treatment of degenerative and

CC disease states related to HBV and HCV infection, replication and gene
 CC expression such as cirrhosis, liver failure, and hepatocellular
 CC carcinoma. The present sequence represents a substrate for one of the HCV
 CC DNazyme or minus strand DNazyme sequences disclosed in the present
 CC invention
 XX
 SQ Sequence 17 BP; 5 A; 3 C; 7 G; 0 T; 2 U; 0 Other;
 Query Match 100.0%; Score 11; DB 8; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.9e+03;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTGGCACTA 11
 DB 17 CTTTGGCACTA 7

RESULT 4
 ACD57843
 ID ACD57843 standard; RNA; 17 BP.
 XX
 AC ACD57843;
 XX
 DT 23-SEP-2003 (first entry)
 XX
 DE HCV DNazyme substrate sequence #541.
 XX
 KW Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
 KW RNA stability; RNA expression; RNA synthesis; antisense;
 KW enzymatic nucleic acid; hammerhead ribozyme; DNazyme; inozyme; zinzyme;
 KW amberyne; G-cleaver ribozyme; decoy molecule; aptamer;
 KW HBV reverse transcriptase; Enhancer I region; viral replication;
 KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;
 KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
 KW virucide; antiinflammatory; substrate; ss.
 XX
 OS Hepatitis C virus.
 XX
 PN WO200281494-A1.
 XX
 PD 17-OCT-2002.
 XX
 PF 26-MAR-2002; 2002WO-US009187.
 XX
 PR 26-MAR-2001; 2001US-00817879.
 PR 08-JUN-2001; 2001US-00877478.
 PR 08-JUN-2001; 2001US-0296876P.
 PR 24-OCT-2001; 2001US-0335059P.
 PR 05-DEC-2001; 2001US-0337055P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MACE/) MACEJAK D.
 PA (MCSW/) MCSWIGGEN J.
 PA (MORR/) MORRISSEY D.
 PA (PAVC/) PAVCO P.
 PA (LEEP/) LEE P.
 PA (DRAP/) DRAPER K.
 PA (ROBE/) ROBERTS E.
 XX
 PI Blatt L, Macejak D, Mcswiggen J, Morrissey J, Pavco P, Lee P;
 PI Draper K, Roberts E;
 XX
 DR WPI; 2003-229207/22.
 XX
 PT Novel compound useful for treating cirrhosis, liver failure,
 PT hepatocellular carcinoma, or condition associated with hepatitis C virus
 PT infection.
 XX
 PS Claim 1; Page 243; 387pp; English.
 XX
 CC The present invention relates to nucleic acid molecules which modulate
 CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or

CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
 CC and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,
 CC inozymes, zinzymes, amberyms, and G-cleaver ribozymes. Also disclosed
 CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse
 CC transcriptase and/or HBV reverse transcriptase primer sequences, as well
 CC as oligonucleotides that specifically bind the Enhancer I region of HBV
 CC DNA. The nucleic acids may be used to modulate the expression of HBV
 CC genes and HBV viral replication. Also disclosed is a method for screening
 CC compounds and/or potential therapies directed against HBV, and compounds
 CC that modulate the expression and/or replication of HCV. The compounds and
 CC methods of the invention are useful for the treatment of degenerative and
 CC disease states related to HBV and HCV infection, replication and gene
 CC expression such as cirrhosis, liver failure, and hepatocellular
 CC carcinoma. The present sequence represents a substrate for one of the HCV
 CC DNazyme or minus strand DNazyme sequences disclosed in the present
 CC invention

SQ Sequence 17 BP; 3 A; 6 C; 4 G; 0 T; 4 U; 0 Other;

Query Match 100.0%; Score 11; DB 8; Length 17;
 Best Local Similarity 63.6%; Pred. No. 1.9e+03;
 Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTGGCACTA 11
 |:::|||||:
 Db 4 CUUUGGCACUA 14

RESULT 5
 ACD57844

ID ACD57844 standard; RNA; 17 BP.

AC ACD57844;

DT 23-SEP-2003 (first entry)

DE HCV DNazyme substrate sequence #542.

XX Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
 KW RNA stability; RNA expression; RNA synthesis; antisense;
 KW enzymatic nucleic acid; hammerhead ribozyme; DNazyme; inozyme; zinzyme;
 KW amberyms; G-cleaver ribozyme; decoy molecule; aptamer;
 KW HBV reverse transcriptase; Enhancer I region; viral replication;
 KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;
 KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
 KW virucide; antiinflammatory; substrate; ss.

XX Hepatitis C virus.

OS WO200281494-A1.

PN 17-OCT-2002.

XX 26-MAR-2002; 2002WO-US009187.

XX 26-MAR-2001; 2001US-00817879.

PR 08-JUN-2001; 2001US-00877478.

PR 08-JUN-2001; 2001US-0296876P.

PR 24-OCT-2001; 2001US-0335059P.

PR 05-DEC-2001; 2001US-0337055P.

XX (RIBO-) RIBOZYME PHARM INC.

PA (BLAT/) BLATT L.

PA (MACE/) MACEJAK D.

PA (MCSW/) MCSWIGGEN J.

PA (MORR/) MORRISSEY D.

PA (PAVC/) PAVCO P.

PA (LEEF/) LEE P.

PA (DRAP/) DRAPER K.

XX

DR WPI; 2003-229207/22.

XX Novel compound useful for treating cirrhosis, liver failure,

PT hepatocellular carcinoma, or condition associated with hepatitis C virus

PT infection.

XX Claim 1; Page 243; 387pp; English.

XX The present invention relates to nucleic acid molecules which modulate
 CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
 CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
 CC and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,
 CC inozymes, zinzymes, amberyms, and G-cleaver ribozymes. Also disclosed
 CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse
 CC transcriptase and/or HBV reverse transcriptase primer sequences, as well
 CC as oligonucleotides that specifically bind the Enhancer I region of HBV
 CC DNA. The nucleic acids may be used to modulate the expression of HBV
 CC genes and HBV viral replication. Also disclosed is a method for screening
 CC compounds and/or potential therapies directed against HBV, and compounds
 CC that modulate the expression and/or replication of HCV. The compounds and
 CC methods of the invention are useful for the treatment of degenerative and
 CC disease states related to HBV and HCV infection, replication and gene
 CC expression such as cirrhosis, liver failure, and hepatocellular
 CC carcinoma. The present sequence represents a substrate for one of the HCV
 CC DNazyme or minus strand DNazyme sequences disclosed in the present
 CC invention

SQ Sequence 17 BP; 2 A; 7 C; 3 G; 0 T; 5 U; 0 Other;

Query Match 100.0%; Score 11; DB 8; Length 17;
 Best Local Similarity 63.6%; Pred. No. 1.9e+03;
 Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTGGCACTA 11
 |:::|||||:
 Db 2 CUUUGGCACUA 12.

RESULT 6

ACD64826/c

ID ACD64826 standard; RNA; 17 BP.

AC ACD64826;

DT 30-SEP-2003 (first entry)

XX HCV minus strand DNazyme substrate sequence #1737.

XX Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
 KW RNA stability; RNA expression; RNA synthesis; antisense;
 KW enzymatic nucleic acid; hammerhead ribozyme; DNazyme; inozyme; zinzyme;
 KW amberyms; G-cleaver ribozyme; decoy molecule; aptamer;
 KW HBV reverse transcriptase; Enhancer I region; viral replication;
 KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;
 KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
 KW virucide; antiinflammatory; substrate; ss.

OS Hepatitis C virus.

XX WO200281494-A1.

PN 17-OCT-2002.

XX 26-MAR-2002; 2002WO-US009187.

XX 26-MAR-2001; 2001US-00817879.

PR 08-JUN-2001; 2001US-00877478.

PR 08-JUN-2001; 2001US-0296876P.

PR 24-OCT-2001; 2001US-0335059P.

PR 05-DEC-2001; 2001US-0337055P.

XX (RIBO-) RIBOZYME PHARM INC.


```
PS Claim 1; SEQ ID NO 4014; 198pp; English.
XX
CC The invention relates to an enzymatic nucleic acid molecule which
CC specifically cleaves RNA derived from hepatitis C virus (HCV), in which
CC the binding arms of the enzymatic nucleic acid molecule comprises
CC sequences complementary to any of the defined substrate sequences given
CC in the specification. The nucleic acid molecule may be administered for
CC the treatment of HCV infections, especially in combination with type I
CC interferons. The present sequence represents a HCV DNazyme substrate
CC sequence.
XX
SQ Sequence 17 BP; 4 A; 4 C; 7 G; 0 T; 2 U; 0 Other;

Query Match      100.0%; Score 11; DB 12; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTGGCACTA 11
Db 15 CTTTGGCACTA 5
    |||||
    |||||

RESULT 9
ADI86767/c
ID ADI86767 standard; RNA; 17 BP.
XX
AC ADI86767;
XX
DT 03-JUN-2004 (first entry)
XX
DE HCV DNazyme substrate sequence #4013.
XX
KW ss; enzymatic nucleic acid; RNA cleavage; hepatitis C virus; HCV;
KW HCV infection; type I interferon; DNazyme.
XX
OS Hepatitis C virus.
XX
PN US2003125270-A1.
XX
PD 03-JUL-2003.
XX
PF 18-DEC-2000; 2000US-00740332.
XX
PR 18-DEC-2000; 2000US-00740332.
XX
PA (BLAT/) BLATT L.
PA (MCSW/) MCSWIGGEN J.
PA (ROBE/) ROBERTS E.
PA (PAVC/) PAVCO P A.
PA (MACE/) MACEJACK D.
XX
PI Blatt L, Mcswiggen J, Roberts E, Pavco PA, Macejack D;
XX
WPI; 2004-031273/03.
XX
PT Enzymatic nucleic acid molecules which specifically cleave RNA derived
PT from hepatitis C virus (HCV), useful for the treatment of HCV infections,
PT especially in combination with type I interferon therapy.
XX
PS Claim 1; SEQ ID NO 4013; 198pp; English.
XX
CC The invention relates to an enzymatic nucleic acid molecule which
CC specifically cleaves RNA derived from hepatitis C virus (HCV), in which
CC the binding arms of the enzymatic nucleic acid molecule comprises
CC sequences complementary to any of the defined substrate sequences given
CC in the specification. The nucleic acid molecule may be administered for
CC the treatment of HCV infections, especially in combination with type I
CC interferons. The present sequence represents a HCV DNazyme substrate
CC sequence.
XX
SQ Sequence 17 BP; 5 A; 3 C; 7 G; 0 T; 2 U; 0 Other;

Query Match      100.0%; Score 11; DB 12; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTGGCACTA 11
Db 15 CTTTGGCACTA 5
    |||||
    |||||

RESULT 9
ADI86767/c
ID ADI86767 standard; RNA; 17 BP.
XX
AC ADI86767;
XX
DT 03-JUN-2004 (first entry)
XX
DE HCV DNazyme substrate sequence #4013.
XX
KW ss; enzymatic nucleic acid; RNA cleavage; hepatitis C virus; HCV;
KW HCV infection; type I interferon; DNazyme.
XX
OS Hepatitis C virus.
XX
PN US2003125270-A1.
XX
PD 03-JUL-2003.
XX
PF 18-DEC-2000; 2000US-00740332.
XX
PR 18-DEC-2000; 2000US-00740332.
XX
PA (BLAT/) BLATT L.
PA (MCSW/) MCSWIGGEN J.
PA (ROBE/) ROBERTS E.
PA (PAVC/) PAVCO P A.
PA (MACE/) MACEJACK D.
XX
PI Blatt L, Mcswiggen J, Roberts E, Pavco PA, Macejack D;
XX
WPI; 2004-031273/03.
XX
PT Enzymatic nucleic acid molecules which specifically cleave RNA derived
PT from hepatitis C virus (HCV), useful for the treatment of HCV infections,
PT especially in combination with type I interferon therapy.
XX
PS Claim 1; SEQ ID NO 4013; 198pp; English.
XX
CC The invention relates to an enzymatic nucleic acid molecule which
CC specifically cleaves RNA derived from hepatitis C virus (HCV), in which
CC the binding arms of the enzymatic nucleic acid molecule comprises
CC sequences complementary to any of the defined substrate sequences given
CC in the specification. The nucleic acid molecule may be administered for
CC the treatment of HCV infections, especially in combination with type I
CC interferons. The present sequence represents a HCV DNazyme substrate
CC sequence.
XX
SQ Sequence 17 BP; 5 A; 3 C; 7 G; 0 T; 2 U; 0 Other;

Query Match      100.0%; Score 11; DB 12; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTGGCACTA 11
Db 15 CTTTGGCACTA 5
    |||||
    |||||

RESULT 9
ADI86767/c
ID ADI86767 standard; RNA; 17 BP.
XX
AC ADI86767;
XX
DT 03-JUN-2004 (first entry)
XX
DE HCV DNazyme substrate sequence #4013.
XX
KW ss; enzymatic nucleic acid; RNA cleavage; hepatitis C virus; HCV;
KW HCV infection; type I interferon; DNazyme.
XX
OS Hepatitis C virus.
XX
PN US2003125270-A1.
XX
PD 03-JUL-2003.
XX
PF 18-DEC-2000; 2000US-00740332.
XX
PR 18-DEC-2000; 2000US-00740332.
XX
PA (BLAT/) BLATT L.
PA (MCSW/) MCSWIGGEN J.
PA (ROBE/) ROBERTS E.
PA (PAVC/) PAVCO P A.
PA (MACE/) MACEJACK D.
XX
PI Blatt L, Mcswiggen J, Roberts E, Pavco PA, Macejack D;
XX
WPI; 2004-031273/03.
XX
PT Enzymatic nucleic acid molecules which specifically cleave RNA derived
PT from hepatitis C virus (HCV), useful for the treatment of HCV infections,
PT especially in combination with type I interferon therapy.
XX
PS Claim 1; SEQ ID NO 542; 198pp; English.
XX
CC The invention relates to an enzymatic nucleic acid molecule which
CC specifically cleaves RNA derived from hepatitis C virus (HCV), in which
CC the binding arms of the enzymatic nucleic acid molecule comprises
CC sequences complementary to any of the defined substrate sequences given
CC in the specification. The nucleic acid molecule may be administered for
CC the treatment of HCV infections, especially in combination with type I
CC interferons. The present sequence represents a HCV DNazyme substrate
CC sequence.
XX
SQ Sequence 17 BP; 2 A; 7 C; 3 G; 0 T; 5 U; 0 Other;

Query Match      100.0%; Score 11; DB 12; Length 17;
Best Local Similarity 63.6%; Pred. No. 1.9e+03;
Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTGGCACTA 11
Db 2 CUUUGGCACUA 12
    |:::|
    |:::|

RESULT 11
AAH23171
ID AAH23171 standard; DNA; 18 BP.
XX
AC AAH23171;
XX
```

DT 17-SEP-2001 (first entry)
 XX Nitric oxide synthase gene nuclear factor 1 (NF-1) binding site.
 DE
 XX Hypertension; renal disease; non insulin dependent diabetes mellitus;
 KW polymorphism; nitric oxide synthase; breast; lung; prostate; cancer;
 KW nephrotropic; vasodilatory; renal injury; NIDDM; SNP; NOS; NF-1;
 XX nuclear factor 1; ss.
 XX Homo sapiens.
 OS
 XX WO200153537-A2.
 PN
 XX 26-JUL-2001.
 XX
 XX 24-JAN-2001; 2001WO-US002260.
 XX
 PR 24-JAN-2000; 2000US-0177775P.
 PR 25-JUL-2000; 2000US-0220662P.
 XX
 XX (DZGE-) DZ GENES LLC.
 PA
 XX Moskowitz DW;
 PI
 XX WPI; 2001-451916/48.
 DR
 XX The diagnosis of disorders, i.e. hypertension and non insulin dependent
 PT diabetes mellitus comprises the identification of single polymorphism(s)
 PT in a nitric oxide synthase gene.
 XX
 XX Example 4; Page 88; 119pp; English.
 PS
 XX The invention relates to diagnosing a genetic predisposition to disease,
 CC condition or disorder i.e. hypertension, non insulin dependent diabetes
 CC mellitus (NIDDM), end stage renal disease due to hypertension and/or
 CC NIDDM mellitus that involves detecting the presence or absence of single
 CC nucleotide polymorphisms (SNP) in the nitric oxide synthase gene (NOS).
 CC The method is also useful for the treatment or prophylaxis of breast,
 CC lung or prostate cancer. The method allows the identification of people
 CC with a predisposition to disorders, before the disease progresses to an
 CC end stage. The present sequence represents a nuclear factor 1 (NF-1)
 CC binding site of the nitric oxide synthase gene, where a disruption occurs
 CC due to a deletion polymorphism at position 1272 of the gene
 XX
 XX Sequence 18 BP; 6 A; 6 C; 2 G; 4 T; 0 U; 0 Other;
 SQ
 Query Match 100.0%; Score 11; DB 4; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.9e+03;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 QY 1 CTTTGGCACTA 11
 Db |||||
 1 CTTTGGCACTA 11
 RESULT 12
 AAX85553
 ID AAX85553 standard; cDNA; 22 BP.
 XX
 AC AAX85553;
 XX
 XX 07-SEP-1999 (first entry)
 DT
 XX PCR primer and probe used to detect human kin17 nucleic acids.
 DE
 XX Human; kin17 protein; cell proliferation; fertility; probe;
 KW hyperproliferative disease; protein interaction; curved DNA;
 KW HIV replication; HIV integration; repair enzyme; PCR primer; ss.
 XX
 XX Synthetic.
 OS
 XX Homo sapiens.
 XX
 XX FR2772046-A1.
 PN

XX 11-JUN-1999.
 PD
 XX 09-DEC-1997; 97FR-00015536.
 PF
 XX 09-DEC-1997; 97FR-00015536.
 PR
 XX (COMS) COMMISSARIAT ENERGIE ATOMIQUE.
 PA
 XX Kannouche P, Mauffrey P, Pinon LG, Biard D, Angulo MJF;
 PI
 XX WPI; 1999-359999/31.
 DR
 XX New DNA coding for human kin17 protein - useful for controlling cell
 PT proliferation or fertility.
 PT
 XX Claim 7; Page 5; 6pp; French.
 PS
 XX AAX8553-69 represent PCR primers and probes used to detect nucleic acids
 CC encoding human kin17 protein. The mammalian kin17 protein is useful for
 CC preparing a medicament for controlling cell proliferation or for
 CC controlling fertility. The medicaments can also be used to treat
 CC hyperproliferative diseases. Fragments between amino acids 55 and 235
 CC (preferably between amino acids 129 and 228) of a mammalian kin17 protein
 CC are useful for regulating the interaction between proteins and curved
 CC DNA. The fragment can be used to block replication of HIV or its
 CC integration into the human genome or to target repair enzymes to curved
 CC DNA sites. Expression vectors for kin17 can be used for controlling cell
 CC proliferation
 XX
 XX Sequence 22 BP; 5 A; 6 C; 6 G; 5 T; 0 U; 0 Other;
 SQ
 Query Match 100.0%; Score 11; DB 2; Length 22;
 Best Local Similarity 100.0%; Pred. No. 1.9e+03;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 QY 1 CTTTGGCACTA 11
 Db |||||
 12 CTTTGGCACTA 22
 RESULT 13
 AAX24199/c
 ID AAX24199 standard; DNA; 23 BP.
 XX
 AC AAX24199;
 XX
 XX 11-SEP-2001 (first entry)
 DT
 XX PCR primer, SEQ ID NO:10, used to isolate ageing inhibition-related DNA.
 DE
 XX Mouse; ageing inhibition-related DNA; ageing inhibitory protein;
 KW recombinant production; transgenic animal; detection; drug screening;
 KW ligand identification; ageing-related disorder; premature ageing;
 KW PCR primer; ss.
 XX
 XX Synthetic.
 OS
 XX WO200138529-A1.
 PN
 XX 31-MAY-2001.
 PD
 XX 17-NOV-2000; 2000WO-JP008121.
 PF
 XX 19-NOV-1999; 99JP-00329649.
 PR
 XX (KYOW) KYOWA HAKKO KOGYO KK.
 PA
 XX Shiraishi N, Sekine S, Nabeshima Y, Fujimori T, Ito S;
 PI
 XX WPI; 2001-367689/38.
 DR
 XX Polypeptide for treatment of premature aging.
 PT

XX Example 1; Page 89; 94pp; Japanese.

PS The invention relates to 3 novel mouse proteins which inhibit ageing

CC (AAH73664-AAH73666) and to the nucleic acids encoding them (AAH24193-
 CC AAH24195). The invention also relates to recombinant vectors, host cells
 CC and transgenic non-human animals comprising DNA encoding a mouse ageing
 CC inhibitory protein of the invention; the recombinant production of a
 CC mouse ageing inhibitory protein; antibodies against the ageing inhibitory
 CC proteins; methods for immunologically assaying the proteins; and methods
 CC for identifying ligands or other modulators of the ageing inhibitory
 CC proteins, and the ligands and modulators thus identified. The ageing
 CC inhibitory proteins, nucleic acids encoding them, and antibodies, ligands
 CC and modulators, may be used in the diagnosis and treatment of ageing
 CC (particularly premature ageing), and ageing-related disorders. Sequences
 CC AAH24198-AAH24199 represent PCR primers used in an exemplification of the
 CC invention to isolate a mouse ageing inhibition-related DNA sequence
 CC (AAH24197)

XX Sequence 23 BP; 8 A; 6 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 11; DB 4; Length 23;
 Best Local Similarity 100.0%; Pred. No. 1.9e+03;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11
 |||||
 Db 13 CTTTGGCACTA 3

RESULT 14

AAH76792

ID AAH76792 standard; DNA; 33 BP.

XX

AC AAH76792;

XX

DT 14-DEC-2001 (first entry)

XX

DE Human bromo-domain 10 PCR primer, SEQ ID NO:6.

XX

Human; bromo-domain 10; recombinant production; malignant tumour; cancer;
 blood disease; HIV infection; human immunodeficiency virus;
 immune disorder; inflammatory condition; cytostatic; anti-HIV;
 antiinflammatory; immunomodulator; PCR primer; ss.

XX Homo sapiens.

OS

XX WO200172812-A1.

PN

XX 04-OCT-2001.

PD

XX 26-MAR-2001; 2001WO-CN000479.

PF

XX 28-MAR-2000; 2000CN-00115196.

PR

XX (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.

PA

XX Mao Y, Xie Y;

PI

XX WPI; 2001-597108/67.

DR

XX Human bromo-domain 10 and encoded polynucleotide, used in diagnosis and
 PT treatment of malignant tumors, hemopathy, human immunodeficiency virus
 PT infection, immunological diseases and inflammation.

XX

PS Example 4; Page 16; 32pp; Chinese.

XX The invention relates to human bromo-domain 10 (AAG66746), nucleic acids
 CC encoding it (AAH76789), and a method for the recombinant production of
 CC bromo-domain 10. The protein has a molecular weight of 10 kD. The present
 CC invention additionally discloses an antagonist of bromo-domain 10 for
 CC therapeutic use, and an antibody which specifically binds to bromo-domain
 CC 10. Bromo-domain 10, and nucleotides which encode it may be used for

CC treating a variety of diseases, such as malignant tumours, blood
 CC diseases, HIV (human immunodeficiency virus) infection, immune disorders
 CC and inflammatory conditions. The protein may also be used to screen for
 CC modulators of its activity or for peptide fingerprinting identification.
 CC The polynucleotide can be used as a primer for nucleic acid amplification.
 CC reactions or as a probe for hybridisation reactions, or in producing gene
 CC chips or microarrays. Sequences AAH76791-AAH76792 represent PCR primers
 CC used in an exemplification of the invention to amplify human bromo-domain
 CC 10 cDNA for cloning

XX

SQ Sequence 33 BP; 8 A; 10 C; 6 G; 9 T; 0 U; 0 Other;

Query Match 100.0%; Score 11; DB 5; Length 33;
 Best Local Similarity 100.0%; Pred. No. 2e+03;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTGGCACTA 11
 |||||
 Db 21 CTTTGGCACTA 31

RESULT 15

AAH38062/c

ID AAD38062 standard; DNA; 47 BP.

XX

AC AAD38062;

XX

DT 10-SEP-2002 (first entry)

XX

DE Maize proRIP DNA amplifying PCR primer, RIP1BP.

XX

KW Maize; transgenic; transgenic plant; ribosome inactivating protein; RIP;
 KW cytotoxicity; nematode resistant plant; sterility; fruit abscission;
 KW viral infection; nematocide; antiviral; PCR; primer; ss.

XX Zea mays.

OS

XX WO200233106-A2.

PN

XX 25-APR-2002.

PD

XX 15-OCT-2001; 2001WO-GB004581.

PF

XX 14-OCT-2000; 2000GB-00025225.

PR

XX (ADTE-) ADVANCED TECHNOLOGIES CAMBRIDGE LTD.

PA

XX Thomas CUR, Mcpherson MJ, Atkinson HJ, Neelam A;

PI

XX WPI; 2002-454604/48.

DR

XX Producing transgenic plant resistant to nematode infection, comprises
 PT transforming plant with chimeric gene having promoter inducible at
 PT nematode feeding site, linked to sequence encoding maize ribosome
 PT inactivating protein.

XX

PS Example; Page 87; 89pp; English.

XX The present invention relates to a novel method for producing transgenic
 CC plants which harbour chimeric genes within the genome of the plant, the
 CC expression of which gene causes plant cytotoxicity at a target site. The
 CC method involves transforming a plant with a chimeric gene comprising a
 CC promoter inducible at and/or adjacent to a target site, operably linked
 CC to a coding sequence encoding a maize ribosome inactivating protein (RIP)
 CC or its portion. The method is useful for producing transgenic plants
 CC harbouring within the genome a chimeric gene which when expressed,
 CC produces a cytotoxic protein. The target site may be a nematode feeding
 CC site and by targeting the nematode feeding site, nematode resistant plant
 CC can be obtained. If the target site is one or more of plant's pollen,
 CC anther or tapetum, the method is useful for effecting the male sterility
 CC in plants and if the target site is ovule of plant, the method is
 CC directed to effecting female sterility in plants. The target site may be
 CC specific parts of the flower or abscission zone of the leaf and/or fruit

CC and the method is useful for manipulating morphology of the flower of a
CC plant and to assist in or promote leaf and/or fruit abscission in plants.
CC The method is also useful for controlling viral infection. The present
CC DNA sequence is a PCR primer which is used to amplify maize proRIP DNA.
CC This primer is used in the exemplification of the invention

XX SQ Sequence 47 BP; 16 A; 9 C; 12 G; 10 T; 0 U; 0 Other;

Query Match 100.0%; Score 11; DB 6; Length 47;

Best Local Similarity 100.0%; Pred. No. 2e+03; Mismatches 0; Indels 0; Gaps 0;
Matches 11; Conservative 0;

OY 1 CTTTGGCACTA 11
|||||
DB 40 CTTTGGCACTA 30
|||||

RESULT 16

AAI22229
ID AAI22229 standard; DNA; 77 BP.

XX AC

AAI22229;

DT 12-OCT-2001 (first entry)

XX DE Probe #12162 for gene expression analysis in human cervical cell sample.

XX KW Probe; human; microarray; gene expression; cervical epithelial cell;

XX KW cervical cancer; ss.

XX OS Homo sapiens.

XX PN WO200157278-A2.

XX PD 09-AUG-2001.

XX PF 30-JAN-2001; 2001WO-US000670.

XX PR 04-FEB-2000; 2000US-0180312P.

XX PR 26-MAY-2000; 2000US-0207456P.

XX PR 30-JUN-2000; 2000US-00608408.

XX PR 03-AUG-2000; 2000US-00632366.

XX PR 21-SEP-2000; 2000US-0234687P.

XX PR 27-SEP-2000; 2000US-0236359P.

XX PR 04-OCT-2000; 2000GB-00024263.

XX PA (MOLE-) MOLECULAR DYNAMICS INC.

XX PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX DR WPI; 2001-488901/53.

XX PT Human genome-derived single exon nucleic acid probes useful for analyzing
XX PT gene expression in human cervical epithelial cells.

XX PS Claim 25; SEQ ID NO 12162; 487pp; English.

XX CC The present invention relates to human single exon nucleic acid probes
XX CC (SENPs). The present sequence is one such probe. The SENPs are derived
XX CC from human HeLa cells. The SENPs can be used to produce a single exon
XX CC microarray, which can be used for measuring human gene expression in a
XX CC sample derived from human cervical epithelial cells. By measuring gene
XX CC expression, the probes are therefore useful in grading and/or staging of
XX CC diseases of the cervix, notably cervical cancer. Note: The sequence data
XX CC for this patent did not form part of the printed specification, but was
XX CC obtained in electronic format directly from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 77 BP; 25 A; 13 C; 18 G; 21 T; 0 U; 0 Other;

Query Match

Best Local Similarity 100.0%; Score 11; DB 4; Length 77;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTTTGGCACTA 11
|||||
DB 34 CTTTGGCACTA 44
|||||

RESULT 17

ABA67308

ID ABA67308 standard; DNA; 77 BP.

XX AC

ABA67308;

XX DT 01-FEB-2002 (first entry)

XX DE Human foetal liver single exon nucleic acid probe #15613.

XX KW Human; foetal liver; gene expression; single exon nucleic acid probe; ss.

XX OS Homo sapiens.

XX PN WO200157277-A2.

XX PD 09-AUG-2001.

XX PF 30-JAN-2001; 2001WO-US000669.

XX PR 04-FEB-2000; 2000US-0180312P.

XX PR 26-MAY-2000; 2000US-0207456P.

XX PR 30-JUN-2000; 2000US-00608408.

XX PR 03-AUG-2000; 2000US-00632366.

XX PR 21-SEP-2000; 2000US-0234687P.

XX PR 27-SEP-2000; 2000US-0236359P.

XX PR 04-OCT-2000; 2000GB-00024263.

XX PA (MOLE-) MOLECULAR DYNAMICS INC.

XX PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX DR WPI; 2001-483447/52.

XX PT Human genome-derived single exon nucleic acid probes useful for analyzing
XX PT gene expression in human fetal liver.
XX PS Claim 4; SEQ ID NO 15613; 639pp + Sequence Listing; English.
XX CC The invention relates to a single exon nucleic acid probe for measuring
XX CC human gene expression in a sample derived from human foetal liver. The
XX CC single exon nucleic acid probes may be used for predicting, measuring and
XX CC displaying gene expression in samples derived from human fetal liver. The
XX CC present sequence is a single exon nucleic acid probe of the invention.
XX CC Note: The sequence data for this patent did not form part of the printed
XX CC specification, but was obtained in electronic format directly from WIPO
XX CC at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 77 BP; 25 A; 13 C; 18 G; 21 T; 0 U; 0 Other;

Query Match 100.0%; Score 11; DB 4; Length 77;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTTTGGCACTA 11
|||||
DB 34 CTTTGGCACTA 44
|||||

RESULT 18

AAI47524

ID AAI47524 standard; DNA; 77 BP.

XX AC

AAI47524;

XX DT 17-OCT-2001 (first entry)

XX XX

DE Probe #16210 used to measure gene expression in human placenta sample.
XX Probe: microarray; human; placenta; antenatal diagnosis;
KW Genetic disorder; ss.
XX Homo sapiens.
XX OS
XX WO200157272-A2.
XX PD
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US000663.
XX
XX 04-FEB-2000; 2000US-0180312P.
XX 26-MAY-2000; 2000US-0207456P.
XX 30-JUN-2000; 2000US-00608408.
XX 03-AUG-2000; 2000US-00632366.
XX 21-SEP-2000; 2000US-0234687P.
XX 27-SEP-2000; 2000US-0236359P.
XX 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488897/53.
XX Human genome-derived single exon nucleic acid probes useful for analyzing
XX gene expression in human placenta.
XX
XX Claim 25; SEQ ID NO 16210; 654pp; English.
XX
XX The present invention relates to single exon nucleic acid probes (SENPs).
XX The present sequence is one such probe. The probes are useful for
XX producing a microarray for predicting, measuring and displaying gene
XX expression in samples derived from human placenta. The probes are useful
XX for antenatal diagnosis of human genetic disorders
XX
XX Sequence 77 BP; 25 A; 13 C; 18 G; 21 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 11; DB 4; Length 77;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CTTTGGCACTA 11
DB 34 CTTTGGCACTA 44
RESULT 19
ABA49398
ID ABA49398 standard; DNA; 77 BP.
XX
XX ABA49398;
AC
XX
XX 01-FEB-2002 (first entry)
DT
DE Human breast cell single exon nucleic acid probe #8093.
DE
XX Human; microarray; single exon probe; gene expression; breast; disease;
KW cancer; ss.
XX
XX Homo sapiens.
XX OS
XX WO200157271-A2.
XX PN
XX 09-AUG-2001.
XX PD
XX
XX 30-JAN-2001; 2001WO-US000662.
XX PF
XX 04-FEB-2000; 2000US-0180312P.
XX 26-MAY-2000; 2000US-0207456P.
XX 30-JUN-2000; 2000US-00608408.
XX 03-AUG-2000; 2000US-00632366.
XX 21-SEP-2000; 2000US-0234687P.
XX 27-SEP-2000; 2000US-0236359P.
XX 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488897/53.
XX Human genome-derived single exon nucleic acid probes useful for analyzing
XX gene expression in human placenta.
XX
XX Claim 25; SEQ ID NO 16210; 654pp; English.
XX
XX The present invention relates to single exon nucleic acid probes (SENPs).
XX The present sequence is one such probe. The probes are useful for
XX producing a microarray for predicting, measuring and displaying gene
XX expression in samples derived from human placenta. The probes are useful
XX for antenatal diagnosis of human genetic disorders
XX
XX Sequence 77 BP; 25 A; 13 C; 18 G; 21 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 11; DB 4; Length 77;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CTTTGGCACTA 11
DB 34 CTTTGGCACTA 44
RESULT 20
AAK41482
ID AAK41482 standard; DNA; 77 BP.
XX
XX AAK41482;
AC
XX
XX 06-NOV-2001 (first entry)
DT
DE Human bone marrow expressed single exon probe SEQ ID NO: 16039.
DE
XX Human; bone marrow expressed exon; gene expression analysis; probe;
KW microarray; cancer; leukaemia; lymphoma; myeloma; ss.
XX
XX Homo sapiens.
XX OS
XX WO200157276-A2.
XX PN
XX 09-AUG-2001.
XX PD
XX
XX 30-JAN-2001; 2001WO-US000668.
XX PF
XX 04-FEB-2000; 2000US-0180312P.
XX 26-MAY-2000; 2000US-0207456P.
XX 30-JUN-2000; 2000US-00608408.
XX 03-AUG-2000; 2000US-00632366.
XX 21-SEP-2000; 2000US-0234687P.
XX

PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-496933/54.
XX New spatially-addressable set of single exon nucleic acid probes, useful
XX for measuring gene expression in sample derived from human breast,
XX comprises number of single exon nucleic acid probes.
XX
XX Claim 4; SEQ ID NO 8093; 327pp + Sequence Listing; English.
XX
XX The invention relates to a spatially-addressable set of single exon
XX nucleic acid probes for measuring gene expression in a sample derived
XX from human breast and Br 474 cells. The method involves contacting the
XX probes with a collection of detectably labelled nucleic acids derived
XX from mRNA of human breast, and then measuring the label bound to each
XX probe of the microarray. The probes are useful for verifying the
XX expression of regions of genomic DNA predicted to encode proteins. They
XX are useful for gene discovery, and for determining predisposition and/or
XX prognosis breast disease. Gene expression analysis is useful for
XX assessing the toxicity of chemical agents on cells. The microarray of
XX this invention presents a far greater diversity of probes for measuring
XX gene expression, with far less bias than expressed sequence tag
XX microarrays. The method is suitable for rapid production of functional
XX information from genomic sequence. The present sequence is a single exon
XX nucleic acid probe of the invention. Note: The sequence data for this
XX patent did not form part of the printed specification, but was obtained
XX in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
SQ Sequence 77 BP; 25 A; 13 C; 18 G; 21 T; 0 U; 0 Other;
Query Match 100.0%; Score 11; DB 4; Length 77;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CTTTGGCACTA 11
DB 34 CTTTGGCACTA 44
RESULT 20
AAK41482
ID AAK41482 standard; DNA; 77 BP.
XX
XX AAK41482;
AC
XX
XX 06-NOV-2001 (first entry)
DT
DE Human bone marrow expressed single exon probe SEQ ID NO: 16039.
DE
XX Human; bone marrow expressed exon; gene expression analysis; probe;
KW microarray; cancer; leukaemia; lymphoma; myeloma; ss.
XX
XX Homo sapiens.
XX OS
XX WO200157276-A2.
XX PN
XX 09-AUG-2001.
XX PD
XX
XX 30-JAN-2001; 2001WO-US000668.
XX PF
XX 04-FEB-2000; 2000US-0180312P.
XX 26-MAY-2000; 2000US-0207456P.
XX 30-JUN-2000; 2000US-00608408.
XX 03-AUG-2000; 2000US-00632366.
XX 21-SEP-2000; 2000US-0234687P.
XX

PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488900/53.
XX Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human bone marrow.
XX Example 4; SEQ ID NO 16039; 659pp + Sequence Listing; English.
XX The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC bone marrow. They can be used to measure gene expression in bone marrow
CC samples, which may enable the improved diagnosis and treatment of cancers
CC such as lymphoma, leukaemia and myeloma. The present sequence is one of
CC the probes of the invention
XX
SQ Sequence 77 BP; 25 A; 13 C; 18 G; 21 T; 0 U; 0 Other;
Query Match 100.0%; Score 11; DB 4; Length 77;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTTTGGCACTA 11
DB 34 CTTTGGCACTA 44
RESULT 21
AAK15744
ID AAK15744 standard; DNA; 77 BP.
XX AAK15744;
XX 05-NOV-2001 (first entry)
XX Human brain expressed single exon probe SEQ ID NO: 15735.
XX Human; brain expressed exon; gene expression analysis; probe; microarray;
KW Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer;
KW ss.
XX Homo sapiens.
XX WO200157275-A2.
XX 09-AUG-2001.
XX 30-JAN-2001; 2001WO-US000667.
XX 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-483446/52.
XX Single exon nucleic acid probes for analyzing gene expression in human
PT brains.
XX Example 4; SEQ ID NO 15735; 650pp + Sequence Listing; English.
XX

CC The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC brain. They can be used to measure gene expression in brain cell samples,
CC which may enable the diagnosis and improved treatment of nervous system
CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
CC epilepsy and cancers. The present sequence is one of the probes of the
CC invention
XX
SQ Sequence 77 BP; 25 A; 13 C; 18 G; 21 T; 0 U; 0 Other;
Query Match 100.0%; Score 11; DB 4; Length 77;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTTTGGCACTA 11
DB 34 CTTTGGCACTA 44
RESULT 22
ABS41072
ID ABS41072 standard; DNA; 77 BP.
XX AC ABS41072;
XX 25-FEB-2003 (first entry)
XX Human liver single exon probe, SEQ ID NO 16062.
XX Human; single exon nucleic acid probe; liver; cirrhosis;
KW hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia;
KW coronary heart disease; ss.
XX Homo sapiens.
XX WO200157273-A2.
XX 09-AUG-2001.
XX 30-JAN-2001; 2001WO-US000664.
XX 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488998/53.
XX Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human adult liver.
XX Claim 4; SEQ ID NO 16062; 659pp; English.
XX The invention relates to a single exon nucleic acid probe (SENP) (I) for
CC measuring human gene expression in a sample derived from human adult
CC liver, comprising one of 13109 defined nucleotide sequences given in the
CC specification (or complements/ fragments). The probe hybridises at high
CC stringency to a nucleic acid molecule expressed in the human adult liver.
CC (I) may be used for predicting, measuring and displaying gene expression
CC in samples derived from human adult liver. The genes identified may be
CC involved in genetic liver diseases such as cirrhosis,
CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is
CC associated with coronary heart disease. ABS25011-ABS51005 represent human
CC liver single exon nucleic acid probes of the invention. Note: The
CC sequence information for this patent does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at

CC ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 77 BP; 25 A; 13 C; 18 G; 21 T; 0 U; 0 Other;

Query Match 100.0%; Score 11; DB 4; Length 77;

Best Local Similarity 100.0%; Pred. No. 2e+03;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTGGCACTA 11

|||||

DB 34 CTTTGGCACTA 44

RESULT 23

AAI07928

ID AAI07928 standard; DNA; 77 BP.

XX

AC AAI07928;

XX

DT 09-OCT-2001 (first entry)

XX

DE Probe #7919 used to measure gene expression in human breast sample.

XX

Probe; human; breast disease; breast cancer; development disorder; ss;

KW inflammatory disease; proliferative breast disease; non-carcinoma tumour.

XX

OS Homo sapiens.

XX

PN WO200157270-A2.

XX

PD 09-AUG-2001.

XX

PF 29-JAN-2001; 2001WO-US000661.

XX

PR 04-FEB-2000; 2000US-0180312P.

XX

PR 26-MAY-2000; 2000US-0207456P.

XX

PR 30-JUN-2000; 2000US-00608408.

XX

PR 03-AUG-2000; 2000US-00632366.

XX

PR 21-SEP-2000; 2000US-0234687P.

XX

PR 27-SEP-2000; 2000US-0236359P.

XX

PR 04-OCT-2000; 2000GB-00024263.

XX

PA (MOLE-) MOLECULAR DYNAMICS INC.

XX

PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX

WPI; 2001-476286/51.

XX

DR Novel single exon nucleic acid probe used to measuring gene expression in

XX

PT a human breast.

XX

PS Claim 25; SEQ ID NO 7919; 322pp; English.

XX

CC The present invention relates to novel single exon nucleic acid probes.

XX

CC The present sequence is one such probe. The probes are useful for

XX

CC measuring human gene expression in a human breast sample, where the probe

XX

CC hybridises at high stringency to a nucleic acid expressed in the human

XX

CC breast. The probes are useful for predicting, diagnosing, grading,

XX

CC staging, monitoring and prognosing diseases of the human breast,

XX

CC particularly those diseases with polygenic aetiology. The diseases

XX

CC include: breast cancer, disorders of development, inflammatory diseases

XX

CC of the breast, fibrocystic changes, proliferative breast disease and non-

XX

CC carcinoma tumours. Note: The sequence data for this patent did not form

XX

CC part of the printed specification, but was obtained in electronic format

XX

CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX

SQ Sequence 77 BP; 25 A; 13 C; 18 G; 21 T; 0 U; 0 Other;

Query Match 100.0%; Score 11; DB 5; Length 77;

Best Local Similarity 100.0%; Pred. No. 2e+03;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTGGCACTA 11

|||||

DB 34 CTTTGGCACTA 44

RESULT 24

ABS15487

ID ABS15487 standard; DNA; 77 BP.

XX

AC ABS15487;

XX

DT 19-AUG-2002 (first entry)

XX

DE Human genome-derived single exon probe ORF from lung SEQ ID No 15478.

XX

Human; ds; single exon probe; asthma; lung cancer; COPD; ILD;

KW chronic obstructive pulmonary disease; interstitial lung disease;

XX

familial idiopathic pulmonary fibrosis; neurofibromatosis;

KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;

XX

Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;

KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome;

XX

pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;

KW primary ciliary dyskinesia; pulmonary hypertension;

XX

hyaline membrane disease; open reading frame; ORF.

OS Homo sapiens.

XX

PN WO200186003-A2.

XX

PD 15-NOV-2001.

XX

PF 30-JAN-2001; 2001WO-US000665.

XX

PR 04-FEB-2000; 2000US-0180312P.

XX

PR 26-MAY-2000; 2000US-0207456P.

XX

PR 30-JUN-2000; 2000US-00608408.

XX

PR 01-SEP-2000; 2000US-00632366.

XX

PR 21-AUG-2000; 2000US-0234687P.

XX

PR 27-SEP-2000; 2000US-0236359P.

XX

PR 04-OCT-2000; 2000GB-00024263.

XX

PA (MOLE-) MOLECULAR DYNAMICS INC.

XX

PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX

WPI; 2002-114183/15.

XX

PT Spatially-addressable set of single exon nucleic acid probes, used to

XX

measure gene expression in human lung samples.

XX

PS Claim 4; SEQ ID NO 15478; 634pp; English.

XX

CC The invention relates to a spatially-addressable set of single exon

XX

CC nucleic acid probes for measuring gene expression in a sample derived

XX

CC from human lung comprising single exon nucleic acid probes having one of

XX

CC 12614 nucleic acid sequences mentioned in the specification, or their

XX

CC complements or the 12387 open reading frames derived from the 12614

XX

CC probes. Also included are a microarray comprising the novel set of probes

XX

CC and the novel set of probes which hybridise at high stringency to a nucleic

XX

CC acid expressed in the human lung; measuring gene expression in a sample

XX

CC derived from human lung, comprising (a) contacting the array with a

CC collection of detectably labeled nucleic acids derived from human lung

CC mRNA, and (b) measuring the label detectably bound to each probe of the

CC array; identifying exons in a eukaryotic genome, comprising (a)

CC algorithmically predicting at least one exon from genomic sequences of

CC the eukaryote; and (b) detecting specific hybridisation of detectably

CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,

CC in the above mentioned microarray; assigning exons to a single gene,

CC comprising (a) identifying exons from genomic sequence by the method

CC above and (b) measuring the expression of each of the exons in several

CC tissues and/or cell types using hybridisation to a single exon

CC microarrays having a probe with the exon, where a common pattern of

CC expression of the exons in the tissues and/or cell types indicates that

CC the exons should be assigned to a single gene; a peptide comprising one
CC of 12011 sequences, mentioned in the specification, or encoded by the
CC probes/open reading frames (ORF). The probes are used for gene expression
CC analysis, and for identifying exons in a gene, particularly using human
CC lung derived mRNA and for the study of lung diseases such as asthma, lung
CC cancer, chronic obstructive pulmonary disease (COPD), interstitial lung
CC disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,
CC tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-
CC Pudiak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary
CC histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis,
CC Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary
CC dyskinesia, pulmonary hypertension and hyaline membrane disease. The
CC present sequence is a single exon probe open reading frame of the
CC invention. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 77 BP; 25 A; 13 C; 18 G; 21 T; 0 U; 0 Other;

Query Match 100.0%; Score 11; DB 6; Length 77;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTGGCACTA 11
DB 34 CTTTGGCACTA 44

RESULT 25

AAC22084
ID AAC22084 standard; cDNA; 100 BP.

XX AAC22084;

DT 06-OCT-2000 (first entry)

DE Human secreted protein 5' EST, SEQ ID NO: 26159.

XX Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW gene therapy; chromosome mapping; ss.

XX Homo sapiens.

XX EP1033401-A2.

XX 06-SEP-2000.

XX 21-FEB-2000; 2000EP-00200610.

XX 26-FEB-1999; 99US-0122487P.

XX (GEST) GENSET.

PI Dumas Milne Edwards J, Duclert A, Giordano J;

XX WPI; 2000-500381/45.

XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
PT diagnostic, forensic, gene therapy and chromosome mapping procedures.

XX Claim 1; SEQ ID NO 26159; 71pp + Sequence Listing; English.

XX The present sequence is one of a large number of 5' ESTs derived from
CC mRNAs encoding secreted proteins. No ORF has yet been conclusively
CC identified within the present sequence. The 5' ESTs were prepared from
CC total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
CC sequences usually correspond mainly to the 3' untranslated region (UTR)
CC of the mRNA because they are often obtained from oligo-dT primed cDNA
CC libraries. Such ESTs are not well suited for isolating cDNA sequences
CC derived from the 5' ends of mRNAs and even in those cases where longer
CC cDNA sequences have been obtained, the full 5' UTR is rarely included. 5'
CC ESTs are derived from mRNAs with intact 5' ends and can therefore be used

CC to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in
CC diagnostic, forensic, gene therapy and chromosome mapping procedures.
CC They are used to obtain upstream regulatory sequences and to design
CC expression and secretion vectors

XX SQ Sequence 100 BP; 32 A; 21 C; 14 G; 33 T; 0 U; 0 Other;

Query Match 100.0%; Score 11; DB 3; Length 100;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTGGCACTA 11
DB 81 CTTTGGCACTA 91

RESULT 26

ABK26046/c

ID ABK26046 standard; DNA; 121 BP.

XX ABK26046;

DT 09-APR-2002 (first entry)

DE Amino acid overproduction genome altering oligonucleotide #118.

XX Chromosomal genomic alteration; genome altering oligonucleotide; PCR; ss;
KW o-methyl modification; LNA modification; phosphorothioate linkage;
KW DNA repair; DNA alteration; environmental tolerance; hygromycin-B;
KW abiotic stress tolerance; improved nutritional value; hygromycin-B;
KW amino acid overproduction; herbicide resistance; glyphosate resistance;
KW imidazolinone herbicide resistance; sulphonylurea herbicide resistance;
KW porphyric herbicide resistance; triazine resistance; disease resistance;
KW modified oil production; modified starch production; waxy starch;
KW altered floral morphology; male-sterile plant; albino mutant;
KW modified fatty acid content; reduced palmitate production; albino plant;
KW increased stearate production; reduced linolenic acid production;
KW photosynthetic process.

XX Oryza sativa.

XX Synthetic.

XX WO200192512-A2.

XX 06-DEC-2001.

XX 01-JUN-2001; 2001WO-US017672.

XX 01-JUN-2000; 2000US-0208538P.

XX 30-OCT-2000; 2000US-0244989P.

XX 27-MAR-2001; 2001US-00818875.

XX (UYDE) UNIV DELAWARE.

XX Kmtec EB, Gamper HB, Rice MC, Kim J;

XX WPI; 2002-106307/14.

XX New oligonucleotides with modified nuclease-resistant termini, useful for
PT creating plants with desired phenotypes, e.g. stress tolerance, improved
PT nutritional value, herbicide or disease resistance, or modified oil
PT production.

XX Claim 7; Page 128; 220pp; English.

XX The invention relates to an oligonucleotide for targeted alteration of a
CC genetic sequence, which comprises a single-stranded oligonucleotide
CC having a DNA domain. The DNA domain has at least one mismatch with
CC respect to the genetic sequence to be altered and further comprises
CC chemical modifications of the oligonucleotide. The chemical modifications
CC consist of o-methyl modification, an LNA modification, two or more
CC phosphorothioate linkages on a terminus, or a combination of any two or
CC more of these modifications. The oligonucleotides are useful for

CC directing repair or alteration of plant genetic information. The
 CC oligonucleotides are particularly useful for creating plants with desired
 CC phenotypes, e.g. environmental or abiotic stress tolerance, improved
 CC nutritional value (e.g. altering amino acid content of plants or
 CC conferring amino acid over production), herbicide resistance (e.g.
 CC glyphosate resistance, imidazolinone and sulphonylurea herbicide
 CC resistance, porphyrin herbicide resistance or triazine resistance),
 CC disease resistance, modified oil production, modified starch production
 CC (e.g. increased starch or production of waxy starch), altered floral
 CC morphology (e.g. male-sterile plants) or modified fatty acid content
 CC (e.g. reduced palmitate, increased stearate or reduced linolenic acid).
 CC The oligonucleotides are also useful for producing albino mutants for the
 CC analysis of photosynthetic processes. This sequence represents a genome
 CC altering oligonucleotide of the invention

SQ Sequence 121 BP; 28 A; 31 C; 24 G; 38 T; 0 U; 0 Other;

Query Match 100.0%; Score 11; DB 6; Length 121;
 Best Local Similarity 100.0%; Pred. No. 2e+03;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTGGCACTA 11
 |||||
 DB 99 CTTTGGCACTA 89

RESULT 27

ABK26045
 ID ABK26045 standard; DNA; 121 BP.

XX AC ABK26045;

DT 09-APR-2002 (first entry)

XX Amino acid overproduction genome altering oligonucleotide #117.

XX Chromosomal genomic alteration; genome altering oligonucleotide; PCR; ss;
 KW o-methyl modification; LNA modification; phosphorothioate linkage;
 KW DNA repair; DNA alteration; environmental tolerance; hygromycin-B;
 KW abiotic stress tolerance; improved nutritional value; hygromycin; primer;
 KW amino acid over production; herbicide resistance; glyphosate resistance;
 KW imidazolinone herbicide resistance; sulphonylurea herbicide resistance;
 KW porphyrin herbicide resistance; triazine resistance; disease resistance;
 KW modified oil production; modified starch production; waxy starch;
 KW altered floral morphology; male-sterile plant; albino mutant;
 KW increased fatty acid content; reduced palmitate production; albino plant;
 KW increased stearate production; reduced linolenic acid production;
 KW photosynthetic process.

OS Oryza sativa.
 OS Synthetic.

XX WO200192512-A2.

PN 06-DEC-2001.

XX 01-JUN-2001; 2001WO-US017672.

XX 01-JUN-2000; 2000US-0208538P.

PR 30-OCT-2000; 2000US-0244989P.

PR 27-MAR-2001; 2001US-00818875.

XX (UYDE) UNIV DELAWARE.

XX Kmiec EB, Gamber HB, Rice MC, Kim J;

PI WPI; 2002-106307/14.

XX New oligonucleotides with modified nuclease-resistant termini, useful for
 PT creating plants with desired phenotypes, e.g. stress tolerance, improved
 PT nutritional value, herbicide or disease resistance, or modified oil
 PT production.

PS Claim 7; Page 128; 220pp; English.

XX The invention relates to an oligonucleotide for targeted alteration of a
 CC genetic sequence, which comprises a single-stranded oligonucleotide
 CC having a DNA domain. The DNA domain has at least one mismatch with
 CC respect to the genetic sequence to be altered and further comprises
 CC chemical modifications of the oligonucleotide. The chemical modifications
 CC consist of o-methyl modification, an LNA modification, two or more
 CC phosphorothioate linkages on a terminus, or a combination of any two or
 CC more of these modifications. The oligonucleotides are useful for
 CC directing repair or alteration of plant genetic information. The
 CC oligonucleotides are particularly useful for creating plants with desired
 CC phenotypes, e.g. environmental or abiotic stress tolerance, improved
 CC nutritional value (e.g. altering amino acid content of plants or
 CC conferring amino acid over production), herbicide resistance (e.g.
 CC glyphosate resistance, imidazolinone and sulphonylurea herbicide
 CC resistance, porphyrin herbicide resistance or triazine resistance),
 CC disease resistance, modified oil production, modified starch production
 CC (e.g. increased starch or production of waxy starch), altered floral
 CC morphology (e.g. male-sterile plants) or modified fatty acid content
 CC (e.g. reduced palmitate, increased stearate or reduced linolenic acid).
 CC The oligonucleotides are also useful for producing albino mutants for the
 CC analysis of photosynthetic processes. This sequence represents a genome
 CC altering oligonucleotide of the invention

SQ Sequence 121 BP; 38 A; 24 C; 31 G; 28 T; 0 U; 0 Other;

Query Match 100.0%; Score 11; DB 6; Length 121;
 Best Local Similarity 100.0%; Pred. No. 2e+03;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTGGCACTA 11
 |||||
 DB 23 CTTTGGCACTA 33

RESULT 28

ADN44736

ID ADN44736 standard; DNA; 121 BP.

XX AC ADN44736;

XX 15-JUL-2004 (first entry)

XX Mutant cell identification-related mutagenic oligonucleotide SeqID1405.

XX cell identification; oligonucleotide-directed sequence alteration;
 KW selectable phenotype; transgenic plant; herbicide resistance;
 KW sterile plant; abiotic stress tolerance; albino plant;
 KW amino acid production; ss.

OS Oryza sativa.

OS Synthetic.

XX WO2004033708-A2.

XX 22-APR-2004.

XX 07-OCT-2003; 2003WO-US031862.

XX 07-OCT-2002; 2002US-0416983P.

PR 07-MAR-2003; 2003US-0453360P.

XX (UYDE) UNIV DELAWARE.

PA (NAPR-) NAPRO BIO THERAPEUTICS INC.

XX Kmiec EB, Van Brabant A;

XX WPI; 2004-340941/31.

XX Identifying a cell with a desired oligonucleotide-directed sequence
 PT alteration at a nucleic acid target site within the cell by identifying
 PT the desired sequence alteration in cells selected for the presence of a

PT selectable phenotype.

XX Example 27; SEQ ID NO 1405; 303pp; English.

PS This invention relates to a novel method of identifying a cell having a

XX desired oligonucleotide-directed sequence alteration at a first nucleic

CC acid target site within the cell. The method comprises identifying the

CC desired sequence alteration in cells that have been selected for the

CC presence of a selectable phenotype conferred by a concurrent

CC oligonucleotide-directed sequence alteration at a second nucleic acid

CC target site within the cells. The method is useful in identifying a cell

CC having a desired oligonucleotide-directed sequence alteration at a first

CC nucleic acid target site within the cell. The method may be useful for

CC the production of plants with herbicide resistance, male or female

CC sterile plants, abiotic stress tolerance, albino plants or plants with

CC altered amino acid production as well as for use in mammalian cell lines.

CC The present sequence is that of a mutagenic oligonucleotide which was

XX used in the exemplification of the invention.

XX SQ Sequence 121 BP; 38 A; 24 C; 31 G; 28 T; 0 U; 0 Other;

Query Match 100.0%; Score 11; DB 12; Length 121;

Best Local Similarity 100.0%; Pred. No. 2e+03; Mismatches 0; Indels 0; Gaps 0;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTGGCACTA 11

DB 23 CTTTGGCACTA 33

RESULT 29

ADN44737/c

ID ADN44737 standard; DNA; 121 BP.

AC ADN44737;

XX 15-JUL-2004 (first entry)

XX Mutant cell identification-related mutagenic oligonucleotide SeqID1406.

DE cell identification; oligonucleotide-directed sequence alteration;

XX selectable phenotype; transgenic plant; herbicide resistance;

KW sterile plant; abiotic stress tolerance; albino plant;

KW amino acid production; ss.

XX Oryza sativa.

OS Synthetic.

XX WO2004033708-A2.

PN 22-APR-2004.

XX 07-OCT-2003; 2003WO-US031862.

PF 07-OCT-2002; 2002US-0416983P.

XX 07-MAR-2003; 2003US-0453360P.

PR (UYDE) UNIV DELAWARE.

XX (NAPRO-) NAPRO BIO THERAPEUTICS INC.

PA Kmiec BB, Van Brabant A;

XX WPI; 2004-340941/31.

DR Identifying a cell with a desired oligonucleotide-directed sequence

XX alteration at a nucleic acid target site within the cell by identifying

PT the desired sequence alteration in cells selected for the presence of a

PT selectable phenotype.

XX Example 27; SEQ ID NO 1406; 303pp; English.

PS This invention relates to a novel method of identifying a cell having a

CC desired oligonucleotide-directed sequence alteration at a first nucleic

CC acid target site within the cell. The method comprises identifying the

CC desired sequence alteration in cells that have been selected for the

CC presence of a selectable phenotype conferred by a concurrent

CC oligonucleotide-directed sequence alteration at a second nucleic acid

CC target site within the cells. The method is useful in identifying a cell

CC having a desired oligonucleotide-directed sequence alteration at a first

CC nucleic acid target site within the cell. The method may be useful for

CC the production of plants with herbicide resistance, male or female

CC sterile plants, abiotic stress tolerance, albino plants or plants with

CC altered amino acid production as well as for use in mammalian cell lines.

CC The present sequence is that of a mutagenic oligonucleotide which was

XX used in the exemplification of the invention.

XX SQ Sequence 121 BP; 38 A; 24 C; 31 G; 28 T; 0 U; 0 Other;

Query Match 100.0%; Score 11; DB 12; Length 121;

Best Local Similarity 100.0%; Pred. No. 2e+03; Mismatches 0; Indels 0; Gaps 0;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTGGCACTA 11

DB 99 CTTTGGCACTA 89

RESULT 30

AAI23415/c

ID AAI23415 standard; DNA; 153 BP.

XX AAI23415;

XX 12-OCT-2001 (first entry)

DE Probe #13348 for gene expression analysis in human cervical cell sample.

XX Probe; human; microarray; gene expression; cervical epithelial cell;

KW cervical cancer; ss.

XX Homo sapiens.

OS WO200157278-A2.

PN 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US000670.

PF 04-FEB-2000; 2000US-0180312P.

XX 26-MAY-2000; 2000US-0207456P.

PR 30-JUN-2000; 2000US-00608408.

XX 03-AUG-2000; 2000US-00632366.

PR 21-SEP-2000; 2000US-0234687P.

XX 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

PA Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-488901/53.

DR Human genome-derived single exon nucleic acid probes useful for analyzing

XX gene expression in human cervical epithelial cells.

PS Claim 25; SEQ ID NO 13348; 487pp; English.

XX The present invention relates to human single exon nucleic acid probes

CC (SENPs). The present sequence is one such probe. The SENPs are derived

CC from human HeLa cells. The SENPs can be used to produce a single exon

CC microarray, which can be used for measuring human gene expression in a

CC sample derived from human cervical epithelial cells. By measuring gene

CC expression, the probes are therefore useful in grading and/or staging of

CC diseases of the cervix, notably cervical cancer. Note: The sequence data

CC for this patent did not form part of the printed specification, but was

CC obtained in electronic format directly from WIPO at

CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 153 BP; 47 A; 33 C; 45 G; 28 T; 0 U; 0 Other;
 Query Match 100.0%; Score 11; DB 4; Length 153;
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CTTTGGCACTA 11
 Db 99 CTTTGGCACTA 89
 RESULT 31
 ABA68523/c
 ID ABA68523 standard; DNA; 153 BP.
 XX
 AC ABA68523;
 XX
 DT 01-FEB-2002 (first entry)
 XX
 DE Human foetal liver single exon nucleic acid probe #16828.
 XX
 KW Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200157277-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 30-JAN-2001; 2001WO-US000669.
 XX
 PR 04-FEB-2000; 2000US-0180312P.
 XX
 PR 26-MAY-2000; 2000US-0207456P.
 XX
 PR 30-JUN-2000; 2000US-00608408.
 XX
 PR 03-AUG-2000; 2000US-00632366.
 XX
 PR 21-SEP-2000; 2000US-0234687P.
 XX
 PR 27-SEP-2000; 2000US-0236359P.
 XX
 PR 04-OCT-2000; 2000GB-00024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX
 PF WPI; 2001-483447/52.
 XX
 DR Human genome-derived single exon nucleic acid probes useful for analyzing
 XX gene expression in human foetal liver.
 XX
 PS Claim 4; SEQ ID NO 16828; 639pp + Sequence Listing; English.
 XX
 CC The invention relates to a single exon nucleic acid probe for measuring
 CC human gene expression in a sample derived from human foetal liver. The
 CC single exon nucleic acid probes may be used for predicting, measuring and
 CC displaying gene expression in samples derived from human foetal liver. The
 CC present sequence is a single exon nucleic acid probe of the invention.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 153 BP; 47 A; 33 C; 45 G; 28 T; 0 U; 0 Other;
 Query Match 100.0%; Score 11; DB 4; Length 153;
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CTTTGGCACTA 11
 Db 99 CTTTGGCACTA 89
 RESULT 32
 ABA50565/c
 ID ABA50565 standard; DNA; 153 BP.
 XX
 AC ABA50565;
 XX
 DT 01-FEB-2002 (first entry)
 XX
 DE Human breast cell single exon nucleic acid probe #9260.
 XX
 KW Human; microarray; single exon probe; gene expression; breast; disease;
 XX cancer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200157271-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 30-JAN-2001; 2001WO-US000663.
 XX
 PR 04-FEB-2000; 2000US-0180312P.
 XX
 PR 26-MAY-2000; 2000US-0207456P.
 XX
 PR 30-JUN-2000; 2000US-00608408.
 XX
 PR 03-AUG-2000; 2000US-00632366.
 XX
 PR 21-SEP-2000; 2000US-0234687P.
 XX
 PR 27-SEP-2000; 2000US-0236359P.
 XX
 PR 04-OCT-2000; 2000GB-00024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX
 PF WPI; 2001-488897/53.
 XX
 DR Human genome-derived single exon nucleic acid probes useful for analyzing
 XX gene expression in human placenta.
 XX
 PS Claim 25; SEQ ID NO 17421; 654pp; English.
 XX
 CC The present invention relates to single exon nucleic acid probes (SENPs).
 CC The present sequence is one such probe. The probes are useful for
 CC producing a microarray for predicting, measuring and displaying gene
 CC expression in samples derived from human placenta. The probes are useful
 CC for antenatal diagnosis of human genetic disorders
 XX
 SQ Sequence 153 BP; 47 A; 33 C; 45 G; 28 T; 0 U; 0 Other;
 Query Match 100.0%; Score 11; DB 4; Length 153;
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CTTTGGCACTA 11
 Db 99 CTTTGGCACTA 89
 RESULT 33
 ABA50565/c
 ID ABA50565 standard; DNA; 153 BP.
 XX
 AC ABA50565;
 XX
 DT 01-FEB-2002 (first entry)
 XX
 DE Human breast cell single exon nucleic acid probe #9260.
 XX
 KW Human; microarray; single exon probe; gene expression; breast; disease;
 XX cancer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200157271-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 30-JAN-2001; 2001WO-US000663.
 XX
 PR 04-FEB-2000; 2000US-0180312P.
 XX
 PR 26-MAY-2000; 2000US-0207456P.
 XX
 PR 30-JUN-2000; 2000US-00608408.
 XX
 PR 03-AUG-2000; 2000US-00632366.
 XX
 PR 21-SEP-2000; 2000US-0234687P.
 XX
 PR 27-SEP-2000; 2000US-0236359P.
 XX
 PR 04-OCT-2000; 2000GB-00024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX
 PF WPI; 2001-488897/53.
 XX
 DR Human genome-derived single exon nucleic acid probes useful for analyzing
 XX gene expression in human placenta.
 XX
 PS Claim 25; SEQ ID NO 17421; 654pp; English.
 XX
 CC The present invention relates to single exon nucleic acid probes (SENPs).
 CC The present sequence is one such probe. The probes are useful for
 CC producing a microarray for predicting, measuring and displaying gene
 CC expression in samples derived from human placenta. The probes are useful
 CC for antenatal diagnosis of human genetic disorders
 XX
 SQ Sequence 153 BP; 47 A; 33 C; 45 G; 28 T; 0 U; 0 Other;

```
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000662.
XX
PR 04-FEB-2000; 2000US-0180312P.
XX
PR 26-MAY-2000; 2000US-0207456P.
XX
PR 30-JUN-2000; 2000US-00608408.
XX
PR 03-AUG-2000; 2000US-00632366.
XX
PR 21-SEP-2000; 2000US-0234687P.
XX
PR 27-SEP-2000; 2000US-0236359P.
XX
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-496933/54.
XX
XX New spatially-addressable set of single exon nucleic acid probes, useful
PT for measuring gene expression in sample derived from human breast,
PT comprises number of single exon nucleic acid probes.
XX
PS Claim 4; SEQ ID NO 9260; 327bp + Sequence Listing; English.
XX
CC The invention relates to a spatially-addressable set of single exon
CC nucleic acid probes for measuring gene expression in a sample derived
CC from human breast and BT 474 cells. The method involves contacting the
CC probes with a collection of detectably labelled nucleic acids derived
CC from mRNA of human breast, and then measuring the label bound to each
CC probe of the microarray. The probes are useful for verifying the
CC expression of regions of genomic DNA predicted to encode proteins. They
CC are useful for gene discovery, and for determining predisposition and/or
CC prognosing breast disease. Gene expression analysis is useful for
CC assessing the toxicity of chemical agents on cells. The microarray of
CC this invention presents a far greater diversity of probes for measuring
CC gene expression, with far less bias than expressed sequence tag
CC microarrays. The method is suitable for rapid production of functional
CC information from genomic sequence. The present sequence is a single exon
CC nucleic acid probe of the invention. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 153 BP; 47 A; 33 C; 45 G; 28 T; 0 U; 0 Other;

Query Match 100.0%; Score 11; DB 4; Length 153;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTGGCACTA 11
DB |||||
99 CTTTGGCACTA 89

RESULT 34
ABA35504/c
ID ABA35504 standard; DNA; 153 BP.
XX
XX ABA35504;
AC
XX
XX 23-JAN-2002 (first entry)
DT
DE
DE Probe #13970 for gene expression analysis in human heart cell sample.
XX
XX Human; gene expression; heart; microarray; vascular system; probe;
KW cardiovascular disease; hypertension; cardiac arrhythmia;
KW congenital heart disease; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200157274-A2.
PN
XX
XX 09-AUG-2001.
PD

PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000666.
XX
PR 04-FEB-2000; 2000US-0180312P.
XX
PR 26-MAY-2000; 2000US-0207456P.
XX
PR 30-JUN-2000; 2000US-00608408.
XX
PR 03-AUG-2000; 2000US-00632366.
XX
PR 21-SEP-2000; 2000US-0234687P.
XX
PR 27-SEP-2000; 2000US-0236359P.
XX
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488899/53.
XX
XX Single exon nucleic acid probes for analyzing gene expression in human
PT hearts.
PT
XX
PS Claim 4; SEQ ID NO 13970; 530pp; English.
XX
CC The present invention relates to single exon nucleic acid probes for
CC measuring human gene expression in a sample derived from human heart. The
CC present sequence is one such probe. The probes may be used for
CC predicting, measuring and displaying gene expression in samples derived
CC from the human heart via microarrays. By measuring gene expression, the
CC probes are useful for predicting, diagnosing, grading, staging,
CC monitoring and prognosing diseases of the human heart and vascular system
CC e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
CC congenital heart disease. Note: The sequence data for this patent did not
CC form part of the printed specification, but was obtained in electronic
CC format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 153 BP; 47 A; 33 C; 45 G; 28 T; 0 U; 0 Other;

Query Match 100.0%; Score 11; DB 4; Length 153;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTGGCACTA 11
DB |||||
99 CTTTGGCACTA 89

RESULT 35
AAK42661/c
ID AAK42661 standard; DNA; 153 BP.
XX
XX AAK42661;
AC
XX
XX 06-NOV-2001 (first entry)
DT
DE
DE Human bone marrow expressed single exon probe SEQ ID NO: 17218.
XX
XX Human; bone marrow expressed exon; gene expression analysis; probe;
KW microarray; cancer; leukaemia; lymphoma; myeloma; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200157276-A2.
PN
XX
XX 09-AUG-2001.
PD

PD 30-JAN-2001; 2001WO-US000668.
XX
XX 04-FEB-2000; 2000US-0180312P.
XX
XX 26-MAY-2000; 2000US-0207456P.
XX
XX 30-JUN-2000; 2000US-00608408.
XX
XX 03-AUG-2000; 2000US-00632366.
XX
XX 21-SEP-2000; 2000US-0234687P.
XX
XX 27-SEP-2000; 2000US-0236359P.
XX
XX 04-OCT-2000; 2000GB-00024263.
XX
```


SQ Sequence 153 BP; 47 A; 33 C; 45 G; 28 T; 0 U; 0 Other;

Query Match 100.0%; Score 11; DB 4; Length 153;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTGGCACTA 11
|||||
Db 99 CTTTGGCACTA 89

RESULT 38

AAI09041/c
ID AAI09041 standard; DNA; 153 BP.

XX AC AAI09041;

DT 09-OCT-2001 (first entry)

DE Probe #9032 used to measure gene expression in human breast sample.

KW Probe; human; breast disease; breast cancer; development disorder; ss;
KW inflammatory disease; proliferative breast disease; non-carcinoma tumour.

XX OS Homo sapiens.

XX PN WO200157270-A2.

XX PD 09-AUG-2001.

XX PF 29-JAN-2001; 2001WO-US000661.

XX PR 04-FEB-2000; 2000US-0180312P.

XX PR 26-MAY-2000; 2000US-0207456P.

XX PR 30-JUN-2000; 2000US-0060840B.

XX PR 03-AUG-2000; 2000US-00632366.

XX PR 21-SEP-2000; 2000US-0234687P.

XX PR 27-SEP-2000; 2000US-0236359P.

XX PR 04-OCT-2000; 2000GB-00024263.

XX PA (MOLE-) MOLECULAR DYNAMICS INC.

XX PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-476286/51.

XX PT Novel single exon nucleic acid probe used to measuring gene expression in

XX PT a human breast.

XX PS Claim 25; SEQ ID NO 9032; 322pp; English.

XX CC The present invention relates to novel single exon nucleic acid probes.

XX CC The present sequence is one such probe. The probes are useful for

XX CC measuring human gene expression in a human breast sample, where the probe

XX CC hybridises at high stringency to a nucleic acid expressed in the human

XX CC breast. The probes are useful for predicting, diagnosing, grading,

XX CC staging, monitoring and prognosing diseases of the human breast,

XX CC particularly those diseases with polygenic aetiology. The diseases

XX CC include: breast cancer, disorders of development, inflammatory diseases

XX CC of the breast, fibrocystic changes, proliferative breast disease and non-

XX CC carcinoma tumours. Note: The sequence data for this patent did not form

XX CC part of the printed specification, but was obtained in electronic format

XX CC directly from WIPO at ftp.wipo.int/pub/published_pt_sequences

RESULT 39

ABS16713/c

ID ABS16713 standard; DNA; 153 BP.

XX AC ABS16713;

DT 19-AUG-2002 (first entry)

XX DE Human genome-derived single exon probe ORF from lung SEQ ID No 16704.

XX KW Human; ds; single exon probe; asthma; lung cancer; COPD; ILD;

XX KW chronic obstructive pulmonary disease; interstitial lung disease;

XX KW familial idiopathic pulmonary fibrosis; neurofibromatosis;

XX KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;

XX KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;

XX KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome;

XX KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;

XX KW primary ciliary dyskinesia; pulmonary hypertension;

XX KW hyaline membrane disease; open reading frame; ORF.

XX OS Homo sapiens.

XX PN WO200186003-A2.

XX PD 15-NOV-2001.

XX PF 30-JAN-2001; 2001WO-US000665.

XX PR 04-FEB-2000; 2000US-0180312P.

XX PR 26-MAY-2000; 2000US-0207456P.

XX PR 30-JUN-2000; 2000US-0060840B.

XX PR 03-AUG-2000; 2000US-00632366.

XX PR 21-SEP-2000; 2000US-0234687P.

XX PR 27-SEP-2000; 2000US-0236359P.

XX PR 04-OCT-2000; 2000GB-00024263.

XX PA (MOLE-) MOLECULAR DYNAMICS INC.

XX PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2002-114183/15.

XX PT Spatially-addressable set of single exon nucleic acid probes, used to

XX PT measure gene expression in human lung samples.

XX PS Claim 4; SEQ ID NO 16704; 634pp; English.

XX CC The invention relates to a spatially-addressable set of single exon

XX CC nucleic acid probes for measuring gene expression in a sample derived

XX CC from human lung comprising single exon nucleic acid probes having one of

XX CC 12614 nucleic acid sequences mentioned in the specification, or their

XX CC complements or the 12387 open reading frames derived from the 12614

XX CC probes. Also included are a microarray comprising the novel set of probes

XX CC ; the novel set of probes which hybridise at high stringency to a nucleic

XX CC acid expressed in the human lung; measuring gene expression in a sample

XX CC derived from human lung, comprising (a) contacting the array with a

XX CC collection of detectably labeled nucleic acids derived from human lung

XX CC mRNA, and (b) measuring the label detectably bound to each probe of the

XX CC array; identifying exons in a eukaryotic genome, comprising (a)

XX CC algorithmically predicting at least one exon from genomic sequences of

XX CC the eukaryote; and (b) detecting specific hybridisation of detectably

XX CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,

XX CC having a fragment identical to the predicted exon, the probe is included

XX CC in the above mentioned microarray; assigning exons to a single gene,

XX CC comprising (a) identifying exons from genomic sequence by the method

XX CC above and (b) measuring the expression of each of the exons in several

XX CC tissues and/or cell types using hybridisation to a single exon

XX CC microarrays having a probe with the exon, where a common pattern of

XX CC expression of the exons in the tissues and/or cell types indicates that

XX CC the exons should be assigned to a single gene; a peptide comprising one

XX CC of 12011 sequences, mentioned in the specification, or encoded by the

CC probes/open reading frames (ORF). The probes are used for gene expression
 CC analysis, and for identifying exons in a gene, particularly using human
 CC lung derived mRNA and for the study of lung diseases such as asthma, lung
 CC cancer, chronic obstructive pulmonary disease (COPD), interstitial lung
 CC disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,
 CC tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hexmanský-
 CC Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary
 CC histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis,
 CC Karagazer syndrome, fibrocystic pulmonary dysplasia, primary ciliary
 CC dyskinesia, pulmonary hypertension and hyaline membrane disease. The
 CC present sequence is a single exon probe open reading frame of the
 CC invention. Note: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 153 BP; 47 A; 33 C; 45 G; 28 T; 0 U; 0 Other;

Query Match 100.0%; Score 11; DB 6; Length 153;
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTGGCACTA 11
 |||||
 Db 99 CTTTGGCACTA 89

RESULT 40
 ACF72987/C
 ID ACF72987 standard; DNA; 204 BP.

XX AC ACF72987;

XX DT 20-NOV-2003 (first entry)

XX DE Staphylococcus aureus DNA #667.

XX KW Antibacterial; vaccine; gene therapy; infection; sepsis; diagnosis;
 KW enzymatic assay; antibiotic target; gene; ds.

XX OS Staphylococcus aureus.

XX PN WO200294868-A2.

XX PD 28-NOV-2002.

XX PF 27-MAR-2002; 2002WO-IB002637.

XX PR 27-MAR-2001; 2001GB-00007661.

XX PA (CHIR-) CHIRON SPA.

XX PI Masignani V, Mora M, Scarselli M;

XX DR WPI; 2003-120786/11.

XX DR P-PSDB; ABW71427.

XX PT New Staphylococcus aureus protein, useful as a vaccine for treating or
 PT preventing Staphylococcal infection, specifically an infection caused by
 PT S. aureus, e.g. sepsis.

XX PS Claim 6; SEQ ID NO 1333; 49pp; English.

XX CC The invention relates to novel genes and encoded proteins from
 CC Staphylococcus aureus. A composition comprising the S. aureus protein, a
 CC nucleic acid encoding the protein, or an antibody to the protein, is
 CC useful as a pharmaceutical, particularly as a vaccine for treating or
 CC preventing infection due to Staphylococcus bacteria, specifically an
 CC infection caused by S. aureus. The composition is particularly useful for
 CC treating or preventing sepsis in a patient. The composition can also be
 CC used for diagnostics. The protein is also used in an assay for enzymatic
 CC studies and as a target for antibiotics. This sequence represents one of
 CC the novel S. aureus genes of the invention

XX

SQ Sequence 204 BP; 76 A; 30 C; 35 G; 63 T; 0 U; 0 Other;

Query Match 100.0%; Score 11; DB 8; Length 204;
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTGGCACTA 11
 |||||
 Db 109 CTTTGGCACTA 99

RESULT 41
 ABS68966
 ID ABS68966 standard; DNA; 213 BP.

XX AC ABS68966;

XX DT 21-NOV-2002 (first entry)

XX DE Novel murine polynucleotide isolated using gene trap technology #29.

XX KW Mouse; gene trapped sequence; GTS; functional genomic analysis;
 KW phage display system; gene chip; temporal gene expression;
 KW tissue specific gene expression; antisense inhibition; gene targeting;
 KW development disorder; cell differentiation disorder; aging; cancer;
 KW autoimmune disease; lupus; inflammatory disorder; skin disorder;
 KW degenerative disorder; ds.

XX OS Mus musculus.

XX PN US2002102543-A1.

XX PD 01-AUG-2002.

XX PF 30-NOV-2000; 2000US-00728445.

XX PR 01-DEC-1999; 99US-0168358P.

XX PA (FRIE/) FRIEDRICH G.

XX PA (ZAMB/) ZAMBROWICZ B.

XX PA (SAND/) SANDS A T.

XX PI Friedrich G, Zambrowicz B, Sands AT;

XX DR WPI; 2002-690598/74.

XX PT Novel murine polynucleotides that individually identify novel genes into
 PT which a retroviral gene trap vector has integrated, useful in genomic
 PT analysis and in discovery, development of therapeutic and diagnostic
 PT agents.

XX PS Claim 1; Page 35; 296pp; English.

XX CC The invention describes an isolated murine polynucleotide (I) comprising
 CC a contiguous stretch of at least 60 nucleotides of one of 265-677
 CC nucleotide 891 OMNIBANK gene trapped sequences (GTSs) (S), given in the
 CC specification. The novel genes and cells are useful in functional genomic
 CC analysis and in the discovery and development of new therapeutic and
 CC diagnostic agents and methods. (I) is useful for identifying the coding
 CC regions of the murine genome, to isolate cDNAs, genomic clones, or full-
 CC length genes/polynucleotides or homologues, heterologues, paralogues, or
 CC orthologues that are capable of hybridising to one or more of the GTSs
 CC under stringent conditions. (I) can be incorporated into a phage display
 CC system that can be used to screen for proteins, or other ligands, that
 CC are capable of binding an amino acid sequence encoded by an
 CC oligonucleotide or polynucleotide sequence in at least one of the TS
 CC sequences. (I) is useful in addressable arrays, such as gene chips, to
 CC identify and characterise temporal and tissue specific gene expression,
 CC to identify the gene of interest from many sources and for genetic
 CC manipulations such as antisense inhibition and gene targeting. Decreasing
 CC the level of expression of (I) and/or down regulating the activity of
 CC peptides or proteins encoded by (I) is useful for treating development
 CC and cell differentiation disorders, aging, cancer, autoimmune disease,

CC lupus, inflammatory disorders, skin disorders and degenerative disorders.
CC This sequence represents a murine cDNA isolated using gene trap
CC technology

SQ Sequence 213 BP; 53 A; 37 C; 36 G; 87 T; 0 U; 0 Other;
Query Match 100.0%; Score 11; DB 6; Length 213;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGGCACTA 11
|||
Db 175 CTTGGCACTA 185

RESULT 42
ABL71901/C
ID ABL71901 standard; cDNA; 240 BP.

XX ABL71901;

XX 14-MAY-2002 (first entry)

DE Corn tassel-derived polynucleotide (cdps) SEQ ID NO:1275.

XX Corn; corn tassel-derived polynucleotide; cdps; hybrid breeding; CDPS;
KW inheritance; characteristic; growth; development; disease resistance;
KW environmental adaptability; quality; yield; molecular marker;
KW multigene trait; plant breeding; corn tassel; gene; ss.

XX Zea mays.

OS US2001051335-A1.

PN 13-DEC-2001.

PD 16-APR-1999; 99US-00294093.

PF 21-APR-1998; 98US-0082567P.

PR (LALG/) LALGUDI R V.

PA (ITOL/) ITO L Y.

PA (SHER/) SHERMAN B K.

PI Lalgudi RV, Ito LY, Sherman BK;

XX WPI; 2002-163647/21.

XX Novel purified corn tassel-derived polynucleotide useful for determining
PT altered gene expression, to recover regulatory elements and to follow
PT inheritance of desirable characteristics through hybrid breeding
PT programs.

XX Claim 1; SEQ ID NO 1275; 201pp; English.

XX The present sequence describes a purified corn tassel-derived
CC polynucleotide sequence (cdps) comprising a nucleic acid sequence
CC selected from those given in ABL7627 to ABL76833. The cdps sequences
CC encode corn tassel-derived polypeptides (CDPs). The cdps sequences (I)
CC can be used for determining altered gene expression, to recover
CC regulatory elements and to follow inheritance of desirable
CC characteristics through hybrid breeding programs. (I) are also useful in
CC the evaluation, and alteration of desired characteristics associated with
CC growth and development, disease resistance, environmental adaptability,
CC quality and yield, and as molecular markers for studying inheritance of
CC multigene traits in a plant breeding program. (I) can be used to produce
CC a tassel-specific profile of gene transcription, a transcript image, to
CC clone regulatory elements for use in transformation vectors, to express a
CC polypeptide, to identify, isolate or extend identical or related corn
CC tassel nucleic acid sequences from DNA libraries, in nucleic acid
CC hybridisation or amplification technologies, as query sequences to
CC determine homology of known sequences, as probe for use in Southern or
CC Northern hybridisation, and to identify the presence of and/or to

CC determine the degree of similarity between two (or more) nucleic acid
CC sequences

SQ Sequence 240 BP; 79 A; 68 C; 49 G; 44 T; 0 U; 0 Other;

Query Match 100.0%; Score 11; DB 6; Length 240;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGGCACTA 11
|||
Db 120 CTTGGCACTA 110

RESULT 43
ABAL1368
ID ABAL1368 standard; cDNA; 245 BP.

XX ABAL1368;

XX 23-JAN-2002 (first entry)

DE Human nervous system related polynucleotide SEQ ID NO 375.

XX Human; nootropic; neuroprotective; cytostatic; dermatological; virucide;
KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnery;
KW antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer;
KW antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;
KW antiallergic; antidiabetic; antitumor; antitumor; antitumor;
KW antiparasitic; cardiant; immune disorder; cardiovascular disorder;
KW neurological disease; infection; nephrotropic; gene therapy; vaccine; ss.

OS Homo sapiens.

XX WO200159063-A2.

XX 16-AUG-2001.

XX 17-JAN-2001; 2001WO-US001334.

XX 31-JAN-2000; 2000US-0179065P.

PR 04-FEB-2000; 2000US-0180628P.

PR 24-FEB-2000; 2000US-0184664P.

PR 02-MAR-2000; 2000US-0186350P.

PR 16-MAR-2000; 2000US-0189874P.

PR 17-MAR-2000; 2000US-0190076P.

PR 18-APR-2000; 2000US-0198123P.

PR 19-MAY-2000; 2000US-0205515P.

PR 07-JUN-2000; 2000US-0209467P.

PR 28-JUN-2000; 2000US-0214886P.

PR 30-JUN-2000; 2000US-0215135P.

PR 07-JUL-2000; 2000US-0216647P.

PR 07-JUL-2000; 2000US-0216880P.

PR 11-JUL-2000; 2000US-0217487P.

PR 14-JUL-2000; 2000US-0218290P.

PR 26-JUL-2000; 2000US-0220963P.

PR 26-JUL-2000; 2000US-0220964P.

PR 14-AUG-2000; 2000US-0224518P.

PR 14-AUG-2000; 2000US-0224519P.

PR 14-AUG-2000; 2000US-0225213P.

PR 14-AUG-2000; 2000US-0225214P.

PR 14-AUG-2000; 2000US-0225266P.

PR 14-AUG-2000; 2000US-0225267P.

PR 14-AUG-2000; 2000US-0225268P.

PR 14-AUG-2000; 2000US-0225270P.

PR 14-AUG-2000; 2000US-0225447P.

PR 14-AUG-2000; 2000US-0225757P.

PR 14-AUG-2000; 2000US-0225758P.

PR 18-AUG-2000; 2000US-0225759P.

PR 22-AUG-2000; 2000US-0226681P.

PR 22-AUG-2000; 2000US-0226686P.

PR 22-AUG-2000; 2000US-0227182P.
 PR 23-AUG-2000; 2000US-0227009P.
 PR 30-AUG-2000; 2000US-0228924P.
 PR 01-SEP-2000; 2000US-0229287P.
 PR 01-SEP-2000; 2000US-0229343P.
 PR 01-SEP-2000; 2000US-0229344P.
 PR 01-SEP-2000; 2000US-0229345P.
 PR 05-SEP-2000; 2000US-0229509P.
 PR 05-SEP-2000; 2000US-0229513P.
 PR 06-SEP-2000; 2000US-0230437P.
 PR 06-SEP-2000; 2000US-0230438P.
 PR 08-SEP-2000; 2000US-0231242P.
 PR 08-SEP-2000; 2000US-0231243P.
 PR 08-SEP-2000; 2000US-0231244P.
 PR 08-SEP-2000; 2000US-0231413P.
 PR 08-SEP-2000; 2000US-0231414P.
 PR 08-SEP-2000; 2000US-0232080P.
 PR 08-SEP-2000; 2000US-0232081P.
 PR 12-SEP-2000; 2000US-0231969P.
 PR 14-SEP-2000; 2000US-0232397P.
 PR 14-SEP-2000; 2000US-0232398P.
 PR 14-SEP-2000; 2000US-0232399P.
 PR 14-SEP-2000; 2000US-0232400P.
 PR 14-SEP-2000; 2000US-0232401P.
 PR 14-SEP-2000; 2000US-0233063P.
 PR 14-SEP-2000; 2000US-0233064P.
 PR 14-SEP-2000; 2000US-0233065P.
 PR 21-SEP-2000; 2000US-0234223P.
 PR 21-SEP-2000; 2000US-0234274P.
 PR 25-SEP-2000; 2000US-0234977P.
 PR 25-SEP-2000; 2000US-0234998P.
 PR 26-SEP-2000; 2000US-0235484P.
 PR 27-SEP-2000; 2000US-0235834P.
 PR 27-SEP-2000; 2000US-0235835P.
 PR 29-SEP-2000; 2000US-0236327P.
 PR 29-SEP-2000; 2000US-0236367P.
 PR 29-SEP-2000; 2000US-0236368P.
 PR 29-SEP-2000; 2000US-0236369P.
 PR 29-SEP-2000; 2000US-0236370P.
 PR 02-OCT-2000; 2000US-0236802P.
 PR 02-OCT-2000; 2000US-0237037P.
 PR 02-OCT-2000; 2000US-0237038P.
 PR 02-OCT-2000; 2000US-0237039P.
 PR 13-OCT-2000; 2000US-0237040P.
 PR 13-OCT-2000; 2000US-0239935P.
 PR 13-OCT-2000; 2000US-0239937P.
 PR 20-OCT-2000; 2000US-0240960P.
 PR 20-OCT-2000; 2000US-0241785P.
 PR 20-OCT-2000; 2000US-0241786P.
 PR 20-OCT-2000; 2000US-0241787P.
 PR 20-OCT-2000; 2000US-0241808P.
 PR 20-OCT-2000; 2000US-0241809P.
 PR 20-OCT-2000; 2000US-0241828P.
 PR 20-OCT-2000; 2000US-0242221P.
 PR 01-NOV-2000; 2000US-0244617P.
 PR 08-NOV-2000; 2000US-0246474P.
 PR 08-NOV-2000; 2000US-0246475P.
 PR 08-NOV-2000; 2000US-0246476P.
 PR 08-NOV-2000; 2000US-0246477P.
 PR 08-NOV-2000; 2000US-0246478P.
 PR 08-NOV-2000; 2000US-0246523P.
 PR 08-NOV-2000; 2000US-0246524P.
 PR 08-NOV-2000; 2000US-0246525P.
 PR 08-NOV-2000; 2000US-0246526P.
 PR 08-NOV-2000; 2000US-0246527P.
 PR 08-NOV-2000; 2000US-0246528P.
 PR 08-NOV-2000; 2000US-0246532P.
 PR 08-NOV-2000; 2000US-0246609P.
 PR 08-NOV-2000; 2000US-0246610P.
 PR 08-NOV-2000; 2000US-0246611P.
 PR 08-NOV-2000; 2000US-0246613P.
 PR 17-NOV-2000; 2000US-0249207P.
 PR 17-NOV-2000; 2000US-0249208P.

PR 17-NOV-2000; 2000US-0249209P.
 PR 17-NOV-2000; 2000US-0249210P.
 PR 17-NOV-2000; 2000US-0249211P.
 PR 17-NOV-2000; 2000US-0249212P.
 PR 17-NOV-2000; 2000US-0249213P.
 PR 17-NOV-2000; 2000US-0249214P.
 PR 17-NOV-2000; 2000US-0249215P.
 PR 17-NOV-2000; 2000US-0249216P.
 PR 17-NOV-2000; 2000US-0249217P.
 PR 17-NOV-2000; 2000US-0249218P.
 PR 17-NOV-2000; 2000US-0249244P.
 PR 17-NOV-2000; 2000US-0249245P.
 PR 17-NOV-2000; 2000US-0249264P.
 PR 17-NOV-2000; 2000US-0249265P.
 PR 17-NOV-2000; 2000US-0249297P.
 PR 17-NOV-2000; 2000US-0249299P.
 PR 17-NOV-2000; 2000US-0249300P.
 PR 01-DEC-2000; 2000US-0250391P.
 PR 01-DEC-2000; 2000US-0251160P.
 PR 05-DEC-2000; 2000US-0251030P.
 PR 05-DEC-2000; 2000US-0251988P.
 PR 05-DEC-2000; 2000US-0256719P.
 PR 06-DEC-2000; 2000US-0251479P.
 PR 08-DEC-2000; 2000US-0251856P.
 PR 08-DEC-2000; 2000US-0251856P.
 PR 08-DEC-2000; 2000US-0251859P.
 PR 08-DEC-2000; 2000US-0251989P.
 PR 08-DEC-2000; 2000US-0251990P.
 PR 11-DEC-2000; 2000US-0254097P.
 PR 05-JAN-2001; 2001US-0259678P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Barash SC, Ruben SM;

XX WPI; 2001-541565/60.

DR P-PSDB; ABB15042.

XX Nucleic acids encoding 3224 human nervous system antigen polypeptides,
 PT useful for preventing, diagnosing and/or treating nervous system cancers
 PT and metastases.

XX Claim 1; SEQ ID NO 375; 1701bp + Sequence Listing; English.

XX The invention relates to novel genes (ABA11004-ABA21534) and proteins
 CC (ABB14678-ABB18001) useful for preventing, treating or ameliorating
 CC medical conditions e.g. by protein or gene therapy. The genes are
 CC isolated from a range of human tissues disclosed in the specification.
 CC The nucleic acids, proteins, antibodies and (ant)agonists are useful in
 CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and
 CC ovarian cancer and other cancers of the adrenal gland, bone, bone marrow,
 CC breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune
 CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic
 CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
 CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)
 CC cardiovascular disorders such as myocardial ischaemia; (d) wound healing
 CC ; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)
 CC infectious diseases such as viral, bacterial, fungal and parasitic
 CC infections. Note: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 245 BP; 35 A; 66 C; 82 G; 60 T; 0 U; 2 Other;

Query Match 100.0%; Score 11; DB 5; Length 245;
 Best Local Similarity 100.0%; Pred. NO. 2.1e+03;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTTTGGGCACTA 11
 |||||
 DB 107 CTTTGGGCACTA 117

RESULT 44
ABN24053/c
ID ABN24053 standard; cDNA; 246 BP.
XX
AC ABN24053;
XX
DT 24-JUN-2002 (first entry)
XX
DE Human ORFX polynucleotide sequence SEQ ID NO:16583.
XX
KW Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis;
KW hyperproliferative disorder; psoriasis; benign tumour; haemorrhage;
KW degenerative disorder; osteoarthritis; neurodegenerative disorder;
KW cardiovascular disease; diabetes mellitus; systemic lupus erythematosus;
KW hypertension; hypothyroidism; cholesterol ester storage disease;
KW immune deficiency; immune disorder; infectious disease;
KW autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
KW myasthenia gravis; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200192523-A2.
XX
PD 06-DEC-2001.
XX
PF 29-MAY-2001; 2001WO-US010836.
XX
PR 30-MAY-2000; 2000US-0206132P.
PR 29-AUG-2000; 2000US-0228716P.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shinkets RA, Leach MD;
XX
DR WPI; 2002-106308/14.
XX
PR P-PSDB; ABP08301.
XX
PT Novel human polypeptides and polynucleotides useful for diagnosing,
PT preventing and treating cardiovascular disease, neurodegenerative,
PT hyperproliferative disorders and autoimmune disorders.
XX
PS Disclosure; SEQ ID NO 16583; 1037pp; English.
XX
CC The present invention describes substantially purified human proteins
CC (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1
CC in the specification). ABN15762 to ABN27252 encode the human ORFX
CC proteins given in ABP0010 to ABP1500. ORFX proteins are useful for
CC treating or preventing a pathology associated with an ORFX-associated
CC disorder in humans, and in the manufacture of a medicament for treating a
CC syndrome associated with ORFX-associated disorder. ORFX polynucleotide
CC sequences can be used in gene therapy. ORFX sequences can be used in the
CC treatment of cancer, hyperproliferative disorders, cirrhosis of liver,
CC psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage,
CC osteoarthritis, neurodegenerative disorders, disorders related to organ
CC transplantation, cardiovascular diseases, diabetes mellitus, systemic
CC lupus erythematosus, hypertension, hypothyroidism, cholesterol ester
CC storage disease, various immune deficiencies and disorders, infectious
CC diseases, autoimmune disorders such as multiple sclerosis, rheumatoid
CC arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host
CC disease and autoimmune inflammatory eye disease. ORFX proteins are also
CC useful for treating burns, incisions, ulcers, for treating osteoporosis,
CC bone degenerative disorders, or periodontal disease, and for gut
CC protection or regeneration and treatment of lung or liver fibrosis,
CC reperfusion injury in various tissues and conditions resulting from
CC systemic cytokine damage. N.B. The sequence data for this patent did not
CC form part of the printed specification, but was obtained in electronic
CC format directly from WIPO at ftp.wipo.int/pub/published_pat_sequences
XX
SQ Sequence 246 BP; 85 A; 31 C; 53 G; 72 T; 0 U; 5 Other;

Query Match 100.0%; Score 11; DB 6; Length 246;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTGGCACTA 11
DB |||||
24 CTTTGGCACTA 14
RESULT 45
AAH81973/c
ID AAH81973 standard; DNA; 255 BP.
XX
AC AAH81973;
XX
DT 21-SEP-2001 (first entry)
XX
DE Rat differential transcription-associated cDNA SEQ ID 482.
XX
KW Differential transcription; human; rat; tumour cell; cytostatic;
KW Ras modulator; Class II tumour suppressor gene; gene therapy; ss.
XX
OS Rattus sp.
XX
PN WO200157058-A2.
XX
PD 09-AUG-2001.
XX
PF 31-JAN-2001; 2001WO-EP001003.
XX
PR 31-JAN-2000; 2000DE-01004102.
XX
PA (META-) METAGEN GES GENOMFORSCHUNG MBH.
XX
PI Rosenthal A, Hinzmann B, Schaefer R, Zuber J, Tchernitsa O;
PI Grips M, Hellriegel M, Schmitz A, Sers C;
XX
DR WPI; 2001-483415/52.
XX
PT Nucleic acids differentially expressed between tumor and normal cells,
PT useful for diagnosis or therapy of tumors and for screening active
PT agents.
XX
PS Claim 6; Page 505; 579pp; German.
XX
CC This invention describes a nucleic acid (I) with differential expression
CC between tumour and normal cells and which has cytostatic activity. (I)
CC work as modulators of Ras activity by inducing expression of tumour
CC suppressor genes. (I), and polypeptides encoded by them, are useful as
CC targets for diagnosis or therapy and in screening to determine the
CC effects of an active compound (potential pharmaceutical) on a cell line,
CC particularly for diagnosis and treatment of tumors, especially by
CC modulating expression of (I) (by gene therapy, antisense RNA or ribozyme
CC methods) or by modulating the amount and/or location of (I)-encoded
CC polypeptides (by administration of the polypeptide or its activator,
CC antibody (optionally as a conjugate) or inhibitor). The method allows
CC identification of many Class II tumour suppressor genes (i.e. genes that
CC are not primary targets for tumour-initiating mutations). AAH81492-
CC AAH82376 represent the human and rat derived nucleic acid fragments
CC described in the method of the invention
XX
SQ Sequence 255 BP; 73 A; 66 C; 51 G; 65 T; 0 U; 0 Other;
Query Match 100.0%; Score 11; DB 5; Length 255;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTTTGGCACTA 11
DB |||||
247 CTTTGGCACTA 237
RESULT 46
ADS68954
ID ADS68954 standard; cDNA; 256 BP.
XX

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AC ADS68954;
XX
XX DT 18-NOV-2004 (first entry)
XX DE
XX DE Corn seedling-derived polynucleotide (cpds), SEQ ID 3970.
XX DE
XX DE Corn; seedling-derived polynucleotide; cdp; ss; plant; seed growth;
XX DE seed development; disease resistance; insect infestation; fungal disease;
XX DE bacterial infection; Goss' Bacterial Wilt; blight;
XX DE Stewart's bacterial Wilt; Holcus spot; bacterial leaf blight; leaf spot;
XX DE bacterial stripe; maize dwarf mosaic virus infection;
XX DE environmental stress; water stress; pH stress; temperature stress;
XX DE pollution; injury; pesticide.
XX OS
XX OS Zea mays.
XX PN
XX PN US2003237110-A9.
XX PD
XX PD 25-DEC-2003.
XX PF
XX PF 06-AUG-2001; 2001US-00923876.
XX PR
XX PR 12-MAY-1998; 98US-0085331P.
XX PR 21-APR-1999; 99US-00298329.
XX PR
XX PR (INCY-) INCYTE PHARM INC.
XX PA
XX PA Lalgudi RV, Ito LY, Sherman BK;
XX PI
XX PI WPI; 2002-195165/25.
XX DR
XX DR New corn seedling-derived polynucleotides and polypeptides, useful in
XX PT identifying and altering desired characteristics associated with growth
XX PT and development, disease resistance, environmental adaptability, quality
XX PT and yield.
XX PT
XX PS Claim 1; SEQ ID NO 3970; 33pp; English.
XX
XX CC The invention relates to a corn seedling-derived polynucleotide (cdp)
XX CC selected from ADS64985-ADS71316, or their complements and fragments. Also
XX CC included are a composition for the detection of altered expression of a
XX CC cdp (comprising a polynucleotide selected from ADS64985-ADS71316), a
XX CC method of detecting a polynucleotide in a biological sample using a cdp,
XX CC a method for using oligomers (and amplification) to recover a regulatory
XX CC element from a DNA library using oligomers designed against a cdp, a
XX CC seedling specific regulatory element that regulates the expression of a
XX CC cdp, an expression vector containing a cdp or regulatory element, a plant
XX CC transformed with the vector, a host cell containing the vector (and
XX CC expressing a corn seedling derived protein, CDP), an anti-CDP antibody,
XX CC identifying a compound which binds a CDP and screening a plurality of
XX CC compounds for binding to cdp polynucleotide. The cdp polynucleotides,
XX CC proteins, vectors, cells and antibodies are useful for the
XX CC identification, evaluation and alteration of seed growth and development,
XX CC disease resistance (e.g. to insect infestation, fungal disease, bacterial
XX CC infection, Goss' Bacterial Wilt, blight, Stewart's bacterial Wilt, Holcus
XX CC spot, bacterial leaf blight, leaf spot, bacterial stripe and maize dwarf
XX CC mosaic virus infection) and resistance to environmental stresses (e.g.
XX CC water stress, pH stress, temperature stress, pollution, injury or
XX CC pesticides. The present sequence is cdp cDNA sequence.
XX CC
XX SQ Sequence 256 BP; 77 A; 57 C; 55 G; 65 T; 0 U; 2 Other;

Query Match 100.0%; Score 11; DB 7; Length 256;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTGGCACTA 11
DB 65 CTTTGGCACTA 75

RESULT 47
ABQ67322/c
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ID ABQ67322 standard; DNA; 273 BP.
XX
XX AC ABQ67322;
XX
XX DT 29-AUG-2002 (first entry)
XX DE
XX DE Listeria innocua DNA sequence #124.
XX DE
XX DE Antibacterial; Listeria; food contamination; mutational analysis;
XX DE infection; ds.
XX DE
XX OS Listeria innocua.
XX
XX PN WO200228891-A2.
XX
XX PD 11-APR-2002.
XX PF
XX PF 04-OCT-2001; 2001WO-FR003061.
XX PR
XX PR 04-OCT-2000; 2000FR-00012697.
XX PR
XX PR (INSP ) INST PASTEUR.
XX PA (CNRS ) CNRS CENT NAT RECH SCI.
XX
XX PI Kunst F, Glaser P;
XX
XX WPI; 2002-332479/37.
XX
XX DE New genomic sequences from Listeria species, useful for detection,
XX PT treatment and prevention of infection, also related polypeptides,
XX PT antibodies and modulators.
XX PT
XX PS Claim 7; SEQ ID NO 135; 180pp; French.
XX
XX CC The present invention relates to nucleic acid sequences (ABQ67188-
XX CC ABQ71212) from Listeria sp. The sequences are useful as probes and
XX CC primers for identification and/or detection of Listeria (e.g. as
XX CC contaminants in foods, or mutational analysis) and for analysis of gene
XX CC expression. Proteins encoded by the nucleic acid sequences can be used to
XX CC screen for compounds that modulate gene expression, replication and
XX CC pathogenicity of Listeria (potential therapeutic agents), also for
XX CC treating infections by Listeria, and are useful as immunogens in anti-
XX CC Listeria vaccines. Note: The sequence data for this patent did not form
XX CC part of the printed specification, but was obtained in electronic format
XX CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 273 BP; 90 A; 53 C; 39 G; 91 T; 0 U; 0 Other;

Query Match 100.0%; Score 11; DB 6; Length 273;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTGGCACTA 11
DB 85 CTTTGGCACTA 75

RESULT 48
AAC23036
ID AAC23036 standard; cDNA; 276 BP.
XX
XX AC AAC23036;
XX
XX DT 06-OCT-2000 (first entry)
XX DE
XX DE Human secreted protein 5' EST, SEQ ID NO: 27111.
XX
XX DE Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
XX KW gene therapy; chromosome mapping; ss.
XX
XX OS Homo sapiens.
XX
XX PN EP1033401-A2.
```

XX 06-SEP-2000.
 XX
 XX 21-FEB-2000; 2000EP-00200610.
 XX
 XX 26-FEB-1999; 99US-0122487P.
 XX
 XX (GEST) GENSET.
 XX
 XX Dumas Milne Edwards J, Duclert A, Giordano J;
 XX
 XX WPI; 2000-500381/45.
 XX
 XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for
 PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
 PT diagnostic, forensic, gene therapy and chromosome mapping procedures.
 XX
 XX Claim 1; SEQ ID NO 27111; 71pp + Sequence Listing; English.
 XX
 CC The present sequence is one of a large number of 5' ESTs derived from
 CC mRNAs encoding secreted proteins. No ORF has yet been conclusively
 CC identified within the present sequence. The 5' ESTs were prepared from
 CC total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
 CC sequences usually correspond mainly to the 3' untranslated region (UTR)
 CC of the mRNA because they are often obtained from oligo-dT primed cDNA
 CC libraries. Such ESTs are not well suited for isolating cDNA sequences
 CC derived from the 5' ends of mRNAs and even in those cases where longer
 CC cDNA sequences have been obtained, the full 5' UTR is rarely included. 5'
 CC ESTs are derived from mRNAs with intact 5' ends and can therefore be used
 CC to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in
 CC diagnostic, forensic, gene therapy and chromosome mapping procedures.
 CC They are used to obtain upstream regulatory sequences and to design
 CC expression and secretion vectors
 XX
 XX Sequence 276 BP; 100 A; 49 C; 48 G; 77 T; 0 U; 2 Other;
 SQ
 Query Match 100.0%; Score 11; DB 3; Length 276;
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CTTTGGCACTA 11
 DB 219 CTTTGGCACTA 229
 RESULT 49
 AAL23068
 ID AAL23068 standard; cDNA; 284 BP.
 XX
 XX AAL23068;
 AC
 DT 07-DEC-2001 (first entry)
 XX
 DE Human breast cancer expressed polynucleotide 15525.
 XX
 KW Human; breast cancer; cell marker; cytostatic; ss.
 XX
 OS Homo sapiens.
 XX
 XX WO200151628-A2.
 PN
 XX 19-JUL-2001.
 PD
 XX 10-JAN-2001; 2001WO-US000798.
 PF
 XX 14-JAN-2000; 2000US-0176077P.
 PR
 XX 14-MAR-2000; 2000US-0189167P.
 PR
 XX 24-MAR-2000; 2000US-0192099P.
 PR
 XX 29-MAR-2000; 2000US-0193480P.
 PR
 XX 15-MAY-2000; 2000US-0205230P.
 PR
 XX 09-JUN-2000; 2000US-0211315P.
 PR
 XX 25-JUL-2000; 2000US-0220534P.
 XX

PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 XX
 XX Lillie J, Xu Y, Wang Y, Steinmann K;
 XX
 XX WPI; 2001-451856/48.
 XX
 XX New peptide useful as a marker for the diagnosis of breast cancer.
 PT
 XX Claim 1; Page 2821; 3695pp; English.
 PS
 XX The invention relates to human breast cancer expressed polynucleotides
 CC (AAL07544-AAL26789) and methods of assessing whether a patient is
 CC afflicted with breast cancer by examining the correlation between the
 CC expression of certain markers and the cancerous state of breast cells.
 CC The polynucleotides and encoded polypeptides are potential markers for
 CC detecting, diagnosing, monitoring, characterising treating and
 CC potentially preventing breast cancer. The polynucleotides and encoded
 CC polypeptides are also useful for isolating compounds with cytostatic
 CC activity
 XX
 XX Sequence 284 BP; 75 A; 65 C; 52 G; 92 T; 0 U; 0 Other;
 SQ
 Query Match 100.0%; Score 11; DB 4; Length 284;
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CTTTGGCACTA 11
 DB 105 CTTTGGCACTA 115
 RESULT 50
 AAS60629/c
 ID AAS60629 standard; cDNA; 286 BP.
 XX
 XX AAS60629;
 AC
 XX 29-JAN-2002 (first entry)
 DT
 XX Human cancer agent-resistance marker #384.
 DE
 XX Human; cancer cell marker; TAXOL; cytostatic; tumour; carcinoma;
 KW squamous cell carcinoma; sarcoma; fibrosarcoma; leukaemia;
 KW lymphocytic leukaemia; lymphoma; plasmocytoma; reticulum cell sarcoma;
 KW Hodgkin's disease; glioma; ss.
 XX
 XX Homo sapiens.
 OS
 XX WO200179556-A2.
 PN
 XX 25-OCT-2001.
 PD
 XX 13-APR-2001; 2001WO-US012132.
 PF
 XX 14-APR-2000; 2000US-0197538P.
 PR
 XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 PA
 XX Lillie J, Brown JL, Bolt A, Van Huffel C;
 PI
 XX WPI; 2001-602933/68.
 DR
 XX Novel nucleic acid, used as a marker to determine the effectiveness of
 PT using TAXOL to treat cancer cell growth in individuals.
 PT
 XX Claim 1; Page 262; 527pp; English.
 PS
 XX The invention relates to 1046 novel nucleic acids which are used as
 CC markers for determining the sensitivity of a cancer cell to the
 CC anticancer agent TAXOL. Cancer cells can be treated with TAXOL when they
 CC are shown to express one of the 242 sensitivity markers or the cells are
 CC shown not to express one of the 804 resistance markers. The methods can
 CC be used to determine the effectiveness of TAXOL in the treatment of

CC cancer cell growth in an individual. The markers can be used as targets
CC in developing anti-cancer agents such as chemotherapeutic compounds. The
CC markers can also be used as targets in developing treatments for cancer,
CC particularly those cancers which display resistance to agents and exhibit
CC expression of the markers. The anticancer agents developed by the novel
CC method can be used to treat cancer. Probes based on the markers can be
CC used to detect transcripts or genomic sequences corresponding to the
CC markers, in the identification of cells or tissues which mis-express the
CC protein. Cancers which may be targeted include carcinoma (e.g. squamous
CC cell carcinoma), sarcoma (e.g. fibrosarcoma) leukaemia (e.g. lymphocytic
CC leukaemia), lymphoma, plasmocytoma, reticulum cell sarcoma, Hodgkin's
CC disease and tumours (e.g. glioma). The present sequence is one of the
CC 1046 novel cancer cell markers
XX

SQ Sequence 286 BP; 95 A; 55 C; 62 G; 74 T; 0 U; 0 Other;

Query Match 100.0%; Score 11; DB 4; Length 286;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTGGCACTA 11
|||
Db 192 CTTTGGCACTA 182

Search completed: March 12, 2005, 10:04:52
Job time : 266 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: March 12, 2005, 10:04:58 ; Search time 56.5 Seconds
(without alignments)
150.597 Million cell updates/sec

Title: US-10-070-588a-112

Perfect score: 3

Sequence: 1 ctttggcacta 11

Scoring table:

OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2105692 seqs, 386760381 residues

Word size: 1

Total number of hits satisfying chosen parameters: 3949848

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 500 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DEV=xlh
-O=/cgn2_1/USPNO.spool/US10070588/runat 10032005 120704 15234/app.query.fasta_1.199
-DB=A_Geneseq16Dec04 -QWTFastan -SUFFIX=olin2p.rag -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi
-LIST=500 -DOALIGN=200 -THR SCORE=quality -THR MIN=1 -ALIGN=50 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USR=US10070588 @CGN 1 1 137 @runat 10032005 120704 15234 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database :
1: Geneseq16Dec04:
17: Geneseq1980s:
2: Geneseq1990s:
3: Geneseq2000s:
4: Geneseq2001s:
5: Geneseq2002s:
6: Geneseq2003as:
7: Geneseq2003bs:
8: Geneseq2004s:

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	3	100.0	8	1	AA81949 8 amino a
2	3	100.0	8	2	AA35903 Hepatitis
3	3	100.0	8	2	AA35885 Hepatitis
4	3	100.0	8	2	AA35884 Hepatitis
5	3	100.0	8	2	AA35882 Hepatitis
6	3	100.0	8	2	AA35883 Hepatitis
7	3	100.0	8	2	AA42565 Tri-/tetra
8	3	100.0	8	2	AA56998 N-termina
9	3	100.0	8	2	AA73487 Human TSH
10	3	100.0	8	2	AA73488 Human TSH

11	3	100.0	8	2	AA73476 Human TSH
12	3	100.0	8	2	AA73413 Human TSH
13	3	100.0	8	2	AA73414 Human TSH
14	3	100.0	8	2	AA73474 Human TSH
15	3	100.0	8	2	AA73475 Human TSH
16	3	100.0	8	2	AA73489 Human TSH
17	3	100.0	8	2	AA73412 Human TSH
18	3	100.0	8	2	AA84449 Hepatitis
19	3	100.0	8	2	AA84450 Hepatitis
20	3	100.0	8	2	ADC81358 Bovin THP
21	3	100.0	8	2	AAW36922 Peptide e
22	3	100.0	8	2	AAW36925 Peptide e
23	3	100.0	8	2	AAW79266 Bovine gl
24	3	100.0	8	2	AAW56853 Enzyme in
25	3	100.0	8	2	AAW75829 Mouse mas
26	3	100.0	8	2	AAW20315 Human mic
27	3	100.0	8	2	AAW59492 Human pro
28	3	100.0	8	2	AAW78686 SH2 domai
29	3	100.0	8	2	AAW78521 SH2 domai
30	3	100.0	8	2	AAW67227 aPL immun
31	3	100.0	8	2	AAW67141 Antibody
32	3	100.0	8	2	AAW29699 TNF recep
33	3	100.0	8	2	AAW29698 TNF recep
34	3	100.0	8	2	AAW29700 TNF recep
35	3	100.0	8	2	AAW29697 TNF recep
36	3	100.0	8	2	AAW47925 Human MHC
37	3	100.0	8	2	AAW67654 LXXLL sig
38	3	100.0	8	2	AAW16865 Heat shoc
39	3	100.0	8	2	AAW16846 Heat shoc
40	3	100.0	8	2	AAW93856 Mouse BR9
41	3	100.0	8	3	AAW28324 Human sec
42	3	100.0	8	3	AAW69116 Subsequen
43	3	100.0	8	3	AAW69128 Subsequen
44	3	100.0	8	3	AAW84485 Amino aci
45	3	100.0	8	3	AAW84484 Amino aci
46	3	100.0	8	3	AAW84483 Amino aci
47	3	100.0	8	3	AAW84500 Amino aci
48	3	100.0	8	3	AAW84489 Amino aci
49	3	100.0	8	3	AAW69217 Tryptic p
50	3	100.0	8	3	AAW29524 E9K pepti
51	3	100.0	8	3	AAW34118 Human sec
52	3	100.0	8	3	AAW21147 Preferred
53	3	100.0	8	3	AAW21145 Preferred
54	3	100.0	8	3	AAW35995 Sorbitol
55	3	100.0	8	3	AAW35815 T7 phage
56	3	100.0	8	3	AAW38150 Alpha-mel
57	3	100.0	8	3	AAW28146 Alpha-mel
58	3	100.0	8	4	AAW88783 Human int
59	3	100.0	8	4	AAW81474 Synthetic
60	3	100.0	8	4	AAW10659 Human Asp
61	3	100.0	8	4	AAW23420 HIV pepti
62	3	100.0	8	4	AAW68496 Human Bre
63	3	100.0	8	4	AAW02611 Human Asp
64	3	100.0	8	4	AAW20363 Mouse pro
65	3	100.0	8	4	AAW65143 Synthetic
66	3	100.0	8	4	AAW75136 Collagena
67	3	100.0	8	4	AAW88960 HER2/neu
68	3	100.0	8	4	AAW88958 HER2/neu
69	3	100.0	8	4	AAW37498 Flagellin
70	3	100.0	8	4	AAW22004 HIV A03 m
71	3	100.0	8	4	AAW22094 HIV A03 m
72	3	100.0	8	4	ABP12087 HIV A02 s
73	3	100.0	8	4	ABP13233 HIV A02 s
74	3	100.0	8	4	ABP13234 HIV A02 s
75	3	100.0	8	4	ABP20019 HIV A03 m
76	3	100.0	8	4	ABP24350 HIV A24 m
77	3	100.0	8	4	ABP14056 HIV A02 s
78	3	100.0	8	4	ABP16447 HIV A24 s
79	3	100.0	8	4	ABP16448 HIV A24 s
80	3	100.0	8	4	ABP11534 HIV A01 s
81	3	100.0	8	4	ABP19597 HIV B62 s
82	3	100.0	8	4	ABP20060 HIV A03 m
83	3	100.0	8	4	ABP22036 HIV A03 m

84	3	100.0	8	4	ABP24334	Abp24334	HIV A24 m	157	3	100.0	8	7	AD123971	Adi233971	A541 locu
85	3	100.0	8	4	ABP24335	Abp24335	HIV A24 m	158	3	100.0	8	7	AD123970	Adi23970	A541 locu
86	3	100.0	8	4	ABP15177	Abp15177	HIV A24 s	159	3	100.0	8	7	ADJ90992	Adj90992	Foot-and-
87	3	100.0	8	4	ABP22422	Abp22422	HIV A11 m	160	3	100.0	8	7	ADJ90993	Adj90993	Foot-and-
88	3	100.0	8	4	ABP14057	Abp14057	HIV A02 s	c 161	3	100.0	8	8	ADH34507	Adh34507	Alpha-mel
89	3	100.0	8	4	ABP16446	Abp16446	HIV A02 s	c 162	3	100.0	8	8	ADG94474	Adg94474	Human JAM
90	3	100.0	8	4	ABP20156	Abp20156	HIV A03 m	c 163	3	100.0	8	8	ADH44539	Adh44539	Animal pr
91	3	100.0	8	4	ABP23849	Abp23849	HIV A11 m	164	3	100.0	8	8	ADH62069	Adh62069	Cyclic an
92	3	100.0	8	4	ABP14058	Abp14058	HIV A02 s	165	3	100.0	8	8	ADH62086	Adh62086	Cyclic an
93	3	100.0	8	4	ABP14061	Abp14061	HIV A02 s	166	3	100.0	8	8	ADH62100	Adh62100	Cyclic an
94	3	100.0	8	4	ABP15206	Abp15206	HIV A24 s	167	3	100.0	8	8	ADH62067	Adh62067	Cyclic an
95	3	100.0	8	4	ABP15032	Abp15032	HIV A03 s	168	3	100.0	8	8	ADH62075	Adh62075	Cyclic an
96	3	100.0	8	4	ABP18188	Abp18188	HIV B58 s	169	3	100.0	8	8	ADH62065	Adh62065	Cyclic an
97	3	100.0	8	4	ABP14059	Abp14059	HIV A02 s	170	3	100.0	8	8	ADH62068	Adh62068	Cyclic an
98	3	100.0	8	4	ABP15031	Abp15031	HIV A03 s	171	3	100.0	8	8	ADH76551	Adh76551	Human neu
99	3	100.0	8	4	ABP14060	Abp14060	HIV A02 s	c 172	3	100.0	8	8	ADJ72154	Adj72154	Cyclin re
100	3	100.0	8	4	ABP12062	Abp12062	HIV A02 s	c 173	3	100.0	8	8	ADJ72147	Adj72147	Cyclin re
101	3	100.0	8	4	ABP12088	Abp12088	HIV A02 s	c 174	3	100.0	8	8	ADJ78900	Adj78900	Peptide #
102	3	100.0	8	4	ABP12086	Abp12086	HIV A02 s	c 175	3	100.0	8	8	ADJ78905	Adj78905	Peptide #
103	3	100.0	8	4	ABP23894	Abp23894	HIV A11 m	c 176	3	100.0	8	8	ADJ78899	Adj78899	Peptide #
104	3	100.0	8	4	ABP17722	Abp17722	HIV B58 s	c 177	3	100.0	8	8	ADJ78907	Adj78907	Peptide #
105	3	100.0	8	4	ABP15205	Abp15205	HIV A24 s	c 178	3	100.0	8	8	ADJ78893	Adj78893	Peptide #
106	3	100.0	8	4	ABP16445	Abp16445	HIV A24 s	c 179	3	100.0	8	8	ADJ78898	Adj78898	Peptide #
107	3	100.0	8	4	ABP18392	Abp18392	HIV B58 s	c 180	3	100.0	8	8	ADJ78895	Adj78895	Peptide #
108	3	100.0	8	4	ABP18591	Abp18591	HIV B62 s	c 181	3	100.0	8	8	ADJ78901	Adj78901	Peptide #
109	3	100.0	8	4	AAB80496	Aab80496	PTH2 rece	c 182	3	100.0	8	8	ADJ78902	Adj78902	Peptide #
110	3	100.0	8	4	AAB80571	Aa800571	Hepatit	c 183	3	100.0	8	8	ADJ78894	Adj78894	Peptide #
111	3	100.0	8	4	AJA01167	Aaj01167	Hepatit	c 184	3	100.0	8	8	ADJ78896	Adj78896	Peptide #
112	3	100.0	8	4	AJA01699	Aaj01699	Hepatit	c 185	3	100.0	8	8	ADJ78892	Adj78892	Peptide #
113	3	100.0	8	4	AJA00550	Aaj00550	Hepatit	c 186	3	100.0	8	8	ADJ78897	Adj78897	Peptide #
114	3	100.0	8	4	AJA00939	Aaj00939	Hepatit	c 187	3	100.0	8	8	ADJ78903	Adj78903	Peptide #
115	3	100.0	8	4	AJA01326	Aaj01326	Hepatit	c 188	3	100.0	8	8	ADJ78906	Adj78906	Peptide #
116	3	100.0	8	4	AJA01732	Aaj01732	Hepatit	c 189	3	100.0	8	8	ADJ78905	Adj78905	Peptide #
117	3	100.0	8	4	AJA01023	Aaj01023	Hepatit	c 190	3	100.0	8	8	ADJ78906	Adj78906	Peptide #
118	3	100.0	8	4	AJA00406	Aaj00406	Hepatit	c 191	3	100.0	8	8	ADK08449	Adk08449	Human pap
119	3	100.0	8	4	AJA01654	Aaj01654	Hepatit	c 192	3	100.0	8	8	ADK10015	Adk10015	Human pap
120	3	100.0	8	5	ABE25496	Abb25496	Enzyme cl	c 193	3	100.0	8	8	ADK08872	Adk08872	Human pap
121	3	100.0	8	5	ABE25496	Aae25496	CAP1-29 t	c 194	3	100.0	8	8	ADK09291	Adk09291	Human pap
122	3	100.0	8	5	ABE25496	Aae25496	Enzyme cl	c 195	3	100.0	8	8	ADK08841	Adk08841	Human pap
123	3	100.0	8	5	ABG71053	Abg71053	Tumour ne	c 196	3	100.0	8	8	ADK08873	Adk08873	Human pap
124	3	100.0	8	5	ABG71053	Abg71053	Tumour ne	c 197	3	100.0	8	8	ADK10131	Adk10131	Human pap
125	3	100.0	8	5	ABG71050	Abg71050	Tumour ne	c 198	3	100.0	8	8	ADK08088	Adk08088	Human pap
126	3	100.0	8	5	ABG35001	Abg35001	Human pro	c 199	3	100.0	8	8	ADK10830	Adk10830	Human pap
127	3	100.0	8	5	AAE26705	Aae26705	Matrix me	c 200	3	100.0	8	8	ADK03860	Adk03860	Hepatit
128	3	100.0	8	5	ABP53319	Abp53319	Alpha-mel	c 201	3	100.0	8	8	ADL95921	Adl95921	Antibody-
129	3	100.0	8	5	ABP78620	Abp78620	Human Asp	c 202	3	100.0	8	8	ADM73301	Adm73301	Human SCP
130	3	100.0	8	5	ABG67499	Abg67499	Human ADP	c 203	3	100.0	8	8	ADM73308	Adm73308	Human SCP
131	3	100.0	8	5	AAE25169	Aae25169	Mouse BR9	c 204	3	100.0	8	8	ADM68731	Adm68731	Human MAG
132	3	100.0	8	5	ABG98330	Abg98330	Secreted	c 205	3	100.0	8	8	ADP67890	Adp67890	Anti-micr
133	3	100.0	8	6	ABJ19705	Abj19705	Human sec	c 206	3	100.0	8	8	ADP67915	Adp67915	Anti-micr
134	3	100.0	8	6	ABG73927	Abg73927	Factor II	c 207	3	100.0	8	8	ADP67880	Adp67880	Anti-micr
135	3	100.0	8	6	ABP99691	Abp99691	Human sec	c 208	3	100.0	8	8	ADP67883	Adp67883	Anti-micr
136	3	100.0	8	6	ABJ20077	Abj20077	MHC bindi	c 209	3	100.0	8	8	ADP67901	Adp67901	Anti-micr
137	3	100.0	8	6	ABR01171	Abro1171	Human gen	c 210	3	100.0	8	8	ADP67884	Adp67884	Anti-micr
138	3	100.0	8	6	ABP74652	Abp74652	Human SCP	c 211	3	100.0	8	8	ADP67882	Adp67882	Anti-micr
139	3	100.0	8	6	ADA44124	Ada44124	Human sec	c 212	3	100.0	8	8	ADP87049	Adp87049	Junctiona
140	3	100.0	8	6	ADA23613	Ada23613	Alzheimer	c 213	3	100.0	8	8	ADQ28101	Adq28101	Excluded
141	3	100.0	8	6	ABR62780	Abro62780	Alpha-MSH	c 214	3	100.0	8	8	ADQ28102	Adq28102	Excluded
142	3	100.0	8	7	ADC20459	Adc20459	Human sec	c 215	3	100.0	8	8	ADQ28109	Adq28109	Excluded
143	3	100.0	8	7	ADC09511	Adc09511	Epitope w	c 216	3	100.0	8	8	ADQ28103	Adq28103	Excluded
144	3	100.0	8	7	ADC33665	Adc33665	Matrix me	c 217	3	100.0	8	8	ADQ28118	Adq28118	Excluded
145	3	100.0	8	7	AAE39184	Aae39184	Angiogene	c 218	3	100.0	8	8	ADQ28128	Adq28128	Excluded
146	3	100.0	8	7	ADC15558	Adc15558	Rho 110 l	c 219	3	100.0	8	8	ADQ28099	Adq28099	Excluded
147	3	100.0	8	7	ABW00631	Abw00631	Mouse BR6	c 220	3	100.0	8	8	ADQ28017	Adq28017	Cyclic an
148	3	100.0	8	7	ADD57117	Add57117	HLA bindi	c 221	3	100.0	8	8	ADR69560	Adr69560	Novel hyb
149	3	100.0	8	7	ADD57541	Add57541	HLA bindi	c 222	3	100.0	8	8	ADR69562	Adr69562	Novel hyb
150	3	100.0	8	7	ADD58002	Add58002	HLA bindi	c 223	3	100.0	8	8	ADR69638	Adr69638	Novel hyb
151	3	100.0	8	7	ADD23843	Add23843	Breast ca	c 224	3	100.0	8	8	ADR69707	Adr69707	Novel hyb
152	3	100.0	8	7	ADD15711	Add15711	Peptide 1	c 225	3	100.0	8	8	ADR69726	Adr69726	Novel hyb
153	3	100.0	8	7	ADD15704	Add15704	Peptide 1	c 226	3	100.0	8	8	ADR69563	Adr69563	Novel hyb
154	3	100.0	8	7	ABW02758	Abw02758	Angiogene	c 227	3	100.0	8	8	ADR69738	Adr69738	Novel hyb
155	3	100.0	8	7	ADG72970	Adg72970	Heat choc	c 228	3	100.0	8	8	ADR70831	Adr70831	Synthetic
156	3	100.0	8	7	ADG72951	Adg72951	Heat choc	c 229	3	100.0	9	2	AAR43247	Aar43247	Cytotoxic

230	3	100.0	9	2	AAR59218	Peptide f	303	3	100.0	9	2	AAW62730	Streptoco
231	3	100.0	9	2	AAR59199	Peptide f	C 304	3	100.0	9	2	AAW71279	P. damsel
232	3	100.0	9	2	AAR59172	Peptide f	C 305	3	100.0	9	2	AAW20755	Human neu
233	3	100.0	9	2	AAR61691	HLA-A2, 1	306	3	100.0	9	2	AAW21455	Human neu
234	3	100.0	9	2	AAR58764	FOKI 11 k	307	3	100.0	9	2	AAW54608	Peptide 1
235	3	100.0	9	2	AAR56351	Peptide 1	308	3	100.0	9	2	AAW54646	Peptide f
236	3	100.0	9	2	AAR56364	Peptide 1	309	3	100.0	9	2	AAW78836	BAGE prot
237	3	100.0	9	2	AAR56340	Peptide 1	310	3	100.0	9	2	AAW60009	HA-2 mino
238	3	100.0	9	2	AAR56376	Peptide 1	311	3	100.0	9	2	AAW71129	BAGE synt
239	3	100.0	9	2	AAR56373	Peptide 1	312	3	100.0	9	2	AAW68375	Human BAG
240	3	100.0	9	2	AAR56377	Peptide 1	313	3	100.0	9	2	AAW46066	Antiphosp
241	3	100.0	9	2	AAR56366	Peptide 1	314	3	100.0	9	2	AAW67101	Antibody
242	3	100.0	9	2	AAR56379	Peptide 1	315	3	100.0	9	2	AAW67118	Antibody
243	3	100.0	9	2	AAR56318	Peptide 1	316	3	100.0	9	2	AAW46351	Amino aci
244	3	100.0	9	2	AAR56326	Peptide 1	317	3	100.0	9	2	AAW46349	Amino aci
245	3	100.0	9	2	AAR56346	Peptide 1	318	3	100.0	9	2	AAW46350	Amino aci
246	3	100.0	9	2	AAR56358	Peptide 1	319	3	100.0	9	2	AAW47937	AE101 ana
247	3	100.0	9	2	AAR56360	Peptide 1	C 320	3	100.0	9	2	AAW97954	Human syn
248	3	100.0	9	2	AAR56330	Peptide 1	321	3	100.0	9	2	AAW10524	HLA Class
249	3	100.0	9	2	AAR56372	Peptide 1	322	3	100.0	9	2	AAW10636	Peptide a
250	3	100.0	9	2	AAR56370	Peptide 1	323	3	100.0	9	2	AAW40233	Amino aci
251	3	100.0	9	2	AAR56363	Peptide 1	324	3	100.0	9	2	AAW47487	Immunogen
252	3	100.0	9	2	AAR56367	Peptide 1	325	3	100.0	9	2	AAW47812	Immunogen
253	3	100.0	9	2	AAR56371	Peptide 1	326	3	100.0	9	2	AAW46853	Immunogen
254	3	100.0	9	2	AAR56375	Peptide 1	327	3	100.0	9	2	AAW46855	Immunogen
255	3	100.0	9	2	AAR56317	Peptide 1	328	3	100.0	9	2	AAW46021	Immunogen
256	3	100.0	9	2	AAR56320	Peptide 1	329	3	100.0	9	2	AAW47488	Immunogen
257	3	100.0	9	2	AAR56327	Peptide 1	330	3	100.0	9	2	AAW47767	Immunogen
258	3	100.0	9	2	AAR56329	Peptide 1	331	3	100.0	9	2	AAW46424	Immunogen
259	3	100.0	9	2	AAR56341	Peptide 1	C 332	3	100.0	9	2	AAW46891	Immunogen
260	3	100.0	9	2	AAR56349	Peptide 1	333	3	100.0	9	2	AAW47722	Immunogen
261	3	100.0	9	2	AAR56359	Peptide 1	334	3	100.0	9	2	AAW46487	Immunogen
262	3	100.0	9	2	AAR56361	Peptide 1	335	3	100.0	9	2	AAW47727	Immunogen
263	3	100.0	9	2	AAR56368	Peptide 1	336	3	100.0	9	2	AAW46776	Immunogen
264	3	100.0	9	2	AAR56325	Peptide 1	C 337	3	100.0	9	2	AAW46675	Immunogen
265	3	100.0	9	2	AAR56339	Peptide 1	338	3	100.0	9	2	AAW03665	Amino aci
266	3	100.0	9	2	AAR56345	Peptide 1	C 339	3	100.0	9	2	AAW93921	Synthetic
267	3	100.0	9	2	AAR56322	Peptide 1	C 340	3	100.0	9	2	AAW93918	Synthetic
268	3	100.0	9	2	AAR56343	Peptide 1	C 341	3	100.0	9	2	AAW93938	Synthetic
269	3	100.0	9	2	AAR56347	Peptide 1	342	3	100.0	9	2	AAW67675	Mutated L
270	3	100.0	9	2	AAR56348	Peptide 1	343	3	100.0	9	2	AAW33152	Human BAG
271	3	100.0	9	2	AAR56369	Peptide 1	344	3	100.0	9	2	AAW25276	HIV Env g
272	3	100.0	9	2	AAR56332	Peptide 1	345	3	100.0	9	2	AAW25241	HIV pol p
273	3	100.0	9	2	AAR56378	Peptide 1	346	3	100.0	9	2	AAW25275	HIV Env g
274	3	100.0	9	2	AAR56342	Peptide 1	347	3	100.0	9	2	AAW25242	HIV pol p
275	3	100.0	9	2	AAR56319	Peptide 1	C 348	3	100.0	9	2	AAW89112	ScFV (dig
276	3	100.0	9	2	AAR56324	Peptide 1	349	3	100.0	9	2	AAW53546	Human BAG
277	3	100.0	9	2	AAR56344	Peptide 1	350	3	100.0	9	2	AAW00811	HLA-A24 a
278	3	100.0	9	2	AAR56350	Peptide 1	351	3	100.0	9	2	AAW26889	Tumour-de
279	3	100.0	9	2	AAR56323	Peptide 1	352	3	100.0	9	2	AAW97259	Cytotoxic
280	3	100.0	9	2	AAR56374	Peptide 1	353	3	100.0	9	2	AAW00690	Tumour an
281	3	100.0	9	2	AAR56331	Peptide 1	354	3	100.0	9	2	AAW31777	Mycobacte
282	3	100.0	9	2	AAR56380	Peptide 1	355	3	100.0	9	2	AAW31775	Mycobacte
283	3	100.0	9	2	AAR56380	Peptide 1	356	3	100.0	9	2	AAW49642	Tumour an
284	3	100.0	9	2	AAR69862	Peptide 1	357	3	100.0	9	2	AAW05025	Tumour an
285	3	100.0	9	2	AAR87312	Plasmodiu	C 358	3	100.0	9	2	AAW96727	IL-8 deri
286	3	100.0	9	2	AAR87269	Antialler	359	3	100.0	9	2	AAW01732	Exemplary
287	3	100.0	9	2	AAR69800	Human MHC	C 360	3	100.0	9	2	AAW43100	Chondroge
288	3	100.0	9	2	AAR87432	HLA-C-clo	361	3	100.0	9	2	AAW94132	Peptide i
289	3	100.0	9	2	AAR89909	BAGE tumo	362	3	100.0	9	3	AAW94132	Peptide i
290	3	100.0	9	2	AAR67810	HPV deriv	363	3	100.0	9	3	AAW71499	Human BAG
291	3	100.0	9	2	AAR84331	FOKI tryp	364	3	100.0	9	3	AAW94359	Human ST4
292	3	100.0	9	2	AAR72807	CTRI seri	365	3	100.0	9	3	AAW94373	Mouse ST4
293	3	100.0	9	2	AAR80577	FOKI rest	366	3	100.0	9	3	AAW78999	Urokinase
294	3	100.0	9	2	AAR66491	BAGE tumo	367	3	100.0	9	3	AAW90783	Human leu
295	3	100.0	9	2	AAW02153	BAGE tumo	368	3	100.0	9	3	AAW70832	BH3 domai
296	3	100.0	9	2	AAW02154	BAGE tumo	C 369	3	100.0	9	3	AAW13745	Peptide f
297	3	100.0	9	2	AAW28811	HPV-16 de	370	3	100.0	9	3	AAW18492	Peptide s
298	3	100.0	9	2	AAW14505	HLA-A2, 1-	371	3	100.0	9	3	AAW98634	wt1 deriv
299	3	100.0	9	2	AAW36923	Peptide e	372	3	100.0	9	3	AAW33648	MHC class
300	3	100.0	9	2	AAW36926	Peptide e	373	3	100.0	9	3	AAW23664	Cytotoxic
301	3	100.0	9	2	AAW22040	Antigenic	374	3	100.0	9	3	AAW20817	D box pep
302	3	100.0	9	2	AAW10399	Antiphosph	375	3	100.0	9	3	AAW92279	BAGE anti
					AAW10275	Antiphosph	375	3	100.0	9	3	AAW66446	HLA-A2-bi

376	3	100.0	9	3	AA556595	BAGE gene
377	3	100.0	9	3	AAY76692	SCP-1 HLA
378	3	100.0	9	3	AB09899	Human gly
379	3	100.0	9	3	AB14892	MCA subet
380	3	100.0	9	3	AY95894	Human MHC
381	3	100.0	9	3	AY84275	Tumour as
382	3	100.0	9	3	AY82958	BAGE tumo
383	3	100.0	9	3	AB02601	Tumour as
384	3	100.0	9	3	AY67271	MMP3 subs
385	3	100.0	9	3	AB08673	Antigenic
386	3	100.0	9	3	AB26353	Human CAS
387	3	100.0	9	3	AB26346	Human CAS
388	3	100.0	9	3	AB26358	Human CAS
389	3	100.0	9	3	AB26364	Human CAS
390	3	100.0	9	3	AB26330	Human CAS
391	3	100.0	9	3	AB33276	HLA A0201
392	3	100.0	9	3	AB33264	HLA A0201
393	3	100.0	9	3	AB08324	Epitope d
394	3	100.0	9	3	AAU68958	Human TAD
395	3	100.0	9	3	AAU68946	Human TAD
396	3	100.0	9	3	AB88782	Human int
397	3	100.0	9	3	AM23477	HIV pepti
398	3	100.0	9	3	AM23447	HIV pepti
399	3	100.0	9	3	AM22224	HIV pepti
400	3	100.0	9	3	AM23460	HIV pepti
401	3	100.0	9	3	AM23445	HIV pepti
402	3	100.0	9	3	AM23427	HIV pepti
403	3	100.0	9	3	AM23428	HIV pepti
404	3	100.0	9	3	AM23459	HIV pepti
405	3	100.0	9	3	AM23479	HIV pepti
406	3	100.0	9	3	AM99546	Vaccine r
407	3	100.0	9	3	AM00185	Laccase a
408	3	100.0	9	3	AM00170	Laccase a
409	3	100.0	9	3	AM00066	Savinas a
410	3	100.0	9	3	AM00054	Savinas a
411	3	100.0	9	3	AB46082	Human TF
412	3	100.0	9	3	AB75673	HLA class
413	3	100.0	9	3	AB75634	HLA class
414	3	100.0	9	3	AAE02090	BAGE huma
415	3	100.0	9	3	AAU70064	Human cal
416	3	100.0	9	3	AAU70073	Human cal
417	3	100.0	9	3	AAU70036	Human cal
418	3	100.0	9	3	AAU70045	Human cal
419	3	100.0	9	3	AAU70060	Human cal
420	3	100.0	9	3	AAU70018	Human cal
421	3	100.0	9	3	AAU70011	Human cal
422	3	100.0	9	3	AAU70015	Human cal
423	3	100.0	9	3	AB68699	Major out
424	3	100.0	9	3	AB95894	MHC class
425	3	100.0	9	3	AA93744	Human BAG
426	3	100.0	9	3	AB47343	Epithelia
427	3	100.0	9	3	AG88385	HER2/NEU
428	3	100.0	9	3	AG88479	HER2/NEU
429	3	100.0	9	3	AG88657	HER2/NEU
430	3	100.0	9	3	AG88445	HER2/NEU
431	3	100.0	9	3	AG88959	HER2/NEU
432	3	100.0	9	3	AG88457	HER2/NEU
433	3	100.0	9	3	AG88591	HER2/NEU
434	3	100.0	9	3	AG88525	HER2/NEU
435	3	100.0	9	3	AB60146	Matrix me
436	3	100.0	9	3	AB68648	HER-2 CTL
437	3	100.0	9	3	AAE07553	Human PUM
438	3	100.0	9	3	AAE07642	Human PUM
439	3	100.0	9	3	AA99417	PRAME der
440	3	100.0	9	3	AA99435	PRAME der
441	3	100.0	9	3	AAU01556	Human SSX
442	3	100.0	9	3	AB46273	HPV type
443	3	100.0	9	3	AG61966	Human WT1
444	3	100.0	9	3	AAE08243	Human str
445	3	100.0	9	3	AAE08251	Human str
446	3	100.0	9	3	AAE08248	Human str
447	3	100.0	9	3	AAU23840	Human MHC
448	3	100.0	9	3	AAU24232	Human MHC

AAU24428	Human MHC
AAU24338	Human MHC
AB19891	Neisseria
AB75866	Influenza
AAU03310	Fruit fly
AB31324	Exemplary
AB37497	Flagellin
ABP16468	HIV A24 s
ABP22010	HIV A03 m
ABP12233	HIV A02 s
ABP14095	HIV A02 s
ABP12234	HIV A02 s
ABP15043	HIV A03 s
ABP20065	HIV A03 m
ABP12212	HIV A02 s
ABP11570	HIV A01 s
ABP15314	HIV A24 s
ABP12210	HIV A02 s
ABP14094	HIV A02 s
ABP15044	HIV A03 s
ABP22497	HIV A11 m
ABP14090	HIV A02 s
ABP20045	HIV A03 m
ABP21987	HIV A03 m
ABP14092	HIV A02 s
ABP15313	HIV A24 s
ABP22096	HIV A03 m
ABP23896	HIV A11 m
ABP14093	HIV A02 s
ABP15312	HIV A24 s
ABP16030	HIV A24 s
ABP20112	HIV A03 m
ABP22009	HIV A03 m
ABP22042	HIV A03 m
ABP23854	HIV A11 m
ABP13232	HIV A02 s
ABP12231	HIV A02 s
ABP12232	HIV A02 s
ABP17683	HIV B58 s
ABP14091	HIV A02 s
ABP14343	HIV A03 s
ABP17625	HIV B58 s
ABP22144	HIV A03 m
ABP13432	HIV A02 s
ABP24348	HIV A24 m
AAU68733	Human Wil
AB45872	Human tum
AAU02236	HLA bindi
AAU02274	HLA bindi
AAU02239	HLA bindi
AAU02263	HLA bindi
AAU02293	HLA bindi

ALIGNMENTS

RESULT 1
AA81949
ID AAP81949 standard; protein; 8 AA.
XX
AC AAP81949;
XX
DT 25-MAR-2003 (revised)
DT 15-OCT-1990 (first entry)
XX
DE 8 amino acid peptide fragment of pure sorbine.
XX sorbine; water and sodium absorption; diarrhoea; pig intestinal mucosa.
XX Sus scrofa.
XX FR2601020-A.
XX

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PD 08-JAN-1988.
PF 03-JUL-1986; 86FR-00609682.
PR 03-JUL-1986; 86FR-00009682.
XX (INRM ) INSERM INST NAT SANTE & RECH MED.
XX Vagnedeser M, Panuescla D, Mutt V, Jornvall H;
XX WPI; 1988-058509/09.
XX
XX New polypeptide sorbose stimulating water and sodium absorption - by the
PT intestine, and its fragments, useful for treating diarrhoea.
XX
XX Claim 3; Page 19; 21pp; French.
XX
XX Fragment forms part of sorbine as purified from pig intestinal mucosa.
CC The final order of the fragments in the intact polypeptide is not known.
CC It is thought, however, that this fragment is the fifth (starting at the
CC N-terminal) in the sequence. see also AAP81945-8 and AAP81950-P81952.
CC (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to
CC correct PR field.) (Updated on 25-MAR-2003 to correct PA field.) (Updated
CC on 25-MAR-2003 to correct PI field.)
XX
SQ Sequence 8 AA;

Alignment Scores:
Pred. No.: 9.59e+07 Length: 8
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-10-070-588A-112 (1-11) x AAP81949 (1-8)

QY 10 AGTGCCAAA 2
DB 1 SerAlalys 3

RESULT 2
AAR35903
ID AAR35903 standard; protein; 8 AA.
XX
AC AAR35903;
XX
XX 25-MAR-2003 (revised)
DT 24-MAY-1993 (first entry)
XX
XX Hepatitis C virus (HCV) epitope.
XX
XX Hepatitis; liver disease; HCV1; monoclonal antibody; epitope;
KW immobilised reagent; immunoassay; diagnosis; detection; treatment;
XX infection.
XX
OS Hepatitis C virus type 1.
XX
XX WO9300365-A2.
XX
XX 07-JAN-1993.
XX
XX 24-JUN-1992; 92WO-US005388.
XX
XX 24-JUN-1991; 91US-00722489.
XX
XX (CHIR ) CHIRON CORP.
XX
XX Chien DY, Rutter W;
XX
XX WPI; 1993-036334/04.
XX
XX Polypeptide(s) comprising truncated hepatitis C virus sequences - for
PT detection, prevention and treatment of hepatitis C infection.

Example A; Page 35; 80pp; English.

This octamer was found to be immunoreactive with anti-HCV anti-sera. In
the epitope mapping experiment three different samples of anti-sera were
reacted with the peptide octamer, and then incubated with HRP-labelled
goat anti-human Ig antiser, to enable detection of binding. This epitope
starts from amino acid 801 of the HCV polypeptide. This was found to be a
weak epitope. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 8 AA;

Alignment Scores:
Pred. No.: 9.59e+07 Length: 8
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x AAR35903 (1-8)

QY 3 TTGCGACTA 11
DB 1 LeuAlaLeu 3

RESULT 3
AAR35885
ID AAR35885 standard; protein; 8 AA.
XX
AC AAR35885;
XX
XX 25-MAR-2003 (revised)
DT 24-MAY-1993 (first entry)
XX
XX Hepatitis C virus (HCV) epitope.
XX
XX Hepatitis; liver disease; HCV1; monoclonal antibody; epitope;
KW immobilised reagent; immunoassay; diagnosis; detection; treatment;
XX infection.
XX
OS Hepatitis C virus type 1.
XX
XX WO9300365-A2.
XX
XX 07-JAN-1993.
XX
XX 24-JUN-1992; 92WO-US005388.
XX
XX 24-JUN-1991; 91US-00722489.
XX
XX (CHIR ) CHIRON CORP.
XX
XX Chien DY, Rutter W;
XX
XX WPI; 1993-036334/04.
XX
XX Polypeptide(s) comprising truncated hepatitis C virus sequences - for
PT detection, prevention and treatment of hepatitis C infection.

Example A; Page 35; 80pp; English.

This octamer was found to be immunoreactive with anti-HCV anti-sera. In
the epitope mapping experiment three different samples of anti-sera were
reacted with the peptide octamer, and then incubated with HRP-labelled
goat anti-human Ig antiser, to enable detection of binding. This epitope
starts from amino acid 613 of the HCV polypeptide. (Updated on 25-MAR-
2003 to correct PN field.)

XX Sequence 8 AA;

Alignment Scores:

```

Pred. No.: 9.59e+07
 Score: 3.00
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 100.00%
 DB: 2
 Gaps: 0

US-10-070-588A-112 (1-11) x AAR35885 (1-8)

QY 1 CTTTGGCAC 9
 |||||
 Db 3 LeuTrpHis 5

RESULT 4

AAR35884
 ID AAR35884 standard; protein; 8 AA.

XX AC AAR35884;

XX DT 25-MAR-2003 (revised)
 XX DT 24-MAY-1993 (first entry)

XX DE Hepatitis C virus (HCV) epitope.

XX KW Hepatitis; liver disease; HCV1; monoclonal antibody; epitope;
 KW immobilised reagent; immunoassay; diagnosis; detection; treatment;
 XX infection.

XX OS Hepatitis C virus type 1.

XX PN WO9300365-A2.

XX PD 07-JAN-1993.

XX PF 24-JUN-1992; 92WO-US005388.

XX PR 24-JUN-1991; 91US-00722489.

XX PA (CHIR) CHIRON CORP.

XX PI Chien DY, Rutter W;

XX DR WPI; 1993-036334/04.

XX PT Polypeptide(s) comprising truncated hepatitis C virus sequences - for
 XX detection, prevention and treatment of hepatitis C infection.

XX PS Example A; Page 35; 80pp; English.

XX CC This octamer was found to be immunoreactive with anti-HCV anti-sera. In
 CC the epitope mapping experiment three different samples of anti-sera were
 CC reacted with the peptide octamer, and then incubated with HRP-labelled
 CC goat anti-human Ig antiserum, to enable detection of binding. This epitope
 CC starts from amino acid 612 of the HCV polypeptide. (Updated on 25-MAR-
 CC 2003 to correct PN field.)

XX SQ Sequence 8 AA;

Alignment Scores:

Pred. No.: 9.59e+07
 Score: 3.00
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 100.00%
 DB: 2
 Gaps: 0

US-10-070-588A-112 (1-11) x AAR35884 (1-8)

QY 1 CTTTGGCAC 9
 |||||
 Db 4 LeuTrpHis 6

RESULT 5

AAR35882
 ID AAR35882 standard; protein; 8 AA.

XX AC AAR35882;

XX DT 25-MAR-2003 (revised)
 XX DT 24-MAY-1993 (first entry)

XX DE Hepatitis C virus (HCV) epitope.

XX KW Hepatitis; liver disease; HCV1; monoclonal antibody; epitope;
 KW immobilised reagent; immunoassay; diagnosis; detection; treatment;
 XX infection.

XX OS Hepatitis C virus type 1.

XX PN WO9300365-A2.

XX PD 07-JAN-1993.

XX PF 24-JUN-1992; 92WO-US005388.

XX PR 24-JUN-1991; 91US-00722489.

XX PA (CHIR) CHIRON CORP.

XX PI Chien DY, Rutter W;

XX DR WPI; 1993-036334/04.

XX PT Polypeptide(s) comprising truncated hepatitis C virus sequences - for
 XX detection, prevention and treatment of hepatitis C infection.

XX PS Example A; Page 35; 80pp; English.

XX CC This octamer was found to be immunoreactive with anti-HCV anti-sera. In
 CC the epitope mapping experiment three different samples of anti-sera were
 CC reacted with the peptide octamer, and then incubated with HRP-labelled
 CC goat anti-human Ig antiserum, to enable detection of binding. This epitope
 CC starts from amino acid 610 of the HCV polypeptide. (Updated on 25-MAR-
 CC 2003 to correct PN field.)

XX SQ Sequence 8 AA;

Alignment Scores:

Pred. No.: 9.59e+07
 Score: 3.00
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 100.00%
 DB: 2
 Gaps: 0

US-10-070-588A-112 (1-11) x AAR35882 (1-8)

QY 1 CTTTGGCAC 9
 |||||
 Db 6 LeuTrpHis 8

RESULT 6

AAR35883
 ID AAR35883 standard; protein; 8 AA.

XX AC AAR35883;

XX DT 25-MAR-2003 (revised)
 XX DT 24-MAY-1993 (first entry)

XX DE Hepatitis C virus (HCV) epitope FB.

XX KW Hepatitis; liver disease; HCV1; monoclonal antibody; epitope;
 KW immobilised reagent; immunoassay; diagnosis; detection; treatment;
 XX infection.

OS Hepatitis C virus type 1.
XX WO9300365-A2.
XX
XX 07-JAN-1993.
XX
XX 24-JUN-1992; 92WO-US005388.
XX
XX 24-JUN-1991; 91US-00722489.
XX
XX (CHIR) CHIRON CORP.
XX
XX Chien DY, Rutter W;
XX
XX WPI; 1993-036334/04.
XX
XX Polypeptide(s) comprising truncated hepatitis C virus sequences - for
XX detection, prevention and treatment of hepatitis C infection.
XX
XX Example A; Page 35; 80pp; English.
XX
XX This octamer was found to be immunoreactive with anti-HCV anti-sera. In
XX the epitope mapping experiment three different samples of anti-sera were
XX reacted with the peptide octamer, and then incubated with HRP-labelled
XX goat anti-human Ig antiserum, to enable detection of binding. This epitope
XX starts from amino acid 611 of the HCV polyprotein. This was found to be a
XX particularly strong epitope. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 8 AA;
SQ
Alignment Scores:
Pred. No.: 9.59e+07 Length: 8
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0
US-10-070-588A-112 (1-11) x AAR35883 (1-8)
QY 1 CTTTGGCAC 9
DB 5 LeuTrpHis 7
RESULT 7
AAR42565
ID AAR42565 standard; peptide; 8 AA.
XX
XX AAR42565;
AC
XX 04-NOV-1994 (first entry)
DT
XX
XX Tri-/tetra-cyclic compound linked peptide #9.
DE
XX Tricyclic; tetracyclic; medicament; manufacture; determination;
XX blood platelet thrombi; fibrinogen antagonists.
KW
XX Synthetic.
OS
XX AU9344935-A.
XX
XX 10-MAR-1994.
PD
XX 26-AUG-1993; 93AU-00044935.
PP
XX 31-AUG-1992; 92CH-00002725.
XX
XX (HOFF) HOFFMANN LA ROCHE & CO AG F.
XX
XX Banwarth W, Gerber F, Griender A, Knierzinger A, Muller K;
XX Obrecht D, Trzeclak A;
XX
XX WPI; 1994-118783/15.
DR

XX New tri- and tetra-cyclic cpds., partic. with peptide chains - used e.g.
XX for determin. of biologically active peptide sequences or as fibrinogen
XX antagonists.
XX
XX Claim 9; Page 120; 131pp; English.
XX
XX The sequences given in AAR42557-68 are peptides which may be linked to
XX the tri- and tetra-cyclic compounds of the invention. These compounds may
XX be used as medicaments or for the manufacture of medicaments. They may
XX esp. be used for the determination of biologically active peptide
XX sequences. Compounds containing the sequence RGDF or RGVV can esp. be
XX used for preventing the formation of blood platelet thrombi, as
XX fibrinogen antagonists
XX
XX Sequence 8 AA;
SQ
Alignment Scores:
Pred. No.: 9.59e+07 Length: 8
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0
US-10-070-588A-112 (1-11) x AAR42565 (1-8)
QY 3 TTGGCACTA 11
DB 5 LeuAlaLeu 7
RESULT 8
AAR56998
ID AAR56998 standard; peptide; 8 AA.
XX
XX AAR56998;
AC
XX 25-MAR-2003 (revised)
DT
XX 15-FEB-1995 (first entry)
DT
XX
XX N-terminal fragment of human histo-blood group A transferase.
DE
XX Blood; group; determinant; antigen; erythrocyte; oligosaccharide;
XX glycoconjugate; glycosphingolipid; glycoprotein; glycosyltransferase;
KW
XX transferase.
KW
XX Homo sapiens.
OS
XX US5326857-A.
XX
XX 05-JUL-1994.
PD
XX
XX 29-AUG-1991; 91US-00752101.
PP
XX
XX 31-AUG-1989; 89US-00402695.
PR
XX
XX (BIOM-) BIOMEMBRANE INST.
PA
XX
XX Hakomori S, Clausen H, Yamamoto F, White T;
PI
XX WPI; 1994-217098/26.
XX
XX Isolated DNA molecules - encode human histo-blood groups A-, B- and O-
XX glycotransferases.
PT
XX
XX Example 2; Col 35; 63pp; English.
PS
XX
XX The histo-blood group ABH determinants are major allogeneic antigens in
XX both erythrocytes and tissues of humans. They generally constitute
XX peripheral parts of the oligosaccharide chains of glycoconjugates
XX i.e. linked to lipids (glycosphingolipids) or to proteins (glycoproteins).
XX It was proposed that the A and B phenotypes were associated with
XX glycosyltransferases that converted the H substance associated with the O

CC phenotype to A and B respectively, through the addition of alpha1-3-N-acetylglactosamine or alpha1-3-galactosyl residues to the H antigen Fuc-alpha1-2Gal-beta1-R. Hence, the primary products of the histo-blood group A and B genes are the respective glycosyltransferases. This is a fragment of the A group transferase. See also AAR56995-R57010. (Updated on 25-MAR-2003 to correct PF field.)

XX Sequence 8 AA;

Alignment Scores:
Pred. No.: 9.59e+07 Length: 8
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x AAR56998 (1-8)

Qy 9 GTGCCAAAG 1
|||||
Db 6 ValProlys 8

RESULT 9
AAR73487

ID AAR73487 standard; peptide; 8 AA.

AC AAR73487;

DT 18-DEC-1995 (first entry)

DE Human TSH receptor (residues 573-580).

KW thyroid stimulating hormone receptor; TSH; human; Homo sapiens; antibody;
KW affinity; detection.

OS Synthetic.

PN JP07089991-A.

PD 04-APR-1995.

PF 28-SEP-1993; 93JP-00240853.

PR 28-SEP-1993; 93JP-00240853.

PA (MITP) MITSUBISHI PETROCHEMICAL CO LTD.

XX WPI; 1995-167251/22.

XX Novel polypeptide(s) having affinity for the human TSH receptor antibody
PT - used in detection of the TSH antibody.

PS Example 1; Page 41; 54pp; Japanese.

XX Peptides with affinity to human TSH (thyroid stimulating hormone)
CC receptor antibody are used for detection of the antibody. (See also
CC AAR73201-592)

XX Sequence 8 AA;

Alignment Scores:
Pred. No.: 9.59e+07 Length: 8
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x AAR73487 (1-8)

Qy 3 TTGGCACTA 11
|||||

Db 6 LeuAlaLeu 8

RESULT 10

AAR73488
ID AAR73488 standard; peptide; 8 AA.

XX AAR73488;

XX 18-DEC-1995 (first entry)

DE Human TSH receptor (residues 575-582).

KW thyroid stimulating hormone receptor; TSH; human; Homo sapiens; antibody;
KW affinity; detection.

OS Synthetic.

PN JP07089991-A.

PD 04-APR-1995.

PF 28-SEP-1993; 93JP-00240853.

PR 28-SEP-1993; 93JP-00240853.

PA (MITP) MITSUBISHI PETROCHEMICAL CO LTD.

XX WPI; 1995-167251/22.

XX Novel polypeptide(s) having affinity for the human TSH receptor antibody
PT - used in detection of the TSH antibody.

PS Example 1; Page 41; 54pp; Japanese.

CC Peptides with affinity to human TSH (thyroid stimulating hormone)
CC receptor antibody are used for detection of the antibody. (See also
CC AAR73201-592)

XX Sequence 8 AA;

Alignment Scores:
Pred. No.: 9.59e+07 Length: 8
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x AAR73488 (1-8)

Qy 3 TTGGCACTA 11
|||||

Db 4 LeuAlaLeu 6

RESULT 11

AAR73476
ID AAR73476 standard; peptide; 8 AA.

XX AAR73476;

XX 18-DEC-1995 (first entry)

DE Human TSH receptor (residues 551-558).

KW thyroid stimulating hormone receptor; TSH; human; Homo sapiens; antibody;
KW affinity; detection.

OS Synthetic.

PN JP07089991-A.

XX 04-APR-1995.

XX


```
PF 28-SEP-1993; 93JP-00240853.
XX
XX
XX 28-SEP-1993; 93JP-00240853.
XX
XX (MITP ) MITSUBISHI PETROCHEMICAL CO LTD.
XX
XX WPI; 1995-167251/22.
XX
XX Novel polypeptide(s) having affinity for the human TSH receptor antibody
XX - used in detection of the TSH antibody.
XX
XX Example 1; Page 39; 54pp; Japanese.
XX
XX Peptides with affinity to human TSH (thyroid stimulating hormone)
XX receptor antibody are used for detection of the antibody. (See also
XX AAR73201-592)
XX
XX Sequence 8 AA;
XX
Alignment Scores:
Pred. No.: 9.59e+07 Length: 8
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0
US-10-070-588A-112 (1-11) x AAR73476 (1-8)
Qy 3 TTGGCACTA 11
Db 2 LeuAlaLeu 4
RESULT 12
AAR73413
ID AAR73413 standard; peptide; 8 AA.
XX
XX AAR73413;
XX
XX 12-DEC-1995 (first entry)
XX
XX Human TSH receptor (residues 425-432).
XX
XX thyroid stimulating hormone receptor; TSH; human; Homo sapiens; antibody;
XX affinity; detection.
XX
XX Synthetic.
XX
XX JP07089991-A.
XX
XX 04-APR-1995.
XX
XX 28-SEP-1993; 93JP-00240853.
XX
XX 28-SEP-1993; 93JP-00240853.
XX
XX (MITP ) MITSUBISHI PETROCHEMICAL CO LTD.
XX
XX WPI; 1995-167251/22.
XX
XX Novel polypeptide(s) having affinity for the human TSH receptor antibody
XX - used in detection of the TSH antibody.
XX
XX Example 1; Page 32; 54pp; Japanese.
XX
XX Peptides with affinity to human TSH (thyroid stimulating hormone)
XX receptor antibody are used for detection of the antibody. (See also
XX AAR73201-592)
XX
XX Sequence 8 AA;
XX
Alignment Scores:
Pred. No.: 9.59e+07 Length: 8
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0
US-10-070-588A-112 (1-11) x AAR73413 (1-8)
Qy 3 TTGGCACTA 11
Db 3 LeuAlaLeu 5
RESULT 13
AAR73414
ID AAR73414 standard; peptide; 8 AA.
XX
XX AAR73414;
XX
XX 12-DEC-1995 (first entry)
XX
XX Human TSH receptor (residues 427-434).
XX
XX thyroid stimulating hormone receptor; TSH; human; Homo sapiens; antibody;
XX affinity; detection.
XX
XX Synthetic.
XX
XX JP07089991-A.
XX
XX 04-APR-1995.
XX
XX 28-SEP-1993; 93JP-00240853.
XX
XX 28-SEP-1993; 93JP-00240853.
XX
XX (MITP ) MITSUBISHI PETROCHEMICAL CO LTD.
XX
XX WPI; 1995-167251/22.
XX
XX Novel polypeptide(s) having affinity for the human TSH receptor antibody
XX - used in detection of the TSH antibody.
XX
XX Example 1; Page 32; 54pp; Japanese.
XX
XX Peptides with affinity to human TSH (thyroid stimulating hormone)
XX receptor antibody are used for detection of the antibody. (See also
XX AAR73201-592)
XX
XX Sequence 8 AA;
XX
Alignment Scores:
Pred. No.: 9.59e+07 Length: 8
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0
US-10-070-588A-112 (1-11) x AAR73414 (1-8)
Qy 3 TTGGCACTA 11
Db 1 LeuAlaLeu 3
RESULT 14
AAR73474
ID AAR73474 standard; peptide; 8 AA.
XX
XX AAR73474;
XX
XX 18-DEC-1995 (first entry)
XX
XX Human TSH receptor (residues 547-554).
```

XX thyroid stimulating hormone receptor; TSH; human; Homo sapiens; antibody;
KW affinity; detection.
XX Synthetic.
XX JP07089991-A.
XX
XX 04-APR-1995.
XX
XX 28-SEP-1993; 93JP-00240853.
XX
XX 28-SEP-1993; 93JP-00240853.
XX
XX (MITP) MITSUBISHI PETROCHEMICAL CO LTD.
XX
XX WPI; 1995-167251/22.
XX
XX Novel polypeptide(s) having affinity for the human TSH receptor antibody
PT - used in detection of the TSH antibody.
XX
XX Example 1; Page 39; 54pp; Japanese.
XX
XX Peptides with affinity to human TSH (thyroid stimulating hormone)
CC receptor antibody are used for detection of the antibody. (See also
CC AAR73201-592)
XX
XX Sequence 8 AA;
SQ
Alignment Scores:
Pred. No.: 9.59e+07 Length: 8
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0
US-10-070-588A-112 (1-11) x AAR73474 (1-8)
Qy 3 TTGGCACTA 11
Db 6 LeuAlaLeu 8
RESULT 15
AAR73475
ID AAR73475 standard; peptide; 8 AA.
XX
XX AAR73475;
XX
XX 18-DEC-1995 (first entry)
XX
XX Human TSH receptor (residues 549-556).
XX
XX thyroid stimulating hormone receptor; TSH; human; Homo sapiens; antibody;
KW affinity; detection.
XX Synthetic.
XX JP07089991-A.
XX
XX 04-APR-1995.
XX
XX 28-SEP-1993; 93JP-00240853.
XX
XX 28-SEP-1993; 93JP-00240853.
XX
XX (MITP) MITSUBISHI PETROCHEMICAL CO LTD.
XX
XX WPI; 1995-167251/22.
XX
XX Novel polypeptide(s) having affinity for the human TSH receptor antibody
PT - used in detection of the TSH antibody.
XX

PS Example 1; Page 39; 54pp; Japanese.
XX
XX Peptides with affinity to human TSH (thyroid stimulating hormone)
CC receptor antibody are used for detection of the antibody. (See also
CC AAR73201-592)
XX
XX Sequence 8 AA;
SQ
Alignment Scores:
Pred. No.: 9.59e+07 Length: 8
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0
US-10-070-588A-112 (1-11) x AAR73475 (1-8)
Qy 3 TTGGCACTA 11
Db 4 LeuAlaLeu 6
RESULT 16
AAR73489
ID AAR73489 standard; peptide; 8 AA.
XX
XX AAR73489;
XX
XX 18-DEC-1995 (first entry)
XX
XX Human TSH receptor (residues 577-584).
XX
XX thyroid stimulating hormone receptor; TSH; human; Homo sapiens; antibody;
KW affinity; detection.
XX Synthetic.
XX JP07089991-A.
XX
XX 04-APR-1995.
XX
XX 28-SEP-1993; 93JP-00240853.
XX
XX 28-SEP-1993; 93JP-00240853.
XX
XX (MITP) MITSUBISHI PETROCHEMICAL CO LTD.
XX
XX WPI; 1995-167251/22.
XX
XX Novel polypeptide(s) having affinity for the human TSH receptor antibody
PT - used in detection of the TSH antibody.
XX
XX Example 1; Page 41; 54pp; Japanese.
XX
XX Peptides with affinity to human TSH (thyroid stimulating hormone)
CC receptor antibody are used for detection of the antibody. (See also
CC AAR73201-592)
XX
XX Sequence 8 AA;
SQ
Alignment Scores:
Pred. No.: 9.59e+07 Length: 8
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0
US-10-070-588A-112 (1-11) x AAR73489 (1-8)
Qy 3 TTGGCACTA 11
Db 2 LeuAlaLeu 4

```

RESULT 17
AAR73412
ID AAR73412 standard; peptide; 8 AA.
AC AAR73412;
XX
XX 12-DEC-1995 (first entry)
XX
XX Human TSH receptor (residues 423-430).
XX
XX thyroid stimulating hormone receptor; TSH; human; Homo sapiens; antibody;
KW affinity; detection.
XX
XX Synthetic.
XX
XX JP07089991-A.
XX
XX 04-APR-1995.
XX
XX 28-SEP-1993; 93JP-00240853.
XX
XX 28-SEP-1993; 93JP-00240853.
XX
XX (MITP ) MITSUBISHI PETROCHEMICAL CO LTD.
XX
XX WPI; 1995-167251/22.
XX
XX Novel polypeptide(s) having affinity for the human TSH receptor antibody
PT - used in detection of the TSH antibody.
XX
XX Example 1; Page 32; 54pp; Japanese.
XX
XX Peptides with affinity to human TSH (thyroid stimulating hormone)
CC receptor antibody are used for detection of the antibody. (See also
CC AAR73201-592)
XX
XX Sequence 8 AA;

Alignment Scores:
Pred. No.: 9.59e+07 Length: 8
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x AAR73412 (1-8)

Qy 3 TTGGCACTA 11
Db 5 LeuAlaLeu 7

RESULT 18
AAR84449
ID AAR84449 standard; peptide; 8 AA.
XX
XX AAR84449;
XX
XX 06-JAN-1997 (first entry)
XX
XX Hepatitis C virus E2 region (611-618) generic sequence.
XX
XX Hepatitis C virus; HCV; immunogen; E2 region; immunodominant;
KW T cell epitope; vaccine.
XX
XX Hepatitis C virus.
XX
XX WO9512677-A2.
XX
XX 11-MAY-1995.
XX
XX 28-OCT-1994; 94WO-EP003555.
XX
XX Hepatitis C virus E2 region (615-622) generic sequence.
XX
XX Hepatitis C virus; HCV; immunogen; E2 region; immunodominant;
KW T cell epitope; vaccine.
XX
XX Hepatitis C virus.
XX
XX WO9512677-A2.
XX
XX 11-MAY-1995.
XX
XX 28-OCT-1994; 94WO-EP003555.
XX
XX Hepatitis C virus immunogenic polypeptide contg. a T-cell stimulating
PT epitope - from core, E1, E2 and NS3 regions, useful in production of
PT vaccines, therapeutic agents, etc.

RESULT 19
AAR84450
ID AAR84450 standard; peptide; 8 AA.
XX
XX AAR84450;
XX
XX 06-JAN-1997 (first entry)
XX
XX Hepatitis C virus E2 region (615-622) generic sequence.
XX
XX Hepatitis C virus; HCV; immunogen; E2 region; immunodominant;
KW T cell epitope; vaccine.
XX
XX Hepatitis C virus.
XX
XX Key Location/Qualifiers
FT Misc-difference 8 /label= ile, Val, Phe, Leu
FT
XX
XX WO9512677-A2.
XX
XX 11-MAY-1995.
XX
XX 28-OCT-1994; 94WO-EP003555.
XX
XX 04-NOV-1993; 93EP-00402718.
XX
XX (INNO-) INNOGENETICS NV.
XX
XX Leroux-Roels G, Deleys R, Maertens G;
XX WPI; 1995-193822/25.
XX
XX Hepatitis C virus immunogenic polypeptide contg. a T-cell stimulating
PT epitope - from core, E1, E2 and NS3 regions, useful in production of
PT vaccines, therapeutic agents, etc.

US-10-070-588A-112 (1-11) x AAR84449 (1-8)

Qy 1 CTTGGCAC 9
Db 5 LeuTrpHis 7

RESULT 19
AAR84450
ID AAR84450 standard; peptide; 8 AA.
XX
XX AAR84450;
XX
XX 06-JAN-1997 (first entry)
XX
XX Hepatitis C virus E2 region (615-622) generic sequence.
XX
XX Hepatitis C virus; HCV; immunogen; E2 region; immunodominant;
KW T cell epitope; vaccine.
XX
XX Hepatitis C virus.
XX
XX Key Location/Qualifiers
FT Misc-difference 8 /label= ile, Val, Phe, Leu
FT
XX
XX WO9512677-A2.
XX
XX 11-MAY-1995.
XX
XX 28-OCT-1994; 94WO-EP003555.
XX
XX 04-NOV-1993; 93EP-00402718.
XX
XX (INNO-) INNOGENETICS NV.
XX
XX Leroux-Roels G, Deleys R, Maertens G;
XX WPI; 1995-193822/25.
XX
XX Hepatitis C virus immunogenic polypeptide contg. a T-cell stimulating
PT epitope - from core, E1, E2 and NS3 regions, useful in production of
PT vaccines, therapeutic agents, etc.
```

XX PS Claim 26; Page 71; 105pp; English.

XX CC Polypeptides comprising 8-20 amino acids from the HCV E2 region sequence

CC in AAR84357 (spanning positions 571-638) and containing a T-cell

CC stimulating epitope are used in HCV immunogenic compositions. The present

CC sequence is a specifically claimed example of such a T-cell epitope-

CC containing region

XX CC Sequence 8 AA;

XX SQ Alignment Scores:

Pred. No.: 9.59e+07 Length: 8

Score: 3.00 Matches: 3

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x AAR84450 (1-8)

QY 1 CTTTGGGAC 9

DB 1 Leutrphis 3

RESULT 20

ADC81358

ID ADC81358 standard; peptide; 8 AA.

XX AC ADC81358;

XX AC

XX DT 01-JAN-2004 (first entry)

XX DE Bovin THF-gamma2 analogue V4-THF gamma2.

XX XX

KW Cow; thymic humoral factor gamma2; THF-gamma2; concanavalin A;

KW Con A-induced interleukin-2 production; mouse spleen cells;

KW granulocyte-monocyte colony forming cell; GM-CFC; mouse bone marrow;

KW immunomodulatory agent; congenital immune defect;

KW primary T cell deficiency; thymic dysplasia; Down's syndrome;

KW viral infection; herpes; adenovirus infection; HIV infection;

KW subacute sclerosing pan-encephalitis; immune suppression; leukopenia;

KW cancer; chemotherapy; radiotherapy; autoimmune inflammatory disorder;

KW rheumatoid arthritis; systemic lupus erythematosus; psoriasis;

KW bone marrow transplantation; atopic condition; asthma; atopic dermatitis;

KW mutant; mutein.

XX OS Synthetic.

OS Bos taurus.

XX XX

XX PH Key Location/Qualifiers

FT Misc-difference 4 /note= "Wild-type Gly substituted by Val"

FT

XX WO9501182-A1.

XX PN

XX PD 12-JAN-1995.

XX XX

XX PF 28-JUN-1994; 94WO-US007304.

XX XX

XX PR 01-JUL-1993; 93IL-00106214.

XX XX

XX PA (YEDA) YEDA RES & DEV CO LTD.

XX XX

XX PI Rycus A, Burstein Y, Trainin N;

XX XX

XX DR WPI; 1995-060814/08.

XX XX

XX PT New thymic humoral factor gamma 2 analogues - used as immunomodulatory

PT agents for treating e.g. immune defects, viral infections or autoimmune

FT disease.

XX XX

XX PS Claim 15; Page 25; 30pp; English.

XX CC A peptide is claimed which is a thymic humoral factor (THF)-gamma2

CC analogue of at least 4 amino acid (AA) residues or a functional

CC derivative or salt, capable of enhancing concanavalin A (Con A)-induced

CC interleukin-2 (IL-2) production in mouse spleen cells and/or the number

CC of granulocyte-monocyte colony forming cells (GM-CFC) of mouse bone

CC marrow. The peptide comprises one or more sequences corresponding to the

CC sequence of the wild-type THF-gamma2 but differing by (i) deletion of one

CC or more AA residues, (ii) addition of one or more AA residues at the N-

CC and/or C-terminus, (iii) substitution of one or more AA residues by a

CC protein natural or non-natural AA residue, (iv) cyclisation through a

CC free carboxyl group and a free amino group or through disulphide bonds of

CC cysteine residues or (v) linkage of two or more sequences or modified

CC sequences corresponding to (i)-(iv), either directly or through a peptide

CC or non-peptide chain. The peptides are used as immunomodulatory agents.

CC They can be used for treating e.g. congenital immune defects involving

CC primary T cell deficiencies such as thymic dysplasia and Down's syndrome,

CC primary and secondary viral infections (e.g. herpes virus, adenovirus and

CC HIV), as well as subacute infections such as subacute sclerosing pan-

CC encephalitis, immune suppression and leukopenia following cancer

CC treatment by chemotherapy and/or radiotherapy, autoimmune inflammatory

CC disorders, e.g. rheumatoid arthritis, systemic lupus erythematosus and

CC psoriasis, in bone marrow transplantation to prevent viral infections and

CC in atopic conditions such as asthma and atopic dermatitis. The present

CC sequence is a bovine THF-gamma2 analogue peptide of the invention.

XX CC

XX SQ Sequence 8 AA;

Alignment Scores:

Pred. No.: 9.59e+07 Length: 8

Score: 3.00 Matches: 3

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x ADC81358 (1-8)

QY 9 GTGCCAAAG 1

DB 4 ValProlys 6

RESULT 21

AAW36922

ID AAW36922 standard; peptide; 8 AA.

XX AC AAW36922;

XX AC

XX DT 17-MAR-1998 (first entry)

XX DE Peptide epitope 17 of CD47 extracellular domain for the C5/D5 antibody.

XX XX

KW CD47 epitope; C5/D5 antibody; colonic epithelial cell; neutrophil; PMN;

KW transmigration; immune response modulation; OVTL3; IAP;

KW extracellular domain.

XX KW

XX OS Homo sapiens.

XX XX

XX PN WO9727873-A1.

XX XX

XX PD 07-AUG-1997.

XX XX

XX PF 28-JAN-1997; 97WO-US001340.

XX XX

XX PR 30-JAN-1996; 96US-00593815.

XX XX

XX PA (BGHM) BRIGHAM & WOMENS HOSPITAL.

XX XX

XX PI Parkos CA, Madara JL;

XX XX

XX DR WPI; 1997-402315/37.

XX XX

XX PT Monoclonal antibody, C5-D5, and related CD47 epitope(s) - used for

PT inhibiting CD47-expressing cell migration, and for modulating immune
 XX responses.

PS Claim 15; Page 65; 87pp; English.

XX Peptides AAW36906-38 represent CD47 epitopes for the C5/D5 antibody. All
 CC of the epitopes are found within an N-terminal fragment of CD47, AAW36904
 CC -5. CD47 is expressed on both colonic epithelial cells, as well as as
 CC neutrophils (PMN). This suggests that CD47 may be utilised by both
 CC epithelia and PMN during transmigration of PMN across columnar epithelia
 CC in vivo. The preferred peptide epitopes are AAW36920 and AAW36934.
 CC Searches for sequence homology of the epitopes revealed a complete match
 CC for AAW36937 and AAW36938 with a membrane protein OVTL3 (also known as
 CC integrin associated protein (IAP)). A novel composition comprises an
 CC inhibitory agent selected from the C5/D5 antibody, functionally active
 CC fragments of this antibody, and monoclonal antibodies with the
 CC characteristics of this antibody. This composition can be used for
 CC inhibiting the migration of a CD47-expressing cell across a cell layer,
 CC extracellular matrix or a filter. C5/D5 can also be used for modulating
 CC an immune response in a subject

SQ Sequence 8 AA;

Alignment Scores: Length: 8
 Pred. No.: 9.59e+07
 Score: 3.00
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 100.00%
 DB: 2
 Indels: 0
 Gaps: 0

US-10-070-588A-112 (1-11) x AAW36922 (1-8)

Qy 10 AGTGCCCAA 2
 Db |||||

2 SerAlaLys 4

RESULT 22

AAW36925
 ID AAW36925 standard; peptide; 8 AA.

XX AAW36925;

XX 17-MAR-1998 (first entry)

XX Peptide epitope 20 of CD47 extracellular domain for the C5/D5 antibody.

XX CD47 epitope; C5/D5 antibody; colonic epithelial cell; neutrophil; PMN;
 KW transmigration; immune response modulation; OVTL3; IAP;
 KW extracellular domain.

XX Homo sapiens.

OS WO9727873-A1.

PN 07-AUG-1997.

XX 28-JAN-1997; 97WO-US001340.

XX 30-JAN-1996; 96US-00593815.

XX (BGHM) BRIGHAM & WOMENS HOSPITAL.

PI Parkos CA, Madara JL;

XX WPI; 1997-402315/37.

XX Monoclonal antibody, C5-D5, and related CD47 epitope(s) - used for
 PT inhibiting CD47-expressing cell migration, and for modulating immune
 PT responses.

PS Claim 15; Page 67; 87pp; English.

XX

CC Peptides AAW36906-38 represent CD47 epitopes for the C5/D5 antibody. All
 CC of the epitopes are found within an N-terminal fragment of CD47, AAW36904
 CC -5. CD47 is expressed on both colonic epithelial cells, as well as as
 CC neutrophils (PMN). This suggests that CD47 may be utilised by both
 CC epithelia and PMN during transmigration of PMN across columnar epithelia
 CC in vivo. The preferred peptide epitopes are AAW36920 and AAW36934.
 CC Searches for sequence homology of the epitopes revealed a complete match
 CC for AAW36937 and AAW36938 with a membrane protein OVTL3 (also known as
 CC integrin associated protein (IAP)). A novel composition comprises an
 CC inhibitory agent selected from the C5/D5 antibody, functionally active
 CC fragments of this antibody, and monoclonal antibodies with the
 CC characteristics of this antibody. This composition can be used for
 CC inhibiting the migration of a CD47-expressing cell across a cell layer,
 CC extracellular matrix or a filter. C5/D5 can also be used for modulating
 CC an immune response in a subject

SQ Sequence 8 AA;

Alignment Scores: Length: 8
 Pred. No.: 9.59e+07
 Score: 3.00
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 100.00%
 DB: 2
 Indels: 0
 Gaps: 0

US-10-070-588A-112 (1-11) x AAW36925 (1-8)

Qy 10 AGTGCCCAA 2

Db |||||

4 SerAlaLys 6

RESULT 23

AAW79266
 ID AAW79266 standard; peptide; 8 AA.

XX AAW79266;

XX 15-FEB-1999 (first entry)

XX Bovine glucuronyl C5-epimerase N-terminal peptide.

XX Glucuronyl C5-epimerase; cattle; D-glucuronic acid; L-iduronic acid;
 KW heparin; heparan sulphate.

XX Bos taurus.

XX Key Location/Qualifiers

FT Misc-difference 4
 FT /note= "unidentified residue"

XX WO9848006-A1.

XX 29-OCT-1998.

XX 17-APR-1998; 98WO-SE000703.

XX 18-APR-1997; 97SE-00001454.

XX (LIND)/ LINDAHL U.

XX (LIJJ)/ LI J.

XX Lindahl U, Li J;

XX WPI; 1998-583655/49.

XX DNA sequence coding for mammalian glucuronyl C5-epimerase and functional
 PT derivatives - capable of converting D-glucuronic acid to L-iduronic acid
 PT in the synthesis of heparin and heparan sulphate.

XX Disclosure; Page 16; 26pp; English.

XX This is an N-terminal peptide of a glucuronyl C5-epimerase purified from

CC bovine liver. It corresponds to amino acid residues 74-86 of the deduced
 CC amino acid sequence (see AAW79263) of the epimerase. N-terminal and
 CC internal peptides (see AAW79264-70) of the epimerase were produced by
 CC digestion of the purified epimerase using a lysine-specific protease. PCR
 CC primers (see AAV62689-91) based on one of these peptides (see AAW79270)
 CC were used to generate a probe that was utilised in the isolation of
 CC glucuronyl C5-epimerase cDNA (see AAV62688) from a bovine lung cDNA
 CC library. The invention relates to isolated or recombinant DNA sequences
 CC for a mammalian (including human) glucuronyl C5-epimerase or its
 CC functional derivative. These can be used for the recombinant production
 CC of the enzyme, which is useful for converting D-glucuronic acid to L-
 CC iduronic acid in the biosynthesis of heparin and heparan sulphate
 XX

SQ Sequence 8 AA;

Alignment Scores:
 Pred. No.: 9.59e+07 Length: 8
 Score: 3.00 Matches: 3
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x AAW79265 (1-8)

QY 9 GTGCCAAG 1
 DB ||||| 6 ValProLys 8

RESULT 24

AAW56853
 ID AAW56853 standard; peptide; 8 AA.

XX AAW56853;

DT 28-JUL-1998 (first entry)

DE Enzyme inhibitor peptide SEQ ID NO:54.

XX Enzyme inhibitor; t-PA; u-PA; chymotrypsin; serine protease; active;
 KW latent; substrate subtraction phage display peptide library;
 KW identification; kinase; phosphatase; serpin.

XX Homo sapiens.

XX WO9747314-A1.

XX 18-DEC-1997.

XX 10-JUN-1997; 97WO-US009760.

XX 10-JUN-1996; 96US-0019495P.

XX (SCRI) SCRIPPS RES INST.

XX Madison EL, Ke S;

XX WPI; 1998-062746/06.

XX Substrate subtraction phage display peptide libraries - used to
 PT distinguish between active and latent forms of enzyme, e.g. serine
 PT protease.

PS Claim 25; Page 58; 138pp; English.

XX The present sequence represents an enzyme inhibitor peptide used in the
 CC method of the invention to distinguish between t-PA and u-PA. The present
 CC invention describes a substrate subtraction library for the
 CC identification of peptide substrates selective between a first enzyme
 CC (E1) and a second enzyme (E2), comprising a collection of different
 CC peptides, substantially lacking peptides that are effective substrates
 CC for E1. Also described are: (1) a method (M1) for identifying peptide
 CC substrates selective between a first enzyme (E1) and a second enzyme (E2)

CC ; (2) a compound comprising the amino acid sequence of a peptide
 CC identified by M1; (3) a polypeptide for use as an enzyme inhibitor
 CC comprising one of 237 amino acid sequences (see AAW56801 to AAW56947, and
 CC AAW56949 to AAW57038); (4) a recombinant DNA vector comprising DNA (I)
 CC encoding a protease inhibitor including the sequence identified by the M1
 CC ; (5) a prokaryotic or eukaryotic cell containing the vector of (4); (6)
 CC an antibody (Ab) immunoreactive with at least one of the peptides
 CC identified by M1; and (7) a diagnostic assay for distinguishing between
 CC active and latent forms of protease inhibitors, that uses (Ab). The
 CC library and method are used for distinguishing between active and latent
 CC forms of enzyme inhibitors, e.g. proteases, kinases and phosphatases.
 CC (Ab) are used for affinity purification of recombinant peptides and in
 CC the identification of naturally occurring protease inhibitors. Enzyme-
 CC inhibiting peptides identified can be used to treat a serpin deficiency
 CC or a disorder of serine proteases
 XX

SQ Sequence 8 AA;

Alignment Scores:
 Pred. No.: 9.59e+07 Length: 8
 Score: 3.00 Matches: 3
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x AAW56853 (1-8)

QY 10 AGTGCCAAA 2

DB ||||| 4 SerAlaLys 6

RESULT 25

AAW75829

ID AAW75829 standard; peptide; 8 AA.

XX AAW75829;

DT 27-OCT-1998 (first entry)

XX Mouse mast cell protease (mMCP-6) susceptible peptide 23.

DE Mast cell protease; MCP; mouse; inhibitor; peptide substrate; asthma;
 KW tryptase-6 protein; inflammatory disorder; allergic rhinitis; urticaria;
 KW anioedema; eczematous dermatitis; atopic dermatitis; anaphylaxis;
 KW hyperproliferative skin disease; peptic ulcer; hyperresponsiveness;
 KW inflammatory skin condition.

XX Synthetic.

XX Mus sp.

XX WO9833812-A1.

XX 06-AUG-1998.

XX 30-JAN-1998; 98WO-US001865.

XX 05-FEB-1997; 97US-0037090P.

XX (SGHM) BRIGHAM & WOMENS HOSPITAL.

XX Stevens RL, Huang C;

XX WPI; 1998-437390/37.

XX Tryptase-6 complex inhibitory peptides - used to treat mast cell-mediated
 PT inflammatory disorders e.g. asthma.

PS Example; Page 26; 69pp; English.

XX Sequences shown in AAW75807 to AAW75835 represent mouse mast cell
 CC protease (mMCP-6) susceptible peptides obtained in the absence of
 CC heparin. The invention provides sequences shown in AAW63160 to AAW63169

CC that are inhibitors of mmp-6. These tryptase-6 complex inhibitor
 CC peptides can be used for treating a mast cell-mediated inflammatory
 CC disorder. The inhibitors can be used to treat inflammatory disorders
 CC including asthma, allergic rhinitis, urticaria and atopic dermatitis, eczematous
 CC dermatitis (atopic dermatitis), hyperproliferative skin disease,
 CC anaphylaxis, peptic ulcers, inflammatory bowel disorder,
 CC hyperresponsiveness and inflammatory skin conditions

CC Sequence 8 AA;

Alignment Scores: Length: 8
 Pred. No.: 9.59e+07
 Score: 3.00
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 100.00%
 DB: 2

US-10-070-588A-112 (1-11) x AAW75829 (1-8)

Oy 3 TTGGCACTA 11

Db 2 LeuAlaLeu 4

RESULT 26

AAAY20315

ID AAY20315 standard; protein; 8 AA.

XX AC AAY20315;

XX DT 22-JUL-1999 (first entry)

XX DE Human microtubule associated protein 2 mutant fragment 11.

XX KW Human; beta-amyloid precursor protein; beta-APP; diagnosis; cancer;
 KW frameshift mutation; age-related disease; neurodegenerative disorder;
 KW Alzheimer's disease; Down's syndrome; myotonic dystrophy; neuronal;
 KW Huntington's disease; multiple sclerosis; alcoholic liver disease;
 KW diabetes mellitus type II; microtubule associated protein; Tau; Big Tau;
 KW ubiquitin B; apolipoprotein E; MAP2; neurofilament-L; neurofilament-M;
 KW neurofilament-F; presenilin I; presenilin II; cellular tumour antigen;
 KW glial fibrillary acidic protein; GFAP; p53; semaphorin III; HUPF-1;
 KW bcl-2; B-cell leukemia/lymphoma 2 proto-oncogene; HMGP-C; NSP-A;
 KW high mobility group protein-C; neuroendocrine specific protein A.

XX OS Synthetic.

XX OS Homo sapiens.

XX PN WO9845322-A2.

XX PD 15-OCT-1998.

XX PF 02-APR-1998; 98WO-IB000705.

XX PR 10-APR-1997; 97US-0043163P.

XX (ROYA-) ROYAL NETHERLANDS ACAD ARTS & SCI.

XX PA (UYRO-) UNIV ROTTERDAM ERASMUS.

XX PA (UYUT-) RIJKSUNIV UTRECHT.

XX PI Van Leeuwen FW, Grosveld FG, Burbach JPH;

XX WPI; 1998-609901/51.

XX N-PSDB; AAX75757.

XX PT Diagnosing disease by detecting frameshift mutations in RNA or
 PT corresponding protein mutations - used to diagnose cancer and
 PT neurological diseases, particularly Alzheimer's disease, and also for
 PT treatment and prevention with specific ribozymes or wild-type RNA.

XX PS Disclosure; Fig 6; 258pp; English.

XX This invention describes a novel method for the diagnosis of a disease

CC caused by, or associated with, an RNA molecule that has a frameshift
 CC mutation. The method is used to diagnose age-related diseases, especially
 CC cancer and a wide range of neurodegenerative disorders (e.g. Alzheimer's
 CC disease, Down's syndrome, myotonic dystrophy, Huntington's disease,
 CC multiple sclerosis, alcoholic liver disease, diabetes mellitus type II
 CC and many others listed) or susceptibility to these disorders. The method
 CC allows a definitive diagnosis of Alzheimer's disease in living patients,
 CC at an early stage. It is based on the observation that disease may be
 CC caused by mutations in RNA rather than DNA. The invention describes the
 CC use of neuronal system RNA molecules, specifically proteins including
 CC beta-amyloid precursor protein (beta-APP), the microtubule associated
 CC proteins tau and big tau, ubiquitin B, apolipoprotein E, microtubule
 CC associated protein 2 (MAP2), neurofilament-L, neurofilament-M,
 CC neurofilament-F, presenilin I, presenilin II, glial fibrillary acidic
 CC protein (GFAP), the cellular tumour antigen p53, B-cell leukemia/lymphoma
 CC 2 (bcl-2) proto-oncogene, semaphorin III, HUPF-1, high mobility group
 CC protein-C (HMGP-C) and neuroendocrine specific protein A

XX SQ Sequence 8 AA;

Alignment Scores:

Pred. No.: 9.59e+07
 Score: 3.00
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 100.00%
 DB: 2

US-10-070-588A-112 (1-11) x AAY20315 (1-8)

Oy 3 TTGGCACTA 11

Db 6 LeuAlaLeu 8

RESULT 27

AAW59492

ID AAW59492 standard; peptide; 8 AA.

XX AC AAW59492;

XX DT 28-AUG-1998 (first entry)

XX DE Human proinsulin C-peptide fragment #5.

XX KW Insulin; C peptide; proinsulin; Na+K-ATPase activity; biomimetic;
 KW renal tubule cell; fibroblast; type I diabetes; treatment; nephropathy;
 KW neuropathy; retinopathy.

XX OS Homo sapiens.

XX PN WO9813384-A1.

XX PD 02-APR-1998.

XX PF 26-SEP-1997; 97WO-GB002627.

XX PR 27-SEP-1996; 96SE-00003533.

XX (CREA-) CREATIVE PEPTIDES SWEDEN AB.

XX PA (DZIE/) DZIEGLEWSKA H E.

XX PI Wahren J, Johansson B, Joernvall H;

XX WPI; 1998-271706/24.

XX PT Human insulin C peptide(s) - stimulate sodium potassium ATPase activity,
 PT useful for combating diabetes and related complications.

XX PS Disclosure; Page 38; 49pp; English.

XX AAW59482-W59494 are fragments of the human insulin C peptide which are
 CC used to stimulate Na+K-ATPase activity. These fragments can be used to
 CC produce a biomimetic organic compound that stimulates Na+K-ATPase

CC activity and which binds to renal tubule cells and fibroblasts and/or
CC cellular binding characteristics. The peptides and biomimetic compounds
CC are used to combat diabetes or diabetic complications, or to stimulate
CC Na-K-ATPase activity in a human or non-human subject. They may be
CC administered alone or in conjunction with another active agent, e.g.
CC insulin. When administered with insulin the compositions can be used to
CC treat type 1 diabetes, optionally with nephropathy, neuropathy or
CC retinopathy or they can be used for retarding the development of late
CC diabetic complications
XX Sequence 8 AA;

Alignment Scores: 9.59e+07 Length: 8
Pred. No.: 3.00 Matches: 3
Score: 100.00% Conservatives: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 2 Gaps: 0
DB:

US-10-070-588A-112 (1-11) x AAW59492 (1-8)

Qy 3 TTGGCACTA 11
 |||||
Db 1 LeuAlaLeu 3

RESULT 28

AAW78686

ID AAW78686 standard; peptide; 8 AA.

XX AC AAW78686;

XX DT 04-NOV-1998 (first entry)

XX DE SH2 domain binding inhibiting peptide SEQ ID NO:181.

XX KW SH2 domain; binding; inhibition; interaction; site specific;

XX KW signal transduction; protein tyrosine kinase; phosphotyrosine;

XX KW growth factor receptor; oncogene; cellular growth; cell proliferation;

XX KW metabolic control; diabetes; PTK; proto-oncogene; insulin receptor.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT Misc-difference 1 /note= "unspecified"

FT Misc-difference 8 /note= "unspecified"

XX PN US5801149-A.

XX PD 01-SEP-1998.

XX PF 21-MAR-1995; 95US-00408604.

XX PR 19-JUN-1991; 91US-00722359.

XX PR 09-OCT-1992; 92US-00959949.

XX PR 08-OCT-1993; 93US-00134558.

XX PA (JOSL-) JOSLIN DIABETES CENT INC.

XX PI Shoelson S;

XX DR WPI; 1998-494822/42.

XX FT Inhibiting site-specific SH2 domain interaction - with peptide containing

XX FT phosphotyrosine or phosphotyrosine mimic.

XX PS Disclosure; Col 109; 70pp; English.

XX CC A method has been developed of inhibiting a site-specific interaction

XX CC between a first molecule having an SH2 domain and a second molecule that

XX CC interacts with the SH2 domain. The method comprises contacting the first

CC molecule with a 4- to 30-mer peptide containing a sequence of formula: R1
CC -Met-R3-Met (I), where R1 = phosphotyrosine (pTyr) or a phosphotyrosine
CC analogue having a hydrolysis-resistant phosphorous moiety, and R3 = any
CC amino acid. AAW78501 to AAW78523 represent specifically claimed examples
CC of the peptides described. The peptides are useful for modulating both
CC cellular growth to control unwanted cell proliferation in e.g. selected
CC malignancies and for metabolic control in e.g. diabetes, by inhibiting
CC signal transduction molecules such as protein tyrosine kinases (PTKs)
CC which include growth factor receptors, proto-oncogene and oncogene
CC products and the insulin receptor. The peptides are also useful for
CC treating and for studying the enzymatic mechanisms of PTPase activity and
CC the metabolic and biochemical roles of PTPases. AAW78524 to AAW78702
CC represent other peptides given in the present invention, but which are
CC not specifically claimed
XX Sequence 8 AA;

Alignment Scores: 9.59e+07 Length: 8
Pred. No.: 3.00 Matches: 3
Score: 100.00% Conservatives: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 2 Gaps: 0
DB:

US-10-070-588A-112 (1-11) x AAW78686 (1-8)

Qy 10 AGTGCCAAA 2

Db 5 SerAlaLys 7

RESULT 29

AAW78521

ID AAW78521 standard; peptide; 8 AA.

XX AC AAW78521;

XX DT 04-NOV-1998 (first entry)

XX DE SH2 domain binding inhibiting peptide SEQ ID NO:207.

XX KW SH2 domain; binding; inhibition; interaction; site specific;

XX KW signal transduction; protein tyrosine kinase; phosphotyrosine;

XX KW growth factor receptor; oncogene; cellular growth; cell proliferation;

XX KW metabolic control; diabetes; PTK; proto-oncogene; insulin receptor.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT Modified-site 1 /note= "acetylated phosphotyrosine"

XX PN US5801149-A.

XX PD 01-SEP-1998.

XX PF 21-MAR-1995; 95US-00408604.

XX PR 19-JUN-1991; 91US-00722359.

XX PR 09-OCT-1992; 92US-00959949.

XX PR 08-OCT-1993; 93US-00134558.

XX PA (JOSL-) JOSLIN DIABETES CENT INC.

XX PI Shoelson S;

XX DR WPI; 1998-494822/42.

XX FT Inhibiting site-specific SH2 domain interaction - with peptide containing

XX FT phosphotyrosine or phosphotyrosine mimic.

XX PS Claim 16; Col 125-126; 70pp; English.

CC A method has been developed of inhibiting a site-specific interaction.
CC between a first molecule having an SH2 domain and a second molecule that
CC interacts with the SH2 domain. The method comprises contacting the first
CC molecule with a 4- to 30-mer peptide containing a sequence of formula: R1
CC -Met-R3-Met (1), where R1 = phosphotyrosine (pTyr) or a phosphotyrosine
CC analogue having a hydrolysis-resistant phosphorous moiety, and R3 = any
CC amino acid. AAW78501 to AAW78523 represent specifically claimed examples
CC of the peptides described. The peptides are useful for modulating both
CC cellular growth to control unwanted cell proliferation in e.g. selected
CC malignancies and for metabolic control in e.g. diabetes, by inhibiting
CC signal transduction molecules such as protein tyrosine kinases (PTKs)
CC which include growth factor receptors, proto-oncogene and oncogene
CC products and the insulin receptor. The peptides are also useful for
CC treating and for studying the enzymatic mechanisms of PTPase activity and
CC the metabolic and biochemical roles of PTPases. AAW78524 to AAW78702
CC represent other peptides given in the present invention, but which are
CC not specifically claimed

XX Sequence 8 AA;

Alignment Scores:
Pred. No.: 9.59e+07 Length: 8
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x AAW78521 (1-8)

Qy 10 AGTGCCAAA 2

Db 5 SerAlalays 7

RESULT 30

AAW67227

ID AAW67227 standard; peptide; 8 AA.

AC AAW67227;

XX 18-DEC-1998 (first entry)

XX aPL immunoreactive peptide derivative #77.

DE antiphospholipid; aPL; analogue; stroke; foetal loss; B cell; epitope;
KW thrombosis; antibody ACA-6641; conjugate; phage library screen;
KW biopanning; micropanning.

XX Synthetic.

XX Key Location/Qualifiers

XX Modified-site 1 /note= "homocysteine"

XX WO9746251-A1.

XX 11-DEC-1997.

XX 06-JUN-1997; 97WO-US010075.

XX 06-JUN-1996; 96US-00660092.

XX 05-DEC-1996; 96US-00760508.

XX (LJOL-) LA JOLLA PHARM CO.

XX Victoria EJ, Marquis DM, Jones DS, Yu L;

XX WPI; 1998-051902/05.

XX New anti-phospholipid analogues and conjugates containing them - are
XX useful in treatment of disorders mediated by antiphospholipid antibody,
XX such as stroke or foetal loss.

XX

PS Disclosure; Page 38; 155pp; English.

XX The invention relates to antiphospholipid (aPL) analogues that bind
CC specifically to B cells to which an aPL epitope binds. Optimised
CC analogues lack T cell epitope(s) and are useful as conjugates for
CC treating aPL antibody-mediated diseases. Conjugates comprising aPL
CC analogues and non-immunogenic valency platform molecules are provided as
CC are novel non-immunogenic valency platform molecules and linkers. Methods
CC of preparing and identifying the analogues, methods of treatment and
CC methods and compositions for preparing conjugates of the analogues and
CC diagnostic immunoassays for aPL antibodies are disclosed. The conjugates
CC are useful for treatment of aPL antibody-mediated diseases, such as
CC stroke, foetal loss, antiphospholipid antibody syndrome or thrombosis.
CC Peptide 6641/3G3 (AAW67144) was isolated from a phage library screen
CC using aPL antibody ACA-6641. This peptide was subjected to a number of
CC analyses, including truncation at both the N-terminus and C-terminus,
CC disulphide substitution, substitution of alanine and glycine for amino
CC acids in positions 2 through 8 etc. The present sequence represents one
CC of these substitutions or truncations. The structure/activity
CC relationship of these substitutions or truncations was determined

XX Sequence 8 AA;

Alignment Scores:
Pred. No.: 9.59e+07 Length: 8
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x AAW67227 (1-8)

Qy 3 TTGGCACTA 11

Db 5 LeuAlaleu 7

RESULT 31

AAW67141

ID AAW67141 standard; peptide; 8 AA.

XX AAW67141;

XX 18-DEC-1998 (first entry)

DE Antibody ACA-6644 epitope isolated from a phage library screen.

XX antiphospholipid; aPL; analogue; stroke; foetal loss; B cell; epitope;
KW thrombosis; antibody ACA-6501; conjugate; phage library screen;
KW biopanning; micropanning.

XX Synthetic.

XX WO9746251-A1.

XX 11-DEC-1997.

XX 06-JUN-1997; 97WO-US010075.

XX 06-JUN-1996; 96US-00660092.

XX 05-DEC-1996; 96US-00760508.

XX (LJOL-) LA JOLLA PHARM CO.

XX Victoria EJ, Marquis DM, Jones DS, Yu L;

XX WPI; 1998-051902/05.

XX New anti-phospholipid analogues and conjugates containing them - are
XX useful in treatment of disorders mediated by antiphospholipid antibody,
XX such as stroke or foetal loss.

XX Disclosure; Page 27; 155pp; English.

XX The invention relates to antiphospholipid (aPL) analogues that bind
 CC specifically to B cells to which an aPL epitope binds. Optimised
 CC analogues lack T cell epitope(s) and are useful as conjugates for
 CC treating aPL antibody-mediated diseases. Conjugates comprising aPL
 CC analogues and non-immunogenic valency platform molecules are provided as
 CC are novel non-immunogenic valency platform molecules and linkers. Methods
 CC of preparing and identifying the analogues, methods of treatment and
 CC methods and compositions for preparing conjugates of the analogues and
 CC diagnostic immunoassays for aPL antibodies are disclosed. The conjugates
 CC are useful for treatment of aPL antibody-mediated diseases, such as
 CC stroke, foetal loss, antiphospholipid antibody syndrome or thrombosis.
 CC The present sequence represents an epitope that was isolated from a phage
 CC library screen using aPL antibody ACA-6644

XX Sequence 8 AA;

Alignment Scores:
 Pred. No.: 9.59e+07 Length: 8
 Score: 3.00 Matches: 3
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x AAW67141 (1-8)

Qy 3 TTGGCACTA 11
 |||||
 Db 3 LeuAlaLeu 5

RESULT 32

AAW29699
 ID AAW29699 standard; peptide; 8 AA.

AC AAW29699;

XX 26-OCT-1998 (first entry)

XX TNF receptor releasing enzyme (TRRE), internal sequence 15.

XX Tumour necrosis factor; TNF; inflammation; autoimmune disease; diabetes;
 KW rheumatoid arthritis; multiple sclerosis; cancer; glioblastoma; melanoma;
 KW neuroblastoma; carcinoma; adenocarcinoma; soft tissue sarcoma; leukaemia;
 KW lymphoma; antibody; enzyme.

XX Synthetic.

XX Homo sapiens.

XX WO9820140-A1.

XX 14-MAY-1998.

XX 05-NOV-1997; 97WO-US019930.

XX 06-NOV-1996; 96US-0030761P.

XX (REGC) UNIV CALIFORNIA.

XX Granger GA, Gatanaga T;

XX WPI; 1998-286955/25.

XX New enzymes that release soluble tumour necrosis factor receptor and
 PT related antibodies - for treatment of inflammation etc., also use of
 PT their inhibitors for treatment of cancer, and diagnosis based on
 PT detecting elevated levels of the enzyme.

XX Claim 8; Page 80; 109pp; English.

XX Sequences AAW29684-W296714 are internal sequences of the TNF receptor
 CC releasing enzyme, which can be used to treat diseases associated with
 CC altered levels of TNF activity, particularly inflammatory diseases and

CC autoimmune diseases e.g. diabetes, rheumatoid arthritis, multiple
 CC sclerosis. Measurement of the TNF receptor releasing enzyme levels can
 CC also be used to diagnose diseases, particularly cancer, e.g.
 CC glioblastoma, melanoma, neuroblastoma, carcinoma, adenocarcinoma, soft
 CC tissue sarcoma, leukaemia and lymphoma. These diseases can be treated
 CC with antibodies that target this enzyme, which will increase the level of
 CC TNF at the site of disease, and may also be administered to subjects at
 CC risk of tumour recurrence

XX Sequence 8 AA;

Alignment Scores:
 Pred. No.: 9.59e+07 Length: 8
 Score: 3.00 Matches: 3
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x AAW29699 (1-8)

Qy 3 TTGGCACTA 11
 |||||
 Db 1 LeuAlaLeu 3

RESULT 33

AAW29698
 ID AAW29698 standard; peptide; 8 AA.

XX AAW29698;

XX 26-OCT-1998 (first entry)

XX TNF receptor releasing enzyme (TRRE), internal sequence 14.

XX Tumour necrosis factor; TNF; inflammation; autoimmune disease; diabetes;
 KW rheumatoid arthritis; multiple sclerosis; cancer; glioblastoma; melanoma;
 KW neuroblastoma; carcinoma; adenocarcinoma; soft tissue sarcoma; leukaemia;
 KW lymphoma; antibody; enzyme.

XX Synthetic.

XX Homo sapiens.

XX WO9820140-A1.

XX 14-MAY-1998.

XX 05-NOV-1997; 97WO-US019930.

XX 06-NOV-1996; 96US-0030761P.

XX (REGC) UNIV CALIFORNIA.

XX Granger GA, Gatanaga T;

XX WPI; 1998-286955/25.

XX New enzymes that release soluble tumour necrosis factor receptor and
 PT related antibodies - for treatment of inflammation etc., also use of
 PT their inhibitors for treatment of cancer, and diagnosis based on
 PT detecting elevated levels of the enzyme.

XX Claim 8; Page 80; 109pp; English.

XX Sequences AAW29684-W296714 are internal sequences of the TNF receptor
 CC releasing enzyme, which can be used to treat diseases associated with
 CC altered levels of TNF activity, particularly inflammatory diseases and
 CC autoimmune diseases e.g. diabetes, rheumatoid arthritis, multiple
 CC sclerosis. Measurement of the TNF receptor releasing enzyme levels can
 CC also be used to diagnose diseases, particularly cancer, e.g.
 CC glioblastoma, melanoma, neuroblastoma, carcinoma, adenocarcinoma, soft
 CC tissue sarcoma, leukaemia and lymphoma. These diseases can be treated
 CC with antibodies that target this enzyme, which will increase the level of

CC TNF at the site of disease, and may also be administered to subjects at
 CC risk of tumour recurrence

SQ Sequence 8 AA;

Alignment Scores:
 Pred. No.: 9.59e+07 Length: 8
 Score: 3.00 Matches: 3
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x AAW29698 (1-8)

OY 3 TTGGCACTA 11
 DB 1 LeuAlaLeu 3

RESULT 34

AAW29700
 ID AAW29700 standard; peptide; 8 AA.

XX AAW29700;

DT 26-OCT-1998 (first entry)

DE TNF receptor releasing enzyme (TRRE), internal sequence 16.

XX Tumour necrosis factor; TNF; inflammation; autoimmune disease; diabetes;
 KW rheumatoid arthritis; multiple sclerosis; cancer; glioblastoma; melanoma;
 KW neuroblastoma; carcinoma; adenocarcinoma; soft tissue sarcoma; leukaemia;
 KW lymphoma; antibody; enzyme.

OS Synthetic.

OS Homo sapiens.

XX WO9820140-A1.

PD 14-MAY-1998.

PF 05-NOV-1997; 97WO-US019930.

PR 06-NOV-1996; 96US-0030761P.

PA (REGC) UNIV CALIFORNIA.

XX Granger GA, Gatanaga T;

DR WPI; 1998-286955/25.

XX New enzymes that release soluble tumour necrosis factor receptor and
 PT related antibodies - for treatment of inflammation etc., also use of
 PT their inhibitors for treatment of cancer, and diagnosis based on
 PT detecting elevated levels of the enzyme.

PS Claim 8; Page 80; 109pp; English.

XX Sequences AAW29684-W296714 are internal sequences of the TNF receptor
 CC releasing enzyme, which can be used to treat diseases associated with
 CC altered levels of TNF activity, particularly inflammatory diseases and
 CC autoimmune diseases e.g. diabetes, rheumatoid arthritis, multiple
 CC sclerosis. Measurement of the TNF receptor releasing enzyme levels can
 CC also be used to diagnose diseases, particularly cancer, e.g.
 CC glioblastoma, melanoma, neuroblastoma, carcinoma, adenocarcinoma, soft
 CC tissue sarcoma, leukaemia and lymphoma. These diseases can be treated
 CC with antibodies that target this enzyme, which will increase the level of
 CC TNF at the site of disease, and may also be administered to subjects at
 CC risk of tumour recurrence

SQ Sequence 8 AA;

Alignment Scores:

Pred. No.: 9.59e+07 Length: 8
 Score: 3.00 Matches: 3
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x AAW29700 (1-8)

OY 3 TTGGCACTA 11
 DB 1 LeuAlaLeu 3

RESULT 35

AAW29697
 ID AAW29697 standard; peptide; 8 AA.

XX AAW29697;

DT 26-OCT-1998 (first entry)

DE TNF receptor releasing enzyme (TRRE), internal sequence 13.

XX Tumour necrosis factor; TNF; inflammation; autoimmune disease; diabetes;
 KW rheumatoid arthritis; multiple sclerosis; cancer; glioblastoma; melanoma;
 KW neuroblastoma; carcinoma; adenocarcinoma; soft tissue sarcoma; leukaemia;
 KW lymphoma; antibody; enzyme.

OS Synthetic.

OS Homo sapiens.

XX WO9820140-A1.

PD 14-MAY-1998.

PF 05-NOV-1997; 97WO-US019930.

PR 06-NOV-1996; 96US-0030761P.

PA (REGC) UNIV CALIFORNIA.

XX Granger GA, Gatanaga T;

DR WPI; 1998-286955/25.

XX New enzymes that release soluble tumour necrosis factor receptor and
 PT related antibodies - for treatment of inflammation etc., also use of
 PT their inhibitors for treatment of cancer, and diagnosis based on
 PT detecting elevated levels of the enzyme.

PS Claim 8; Page 80; 109pp; English.

XX Sequences AAW29684-W296714 are internal sequences of the TNF receptor
 CC releasing enzyme, which can be used to treat diseases associated with
 CC altered levels of TNF activity, particularly inflammatory diseases and
 CC autoimmune diseases e.g. diabetes, rheumatoid arthritis, multiple
 CC sclerosis. Measurement of the TNF receptor releasing enzyme levels can
 CC also be used to diagnose diseases, particularly cancer, e.g.
 CC glioblastoma, melanoma, neuroblastoma, carcinoma, adenocarcinoma, soft
 CC tissue sarcoma, leukaemia and lymphoma. These diseases can be treated
 CC with antibodies that target this enzyme, which will increase the level of
 CC TNF at the site of disease, and may also be administered to subjects at
 CC risk of tumour recurrence

SQ Sequence 8 AA;

Alignment Scores:

Pred. No.: 9.59e+07 Length: 8
 Score: 3.00 Matches: 3
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x AAW29697 (1-8)

QY 3 TTGGCACTA 11
| | | | |
Db 1 LeuAlaLeu 3

RESULT 36

AAW47925
ID AAW47925 standard; peptide; 8 AA.

XX AC AAW47925;

XX DT 12-JUN-1998 (first entry)

XX DE Human MHC class II allele antigenic peptide SEQ ID NO:163.

XX KW Mammalian II key peptide; mammalian invariant chain protein; allergy;
KW immune response; MHC class II; antigenic; autoimmune disease.

XX OS Synthetic.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "Acetylated"

FT Modified-site 8

FT /note= "Amidated"

XX PN WO9749430-Al.

XX PD 31-DEC-1997.

XX PF 09-JUN-1997; 97WO-US009993.

XX PR 26-JUN-1996; 96US-00670605.

XX PA (ANTI-) ANTIGEN EXPRESS INC.

XX PI Humphreys RE, Adams S, Xu M;

XX DR WPI; 1998-076917/07.

XX New mammalian invariant chain protein (Ii) key peptide(s) - used for
modulation of immune response, e.g. for treating malignant, allergic or
autoimmune disease or allograft rejection.

PS Claim 26; Page 142; 149pp; English.

XX The present sequence represents an MHC class II allele antigenic peptide.
The present invention describes a mammalian invariant chain protein (Ii)
key peptide of sequence LRMKLPPKPVSKMR and modifications with the
exclusion of peptide YRMKLPPKPVSKMR. MHC class II molecules are
synthesised in the endoplasmic reticulum with their antigenic peptide
sites blocked by the invariant chain protein (Ii). The products and
method can be used for the modulation of an immune response for
therapeutic or diagnostic purposes. The enhancement of immunity can be
used in the treatment of e.g. malignant or allergic disease. The
immunosuppression can be used for the treatment of autoimmune disease,
e.g. rheumatoid arthritis, multiple sclerosis, diabetes mellitus, lupus
erythematosus, and psoriasis or allograft rejection

XX Sequence 8 AA;

Alignment Scores:

Pred. No.: 9.59e+07 Length: 8
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x AAW47925 (1-8)

QY 10 AGTGCCAAA 2
| | | | |
Db 4 SerAlaLys 6

RESULT 37

AAW67654

ID AAW67654 standard; peptide; 8 AA.

XX AC AAW67654;

XX DT 16-MAR-1999 (first entry)

XX DE LXXLL signature motif #4 from protein RIP140.

XX KW Nuclear protein; signature motif; receptor protein; inflammation; cancer;
interaction; inhibitor; inhibition; transcription factor; ligand.

XX OS Homo sapiens.

XX PN WO9849561-Al.

XX PD 05-NOV-1998.

XX PF 28-APR-1998; 98WO-GB001238.

XX PR 30-APR-1997; 97GB-00008676.

XX PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY.

XX PI Heery DM, Parker MG;

XX DR WPI; 1999-034672/03.

XX Identification of inhibitors of nuclear protein/nuclear receptor
interaction - useful for, e.g. treatment of disease mediated through the
interaction such as inflammation and cancer.

XX Example 1; Fig 1A; 60pp; English.

XX This sequence represents an LXXLL nuclear protein signature motif found
in the 140 kD receptor interacting protein (RIP140) from nuclei. This
peptide corresponds to amino acids 266-273 of RIP140. The invention
relates to the identification of inhibitor compounds capable of reducing
the interaction between a region on a nuclear protein (R1) and a region
on a nuclear receptor (R2), where: (i) R1 is a signature motif; (ii) R2
is the region capable of interacting with the nuclear protein by binding
the signature motif; (iii) the nuclear protein is a bridging factor
responsible for interaction between a liganded nuclear receptor and a
transcription initiation complex involved in gene expression regulation;
(iv) the nuclear receptor is a transcription factor; (v) the signature
motif is a short amino acid sequence which is the key structural element
of a nuclear protein which binds to a liganded nuclear receptor during
activation or repression of target genes. The inhibitors are expected to
be useful in the treatment of any disease mediated through any
interaction between a signature motif on a nuclear protein and a nuclear
receptor, for example inflammation and cancer

XX Sequence 8 AA;

Alignment Scores:

Pred. No.: 9.59e+07 Length: 8
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x AAW67654 (1-8)

QY 3 TTGGCACTA 11
| | | | |

Db 2 LeuAlaLeu 4

RESULT 38
 AAY16865
 ID AAY16865 standard; peptide; 8 AA.
 XX AC AAY16865;
 XX DT 20-JUL-1999 (first entry)
 XX DE Heat shock protein (hsp) binding peptide.
 XX KW Conjugate peptide; heat shock protein; hsp; phage display library; virus;
 KW surface protein; tethering peptide; chaperone process; cytokine; cancer;
 KW neoplastic disease; infectious disease; bacterium; immune system; fungus;
 KW acquired immune deficiency; autoimmune disease.
 XX OS Synthetic.
 XX PN WO9922761-A1.
 XX PD 14-MAY-1999.
 XX PF 22-OCT-1998; 98WO-US022335.
 XX PR 31-OCT-1997; 97US-00961707.
 XX PA (SLOAN) SLOAN KETTERING INST CANCER RES.
 XX PI Rothman JE, Mayhew M, Hoe MH, Houghton A, Hartl U, Querfelli O;
 PI Moroi Y;
 XX WPI; 1999-313177/26.
 XX DR N-PSDB; AAX60765.
 XX PT Identifying peptides which bind heat shock proteins.
 XX PS Disclosure; Fig 2H; 155pp; English.
 XX CC The invention relates to conjugate peptides engineered to noncovalently
 CC bind to heat shock proteins (hsp). A method of identifying a hsp binding
 CC peptide comprises (a) contacting a phage display library having
 CC bacteriophage expressing, in a surface protein, inserted peptides with a
 CC hsp target, and bound to a benzoquinone ansamycin antibiotic (BAA), in a
 CC physiologic binding buffer; (b) isolating a phage binding to the hsp
 CC target; and (c) identifying the inserted peptide expressed. The peptides
 CC which bind to a hsp can be used as tethering peptides for a hsp which may
 CC serve as an accessory in a chaperone process and/or may comprise a
 CC cytokine. They can also be coupled to antigens to induce an immune
 CC response. Such compositions can be used for treating neoplastic disease,
 CC e.g. cancers, infectious diseases, e.g. diseases caused by a bacterium,
 CC virus, protozoan, mycoplasma, fungus, yeast, parasite or prion, or a
 CC disease of the immune system, e.g. acquired immune deficiencies or
 CC autoimmune diseases
 XX SQ Sequence 8 AA;
 Alignment Scores:
 Pred. No.: 9.59e+07 Length: 8
 Score: 3.00 Matches: 3
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 2 Gaps: 0
 US-10-070-588A-112 (1-11) x AAY16865 (1-8)
 QY 3 TTGGCACTA 11
 |||||
 Db 3 LeuAlaLeu 5
 RESULT 39
 AAY16846
 ID AAY16846 standard; peptide; 8 AA.

XX AAY16846;
 XX AC 20-JUL-1999 (first entry)
 XX DT Heat shock protein (hsp) binding peptide.
 XX DE Conjugate peptide; heat shock protein; hsp; phage display library; virus;
 KW surface protein; tethering peptide; chaperone process; cytokine; cancer;
 KW neoplastic disease; infectious disease; bacterium; immune system; fungus;
 KW acquired immune deficiency; autoimmune disease.
 XX OS Synthetic.
 XX PN WO9922761-A1.
 XX PD 14-MAY-1999.
 XX PF 22-OCT-1998; 98WO-US022335.
 XX PR 31-OCT-1997; 97US-00961707.
 XX PA (SLOAN) SLOAN KETTERING INST CANCER RES.
 XX PI Rothman JE, Mayhew M, Hoe MH, Houghton A, Hartl U, Querfelli O;
 PI Moroi Y;
 XX WPI; 1999-313177/26.
 XX DR N-PSDB; AAX60746.
 XX PT Identifying peptides which bind heat shock proteins.
 XX PS Disclosure; Fig 2H; 155pp; English.
 XX CC The invention relates to conjugate peptides engineered to noncovalently
 CC bind to heat shock proteins (hsp). A method of identifying a hsp binding
 CC peptide comprises (a) contacting a phage display library having
 CC bacteriophage expressing, in a surface protein, inserted peptides with a
 CC hsp target, and bound to a benzoquinone ansamycin antibiotic (BAA), in a
 CC physiologic binding buffer; (b) isolating a phage binding to the hsp
 CC target; and (c) identifying the inserted peptide expressed. The peptides
 CC which bind to a hsp can be used as tethering peptides for a hsp which may
 CC serve as an accessory in a chaperone process and/or may comprise a
 CC cytokine. They can also be coupled to antigens to induce an immune
 CC response. Such compositions can be used for treating neoplastic disease,
 CC e.g. cancers, infectious diseases, e.g. diseases caused by a bacterium,
 CC virus, protozoan, mycoplasma, fungus, yeast, parasite or prion, or a
 CC disease of the immune system, e.g. acquired immune deficiencies or
 CC autoimmune diseases
 XX SQ Sequence 8 AA;
 Alignment Scores:
 Pred. No.: 9.59e+07 Length: 8
 Score: 3.00 Matches: 3
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 2 Gaps: 0
 US-10-070-588A-112 (1-11) x AAY16846 (1-8)
 QY 3 TTGGCACTA 11
 |||||
 Db 3 LeuAlaLeu 5
 RESULT 40
 AAW93856
 ID AAW93856 standard; protein; 8 AA.
 XX AC AAW93856;
 XX DT 25-JUN-1999 (first entry)

XX Mouse BR96 receptor light chain CDR L1 variant M131B3-12 protein.
 XX CDR L1; complementarity determining region; receptor; antibody receptor;
 KW BR96; light chain; optimal binding ligand; drug; diagnostic agent.
 XX Synthetic.
 OS Mus sp.
 XX WO9919506-A2.
 XX 22-APR-1999.
 XX 08-OCT-1998; 98WO-US021390.
 XX 09-OCT-1997; 97US-00948187.
 PR 09-OCT-1997; 97US-0112011P.
 XX (IXSY-) IXSYS INC.
 XX Huse WD, Freedman MH;
 PI WPI; 1999-277653/23.
 DR N-PSDB; AAX23892.
 XX Detecting binding between ligand and receptor using collective variants.
 XX Example V; Page 53; 70pp; English.
 PS This invention describes a method which identifies optimal binding
 CC ligands to a receptor. The method involves the binding of receptor (R) to
 CC one or more ligands (L), or of an L to one or more R (or its variants),
 CC and is detected by treating a collective R variant (or L variant)
 CC population with one or more L (or R). The method is used to identify L or
 CC R with optimal binding affinity for a specific target, i.e. potential
 CC drugs and diagnostic agents, or lead compounds for development of
 CC variants with increased binding activity. The method identifies the
 CC optimum binding agent rapidly and efficiently. Using a variant population
 CC for the initial screen increases the chance of detecting a binding event
 CC and quickly provides an enriched population with favourable binding
 CC properties at the target (even those of low affinity for a parent
 CC receptor). Very many different L may be screened with a single variant R
 CC population. The method does not require segregation of the receptor
 CC population, but uses a non-segmented pool, significantly reducing the
 CC contact area/volume needed and thus increasing screening capacity
 XX Sequence 8 AA;

Alignment Scores:
 Pred. No.: 9.59e+07 Length: 8
 Score: 3.00 Matches: 3
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x AAW93856 (1-8)

QY 10 AGTGCCAAA 2
 DB 3 SerAlaLys 5

RESULT 41
 AAB28324
 ID AAB28324 standard; peptide; 8 AA.
 XX AC AAB28324;
 XX 14-FEB-2001 (first entry)
 DT Human secreted peptide #29 encoded by cDNA#48.
 DE Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
 KW

KW antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer;
 KW vulnery; anticonvulsant; antibacterial; antifungal; antiparasitic;
 KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
 XX neurological disease; infection; human; secreted protein.
 OS Homo sapiens.
 XX WO200058355-A1.
 XX 05-OCT-2000.
 XX 22-MAR-2000; 2000WO-US007527.
 XX 26-MAR-1999; 99US-0126501P.
 PR 22-DEC-1999; 99US-0171551P.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX Rosen CA, Ruben SM, Komatsoulis G;
 PI WPI; 2000-602358/57.
 DR N-PSDB; AAC67678.
 XX Nucleic acid molecules encoding human secreted proteins, used in
 PT preventing, treating or ameliorating a disorder, e.g. Alzheimer's and
 PT Parkinson's diseases and cancers.
 XX Claim 11; Page 356; 367pp; English.
 PS Sequences AAB28278-B28326 represent the amino acid sequences of 50 human
 CC secreted proteins encoded by the genes AAC67631-C67680. The genes and
 CC proteins are useful for preventing, ameliorating or treating medical
 CC conditions, e.g. by protein or gene therapy. The genes are isolated from
 CC a range of human tissues disclosed in the specification. The nucleic
 CC acids, proteins, antibodies and (ant)agonists are useful in the
 CC diagnosis, treatment and prevention of: (a) cancer, e.g. breast and
 CC ovarian cancer, and other cancers of the adrenal gland, bone, bone
 CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b)
 CC immune disorders e.g. Addison's disease, diabetes mellitus, Crohn's disease,
 CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease;
 CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)
 CC cardiovascular disorders such as myocardial ischaemias; (d) wound healing
 CC ; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)
 CC infectious diseases such as viral, bacterial, fungal and parasitic
 CC infections
 XX Sequence 8 AA;

Alignment Scores:
 Pred. No.: 9.59e+07 Length: 8
 Score: 3.00 Matches: 3
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 3 Gaps: 0

US-10-070-588A-112 (1-11) x AAB28324 (1-8)

QY 3 TTGGCACTA 11
 DB 6 LeuAlaLeu 8

RESULT 42
 AAY69116
 ID AAY69116 standard; peptide; 8 AA.
 XX AC AAY69116;
 XX 30-MAY-2000 (first entry)
 DT Subsequence which is capable of being digested by a metalloproteinase.
 DE Tropoelastin; derivative; proteolysis; protease; antiwrinkle;
 KW

KW hand lotion; bulking agent; chemotaxis; proliferation; metalloproteinase;
 KW growth inhibition; peptidomimetic; lung damage; elastin; cancer;
 KW metastasis; blood clotting.

OS Homo sapiens.

PN WO200004043-A1.

PD 27-JAN-2000.

PP 19-JUL-1999; 99WO-AU000580.

PR 17-JUL-1998; 98AU-00004723.

PA (UNSY) UNIV SYDNEY.

PI Weiss AS;

PP WPI; 2000-182399/16.

PT New derivatives of tropoelastin useful, e.g. for inducing chemotaxis and cell growth.

PS Claim 68; Page 127; 136pp; English.

XX The present sequence represents a subsequence which is capable of being digested by a metalloproteinase. This sequence can be inserted into human tropoelastin to produce the tropoelastin derivatives of the invention, which have enhanced susceptibility to protease cleavage. The specification describes human tropoelastin derivatives, in which a subsequence has been mutated so that susceptibility to proteolysis is reduced or eliminated, or a subsequence has been inserted so that susceptibility to proteolysis is increased. The derivatives have with reduced susceptibility, and can be used where the wild-type protein would be degraded too easily, e.g. in contact with serum or wound exudate. The tropoelastin derivatives provide competitive inhibition of protease activity. The tropoelastin derivatives, and other polypeptides containing tropoelastin derivative-derived protease-susceptibility sites, are useful in human or veterinary medicine, cosmetics (e.g. antiwrinkle or hand lotions), as bulking agents and for inducing chemotaxis. They are also useful for proliferation or growth inhibition, particularly of smooth muscle cells, epithelial or endothelial cells, fibroblasts, osteocytes, chondrocytes and platelets. Peptidomimetics that mimic the protease cleavage site in tropoelastin derivatives are competitive inhibitors of the protease, and are used for protecting against lung damage caused by elastin, for inhibiting or controlling localized growth of cancers or metastases, or to limit protease activity that causes blood clotting

SQ Sequence 8 AA;

Alignment Scores:
 Pred. NO.: 9.59e+07 Length: 8
 Score: 3.00 Matches: 3
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 3 Gaps: 0

US-10-070-588A-112 (1-11) x AAY69116 (1-8)

Qy 3 TTGGCACTA 11

Db 3 LeuAlaLeu 5

RESULT 43

AAY69128

ID AAY69128 standard; peptide; 8 AA.

XX AC AAY69128;

XX 30-MAY-2000 (first entry)

DE Subsequence which is capable of being digested by a metalloproteinase.

XX Tropoelastin; derivative; proteolysis; protease; antiwrinkle;
 KW hand lotion; bulking agent; chemotaxis; proliferation; metalloproteinase;
 KW growth inhibition; peptidomimetic; lung damage; elastin; cancer;
 KW metastasis; blood clotting.

OS Homo sapiens.

PN WO200004043-A1.

PD 27-JAN-2000.

PP 19-JUL-1999; 99WO-AU000580.

PR 17-JUL-1998; 98AU-00004723.

PA (UNSY) UNIV SYDNEY.

PI Weiss AS;

PP WPI; 2000-182399/16.

PT New derivatives of tropoelastin useful, e.g. for inducing chemotaxis and cell growth.

PS Claim 68; Page 129; 136pp; English.

XX The present sequence represents a subsequence which is capable of being digested by a metalloproteinase. This sequence can be inserted into human tropoelastin to produce the tropoelastin derivatives of the invention, which have enhanced susceptibility to protease cleavage. The specification describes human tropoelastin derivatives, in which a subsequence has been mutated so that susceptibility to proteolysis is reduced or eliminated, or a subsequence has been inserted so that susceptibility to proteolysis is increased. The derivatives have with reduced susceptibility, and can be used where the wild-type protein would be degraded too easily, e.g. in contact with serum or wound exudate. The tropoelastin derivatives provide competitive inhibition of protease activity. The tropoelastin derivatives, and other polypeptides containing tropoelastin derivative-derived protease-susceptibility sites, are useful in human or veterinary medicine, cosmetics (e.g. antiwrinkle or hand lotions), as bulking agents and for inducing chemotaxis. They are also useful for proliferation or growth inhibition, particularly of smooth muscle cells, epithelial or endothelial cells, fibroblasts, osteocytes, chondrocytes and platelets. Peptidomimetics that mimic the protease cleavage site in tropoelastin derivatives are competitive inhibitors of the protease, and are used for protecting against lung damage caused by elastin, for inhibiting or controlling localized growth of cancers or metastases, or to limit protease activity that causes blood clotting

SQ Sequence 8 AA;

Alignment Scores:
 Pred. NO.: 9.59e+07 Length: 8
 Score: 3.00 Matches: 3
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 3 Gaps: 0

US-10-070-588A-112 (1-11) x AAY69128 (1-8)

Qy 3 TTGGCACTA 11

Db 5 LeuAlaLeu 7

RESULT 44

AAY84485

ID AAY84485 standard; peptide; 8 AA.

XX AC AAY84485;

XX 25-JUL-2000 (first entry)

XX DE Amino acid sequence of an epitopic fragment of the C-beta protein.
 XX KW C-beta protein; bactericidal; gram positive bacteria; vaccine;
 XX KW immune response.
 XX OS Streptococcus agalactiae.
 XX PN WO200015760-A1.
 XX PD 23-MAR-2000.
 XX PF 17-SEP-1999; 99WO-US021643.
 XX PR 17-SEP-1998; 98US-0100859P.
 XX PR 19-JUL-1999; 99US-0144324P.
 XX PR 15-SEP-1999; 99US-0154017P.
 XX PA (NAVA-) NORTH AMERICAN VACCINE INC.
 XX PI Long-Rowe KO, Blake MS;
 XX XX WPI; 2000-271404/23.
 XX DR Obtaining substantially pure C-beta protein or fragment and/or mutant for
 XX PT eliciting antibodies which are bactericidal to gram positive bacteria,
 XX PT useful in vaccines.
 XX PS Claim 19; Page 69; 17lpp; English.
 XX CC The specification describes a process for obtaining a substantially pure
 XX CC C-beta protein. The process comprises obtaining the C-beta protein in
 XX CC cell extracts, subjecting the C-beta protein to ion-exchange
 XX CC chromatography and collecting the C-beta protein-containing fractions,
 XX CC pooling and diluting the fractions, and subjecting the fractions to
 XX CC ligand affinity chromatography and collection. The C-beta protein
 XX CC fragments are useful for eliciting antibodies which are bactericidal to
 XX CC gram positive bacteria with complement alone and therefore is useful in a
 XX CC (combination) vaccine together with a pharmaceutically acceptable carrier
 XX CC (and/or optionally at least two protein fragments or peptide-
 XX CC polysaccharide conjugates). The vaccine therefore is useful in a method
 XX CC for inducing an immune response in a mammal. The present sequence
 XX CC represents an epitopic fragment derived from amino acids 827-1028 of the
 XX CC Streptococcus agalactiae C-beta protein
 XX SQ Sequence 8 AA;
 Alignment Scores:
 Pred. No.: 9.59e+07 Length: 8
 Score: 3.00 Matches: 3
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 3 Gaps: 0
 US-10-070-588A-112 (1-11) x AAY84485 (1-8)
 QY 9 GTGCCAAG 1
 DB 1 ValProllys 3
 RESULT 45
 AAY84484
 ID AAY84484 standard; peptide; 8 AA.
 XX AC AAY84484;
 XX XX 25-JUL-2000 (first entry)
 XX DE Amino acid sequence of an epitopic fragment of the C-beta protein.
 XX KW C-beta protein; bactericidal; gram positive bacteria; vaccine;
 XX KW immune response.

XX OS Streptococcus agalactiae.
 XX PN WO200015760-A1.
 XX PD 23-MAR-2000.
 XX PF 17-SEP-1999; 99WO-US021643.
 XX PR 17-SEP-1998; 98US-0100859P.
 XX PR 19-JUL-1999; 99US-0144324P.
 XX PR 15-SEP-1999; 99US-0154017P.
 XX PA (NAVA-) NORTH AMERICAN VACCINE INC.
 XX PI Long-Rowe KO, Blake MS;
 XX XX WPI; 2000-271404/23.
 XX DR Obtaining substantially pure C-beta protein or fragment and/or mutant for
 XX PT eliciting antibodies which are bactericidal to gram positive bacteria,
 XX PT useful in vaccines.
 XX PS Claim 19; Page 69; 17lpp; English.
 XX CC The specification describes a process for obtaining a substantially pure
 XX CC C-beta protein. The process comprises obtaining the C-beta protein in
 XX CC cell extracts, subjecting the C-beta protein to ion-exchange
 XX CC chromatography and collecting the C-beta protein-containing fractions,
 XX CC pooling and diluting the fractions, and subjecting the fractions to
 XX CC ligand affinity chromatography and collection. The C-beta protein
 XX CC fragments are useful for eliciting antibodies which are bactericidal to
 XX CC gram positive bacteria with complement alone and therefore is useful in a
 XX CC (combination) vaccine together with a pharmaceutically acceptable carrier
 XX CC (and/or optionally at least two protein fragments or peptide-
 XX CC polysaccharide conjugates). The vaccine therefore is useful in a method
 XX CC for inducing an immune response in a mammal. The present sequence
 XX CC represents an epitopic fragment derived from amino acids 827-1028 of the
 XX CC Streptococcus agalactiae C-beta protein
 XX SQ Sequence 8 AA;
 Alignment Scores:
 Pred. No.: 9.59e+07 Length: 8
 Score: 3.00 Matches: 3
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 3 Gaps: 0
 US-10-070-588A-112 (1-11) x AAY84484 (1-8)
 QY 9 GTGCCAAG 1
 DB 5 ValProllys 7
 RESULT 46
 AAY84483
 ID AAY84483 standard; peptide; 8 AA.
 XX AC AAY84483;
 XX XX 25-JUL-2000 (first entry)
 XX DE Amino acid sequence of an epitopic fragment of the C-beta protein.
 XX KW C-beta protein; bactericidal; gram positive bacteria; vaccine;
 XX KW immune response.
 XX OS Streptococcus agalactiae.
 XX PN WO200015760-A1.
 XX XX

PI Long-Rowe KO, Blake MS;
XX WPI; 2000-271404/23.
XX
XX
XX Obtaining substantially pure C-beta protein or fragment and/or mutant for
XX eliciting antibodies which are bactericidal to gram positive bacteria,
XX useful in vaccines.
XX
XX
XX Claim 19; Page 69; 171pp; English.
XX
XX The specification describes a process for obtaining a substantially pure
XX C-beta protein. The process comprises obtaining the C-beta protein in
XX cell extracts, subjecting the C-beta protein to ion-exchange
XX chromatography and collecting the C-beta protein-containing fractions,
XX pooling and diluting the fractions, and subjecting the fractions to
XX ligand affinity chromatography and collection. The C-beta protein
XX fragments are useful for eliciting antibodies which are bactericidal to
XX gram positive bacteria with complement alone and therefore is useful in a
XX (combination) vaccine together with a pharmaceutically acceptable carrier
XX (and/or optionally at least two protein fragments or peptide-
XX polysaccharide conjugates). The vaccine therefore is useful in a method
XX for inducing an immune response in a mammal. The present sequence
XX represents an epitopic fragment derived from amino acids 827-1028 of the
XX Streptococcus agalactiae C-beta protein
XX
SQ Sequence 8 AA;
Alignment Scores:
Pred. No.: 9.59e+07 Length: 8
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0
US-10-070-588A-112 (1-11) x AAY84489 (1-8)
QY 3 TTGGCACTA 11
Db 5 LeuAlaLeu 7
RESULT 49
AAY69217
ID AAY69217 standard; peptide; 8 AA.
XX
XX AAY69217;
XX
XX 30-MAY-2000 (first entry)
XX
XX Tryptic peptide of honey bee venom PX3.101 protein.
XX
XX Protein PX3.101; honey bee; venom; interleukin-8; IL-8; receptor; CXCR1;
XX CXCR2; cyclooxygenase; lipoxigenase; phospholipase; protease;
XX inflammatory disease; gene therapy; cancer; autoimmune disease; pain;
XX chemokine imbalance; rheumatoid arthritis; multiple sclerosis; psoriasis;
XX systemic lupus erythematosus; Crohn's disease; vasculitis; scleroderma;
XX metastatic cancer; Alzheimer's disease; wound healing; aging process;
XX antigen.
XX
XX Apis mellifera.
XX
XX
XX Key Location/Qualifiers
XX Misc-difference 1 /note= "unknown amino acid"
XX FT
XX Misc-difference 2 /note= "unknown amino acid"
XX FT
XX
XX GB2341389-A.
XX
XX 15-MAR-2000.
XX
XX 13-SEP-1999; 99GB-00021605.
XX

PR 14-SEP-1998; 98US-0100172P.
XX (PANP-) PAN PACIFIC PHARM INC.
XX
XX
XX Chi X, Lu Y;
XX
XX WPI; 2000-185368/17.
XX
XX Isolated nucleic acids encoding the bee venom protein PX3.101 useful for
XX treating autoimmune and inflammatory disorders such as rheumatoid
XX arthritis.
XX
XX Example 2; Page 52; 83pp; English.
XX
XX The present sequence is derived from the protein PX3.101, which is a
XX honey bee venom isolated Apis mellifera. PX3.101 inhibits the binding of
XX interleukin-8 (IL-8) to its receptor (e.g. CXCR1 and CXCR2) and inhibits
XX a variety of enzymes (e.g. cyclooxygenases, lipoxigenases, phospholipases
XX and proteases) associated with inflammatory diseases. The nucleic acids
XX may be used for the recombinant production of PX3.101 proteins either in
XX vivo (as part of a gene therapy protocol) or in vitro (as a fermentation
XX culture). The nucleic acids may also be used as probes to identify
XX similar sequences in samples. The PX3.101 protein may be used for the
XX treatment of inflammatory diseases, cancers, autoimmune diseases, pain
XX and/or diseases associated with chemokine (especially IL-8) imbalances
XX such as rheumatoid arthritis, multiple sclerosis, psoriasis, systemic
XX lupus erythematosus (SLE), Crohn's disease, vasculitis, scleroderma,
XX metastatic cancer and Alzheimer's disease in humans. It is also disclosed
XX that the proteins may be used to accelerate wound healing, reduce several
XX aging processes and protect against ultraviolet light. The proteins may
XX also be used as antigens in the production of antibodies specific for
XX PX3.101. The antibodies may be used as diagnostic agents to detect
XX CX3.101 protein in samples and to down regulate PX3.101 activity
XX
SQ Sequence 8 AA;
Alignment Scores:
Pred. No.: 9.59e+07 Length: 8
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0
US-10-070-588A-112 (1-11) x AAY69217 (1-8)
QY 9 GTGCCAAAG 1
Db 6 ValProllys 8
RESULT 50
AAB29524
ID AAB29524 standard; peptide; 8 AA.
XX
XX AAB29524;
XX
XX 14-FEB-2001 (first entry)
XX
XX E9K peptide used in a Grb2 protein:peptide binding assay.
XX
XX Fluorescent dye; pH insensitive; trimethine cyanine analogue;
XX immunofluorescence detection system; fluorescence lifetime;
XX fluorescence polarisation; equilibrium-binding assay; binding-pair assay;
XX fluorescence resonance energy transfer; polarisation binding assay;
XX Grb2 protein; E9K peptide.
XX
XX Synthetic.
XX
XX US6133445-A.
XX
XX 17-OCT-2000.
XX
XX 16-DEC-1998; 98US-00212564.
XX

XX 16-DEC-1998; 98US-00212564.
XX (UYCA-) UNIV CARNEGIE MELLON.
XX Waggoner AS, Mujumdar RB;
XX WPI; 2000-678694/66.
XX New bisindolinium(3,2-a,3',2'-a)pyrano(3,2-c:5,6-c')dipyridin-5-ium dye
PT used as fluorescent marker and in fluorescence energy transfer complexes.
PT Example 12; Col 27; 27pp; English.
XX
XX The invention relates to a novel analogue of a trimethine cyanine dye,
CC 6,7,9,10-tetrahydro-2-carboxymethyl-14-sulphonato-16,16,18,18-
CC tetramethyl-7aH,8aH-bisindolinium(3,2-a,3',2'-a)pyrano(3,2-c:5,6-
CC c')dipyridin-5-ium. This compound can be used as a fluorescent marker and
CC in fluorescence energy transfer complexes. It is a bright, highly
CC fluorescent dye compound that absorbs and emits in the 450-600 nm region
CC of the spectrum. It confers high quantum yields of fluorescence, is pH
CC insensitive and extends the range of useful fluorescent labelling agents
CC that can be used in fluorescent detection applications. The compound of
CC the invention can be used in methods to determine the concentration of
CC proteins or other components in a system, for example, in methods to
CC measure the concentration of various labelled analytes using microtitre
CC plate readers or other immunofluorescence detection systems. The novel
CC dye may be used in assay methodologies that use fluorescent labels for
CC the detection of analytes e.g., fluorescence resonance energy transfer
CC (FRET)-based methods, fluorescence lifetime or fluorescence polarisation
CC methods. It may be used in equilibrium-binding assays (e.g.,
CC immunoassays, nucleic acid-hybridisation assays, protein-binding assays,
CC hormone receptor assays), enzyme assays, proteolytic cleavage assays, and
CC in nucleic acid or lipid cleavage assays). It may also be used in
CC specific binding pair assays involving antibodies/antigens, lectins/
CC glycoproteins, biotin/streptavidin, hormones/receptors, enzyme/
CC substrate or co-factor, DNA/DNA, DNA/RNA or DNA/binding protein. The
CC present sequence the E9K peptide which is specifically bound by the Grb2
CC protein and which was used in a protein:peptide polarisation binding
CC assay in an exemplification of the invention
XX
XX SQ Sequence 8 AA;

Alignment Scores:
Pred. No.: 9.59e+07 Length: 8
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-070-588A-112 (1-11) x AAB29524 (1-8)

Qy 9 GTGCCAAG 1
Db |||||
6 ValProlys 8

Search completed: March 12, 2005, 11:05:46
Job time : 66.5 secs

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Result No.	Score	Query Match	Length	DB	ID	Description
C 1	3	100.0	8	2	S37141	tpsa protein - Erw
C 2	3	100.0	9	2	S13333	alpha/beta-gliadin
C 3	3	100.0	11	2	S78765	ribosomal protein
C 4	3	100.0	11	2	S65377	cytochrome-c oxid
C 5	3	100.0	12	2	A26093	microbial collagen
C 6	3	100.0	12	2	A55837	5-aminomidazole r
C 7	3	100.0	12	2	PA0098	ribosomal protein
C 8	3	100.0	12	2	S07206	kassinin - Senegal
C 9	3	100.0	13	2	S03063	Ig lambda chain J
C 10	3	100.0	14	2	PA0094	hyocyanine (6s)-di
C 11	3	100.0	14	2	B34135	DNA-binding protei
C 12	3	100.0	14	2	PH0800	T-cell receptor al
C 13	3	100.0	14	2	PT0210	T-cell receptor al
C 14	3	100.0	14	2	S33801	chaperone, TCPI-re

88	3	100.0	25	2	S47204	T-cell receptor J
89	3	100.0	25	2	S47211	T-cell receptor J
90	3	100.0	25	2	S26651	uterglobin precursor
91	3	100.0	25	2	P70088	arylalkylphosphatase
92	3	100.0	25	2	B49111	POU homeodomain protein
93	3	100.0	25	2	PH1907	T-cell receptor alpha
94	3	100.0	25	2	S47190	T-cell receptor J
95	3	100.0	25	2	I40061	shikimate 5-dehydrogenase
96	3	100.0	25	2	T01689	ATPase-beta chain
97	3	100.0	25	2	I49409	CD2 antigen - west
98	3	100.0	25	2	S65002	glucan 1,3-beta-glucanase
99	3	100.0	25	2	S65729	hemoglobin, extracellular
100	3	100.0	26	2	T12323	NADH2 dehydrogenase
101	3	100.0	26	2	T12327	NADH2 dehydrogenase
102	3	100.0	26	2	T13974	NADH2 dehydrogenase
103	3	100.0	26	2	T14217	NADH2 dehydrogenase
104	3	100.0	26	2	T14221	NADH2 dehydrogenase
105	3	100.0	26	2	T14052	NADH2 dehydrogenase
106	3	100.0	26	2	S8384	T-cell receptor alpha
107	3	100.0	26	2	S32806	transposase - Escherichia
108	3	100.0	26	2	F49164	chromogranin-B - rat
109	3	100.0	27	2	T12314	NADH2 dehydrogenase
110	3	100.0	27	2	T17064	NADH2 dehydrogenase
111	3	100.0	27	2	T14017	NADH2 dehydrogenase
112	3	100.0	27	2	T13836	NADH2 dehydrogenase
113	3	100.0	27	2	T17052	NADH2 dehydrogenase
114	3	100.0	27	2	T17061	NADH2 dehydrogenase
115	3	100.0	27	2	T17055	NADH2 dehydrogenase
116	3	100.0	27	2	T17058	NADH2 dehydrogenase
117	3	100.0	27	2	T17067	NADH2 dehydrogenase
118	3	100.0	27	2	T12306	NADH2 dehydrogenase
119	3	100.0	27	2	T12310	NADH2 dehydrogenase
120	3	100.0	27	2	T12319	NADH2 dehydrogenase
121	3	100.0	27	2	T17070	NADH2 dehydrogenase
122	3	100.0	27	2	I46566	antileukoproteinas
123	3	100.0	27	2	B60630	45k antigen - trichinella
124	3	100.0	27	2	J50676	hypothetical 3.1K
125	3	100.0	27	2	G61002	transformation-sensitizing
126	3	100.0	27	2	A12968	superoxide dismutase
127	3	100.0	27	2	P44234	hypothetical protein
128	3	100.0	27	2	H48200	homeotic protein H
129	3	100.0	27	2	B47235	homeodomain protein
130	3	100.0	28	2	T12301	NADH2 dehydrogenase
131	3	100.0	28	2	I46921	gene Bata protein
132	3	100.0	28	2	T14905	hypothetical protein
133	3	100.0	28	2	S15235	hypothetical protein
134	3	100.0	28	2	S29285	arylalkyl acylamidase
135	3	100.0	28	2	S83502	95k protein - Eubacterium
136	3	100.0	28	2	T06925	hypothetical protein
137	3	100.0	29	1	Q1BP57	gene 1.5 protein - Eubacterium
138	3	100.0	29	2	G61233	conceptus protein
139	3	100.0	29	2	C47719	T-cell receptor alpha
140	3	100.0	29	2	T37306	HLA-DR beta - human
141	3	100.0	29	2	T37534	gene HLA-DRB protein
142	3	100.0	29	2	T37536	MHC class II histocompatibility
143	3	100.0	29	2	T37303	HLA-DR beta - human
144	3	100.0	29	2	T37535	gene HLA-DRB protein
145	3	100.0	29	2	PC4231	ribosomal protein
146	3	100.0	29	2	S26229	ribosomal protein
147	3	100.0	29	2	A35121	hypothetical protein
148	3	100.0	29	2	S05224	photosystem I 4.8K
149	3	100.0	29	2	G64674	pancreatic ribonuclease
150	3	100.0	29	2	G83440	endo-1,4-beta-xylanase
151	3	100.0	29	2	T36654	endo-1,4-beta-xylanase
152	3	100.0	29	2	S73366	epoxide hydrolase

30	2	B84786	hypothetical protein
30	2	B70165	hypothetical protein
30	2	A70209	hypothetical protein
31	2	S13205	glyceraldehyde-3-phosphate dehydrogenase
31	2	S44472	glucagon C2 - N-terminus
31	2	F53480	T-cell receptor alpha chain
31	2	T08489	hypothetical protein
31	2	F72429	hypothetical protein
31	2	C71945	hypothetical protein
31	2	C82175	hypothetical protein
31	2	E82466	hypothetical protein
31	2	S15837	hypothetical protein
31	2	T06934	photosystem I chain
31	2	A05051	hypothetical protein
31	2	S05124	hypothetical protein
31	2	A36221	cecropin P1 - pig
31	2	D82827	hypothetical protein
31	2	T07290	photosystem I protein
31	2	AD2046	hypothetical protein
31	2	AD2046	hypothetical protein
32	2	PC2175	3alpha-hydroxysteroid oxidoreductase
32	2	G46376	1-aminocyclopropanecarboxylate lyase
32	2	A53480	T-cell receptor alpha chain
32	2	A02687	DNA-binding protein
32	2	S11610	ribosomal protein
32	2	PC7067	meltrin beta - mouse
32	2	E82279	hypothetical protein
32	2	C82467	hypothetical protein
32	2	H82416	hypothetical protein
32	2	A05015	hypothetical protein
32	2	C26393	calelectrin - mouse
32	2	A36154	benzphetamine N-decarboxylase
32	2	S43312	2',3'-cyclic-nucleoside 5-phosphorylase
32	2	A44181	Cerastes serine protease
32	2	A61310	nonhistone chromosomal protein
32	2	I61694	myosin - human (fructose-bisphosphate dependent)
32	2	T08018	ycf12 protein - Chlamydia
32	2	A05010	hypothetical protein
32	2	E45557	orf immediately upstream open reading frame
32	2	I51969	neurofibromin - human
32	2	E95133	hypothetical protein
32	2	E43675	orf protein - infectious mononucleosis
32	2	A70159	hypothetical protein
32	2	G82254	hypothetical protein
32	2	E82391	hypothetical protein
32	2	T03346	gene e21 protein - Neurospora
32	2	E82353	hypothetical protein
32	2	S18161	NADH2 dehydrogenase
32	2	A36626	osteogenic protein
32	2	A19197	class II histocompatibility antigen
32	2	E78345	hypothetical protein
32	2	F84079	hypothetical protein
32	2	E82819	hypothetical protein
32	2	S05112	M24 protein - Streptococcus
32	2	S65772	early nodulin 40 - Arabidopsis
32	2	S33666	hypothetical protein
32	2	B41161	29K antigen PEB2 - Pichia
32	2	A45791	hypothetical protein
32	2	E69217	hypothetical protein
32	2	A39830	dentin matrix, incisor
32	2	S08136	hypothetical protein
32	2	S15821	ventricular natriuretic factor
32	2	S70806	hypothetical protein
32	2	S78721	protein YGL006w-a
32	2	A41017	LDL receptor-related protein
32	2	B53480	T-cell receptor alpha chain
32	2	D87544	hypothetical protein
32	2	A81740	hypothetical protein
32	2	E82854	hypothetical protein
32	2	A00066	hypothetical protein
32	2	A80592	probable membrane protein
32	2	G95010	hypothetical protein

Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x S37141 (1-8)

Qy 10 AGTGCCAAA 2
Db 4 SerAlaLys 6

RESULT 2
alpha/beta-gliadin - wheat (fragment)
C/Species: Triticum aestivum (common wheat)
C/Date: 19-Mar-1997 #sequence_revision 30-Jan-1998 #text_change 09-Jul-2004
C/Accession: S13333
R/Arvan, A.P.; An, G.; Okita, T.W.
Mol. Gen. Genet. 225, 65-71, 1991
A/Title: Structural and functional analysis of promoter from gliadin, an endosperm-specific protein
A/Reference number: S13333; MUID:91155936; PMID:2000092
A/Accession: S13333
A/Molecule type: DNA
A/Residues: 1-9 <ARY>
A/Cross-references: UNIPROT:Q41531; UNIPROT:Q41529; UNIPROT:Q41546; UNIPROT:Q41530; UNIPROT:Q41537

Alignment Scores:
Pred. No.: 2.14e+07 Length: 9
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x S13333 (1-9)

Qy 3 TTGGCACTA 11
Db 7 LeuAlaLeu 9

RESULT 3
S78765
ribosomal protein MRP-S24, mitochondrial - bovine (fragment)
C/Species: Bos primigenius taurus (cattle)
C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C/Accession: S78765
R/Graack, H.R.
submitted to the Protein Sequence Database, July 1999
A/Reference number: S78760
A/Accession: S78765
A/Molecule type: protein
A/Residues: 1-11 <GRA>
A/Cross-references: UNIPROT:Q7M374
C/Keywords: mitochondrion
F/1-11/Product: ribosomal protein MRP-S24 (fragment) #status experimental <MAT>

Alignment Scores:
Pred. No.: 8.91e+04 Length: 11
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x S78765 (1-11)

Qy 9 GTGCCAAG 1
Db 5 ValProLys 7

RESULT 4
S65377
cytochrome-c oxidase (EC 1.9.3.1) chain Via-H, cardiac - rat (fragment)
C/Species: Rattus norvegicus (Norway rat)
C/Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004

Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x S65377 (1-11)

Qy 10 AGTGCCAAA 2
Db 2 SerAlaLys 4

RESULT 5
A26093
microbial collagenase (EC 3.4.24.3) 1 - Vibrio alginolyticus chemovar. iophagus (fragment)
N/Alternate names: Achromobacter collagenase
C/Species: Vibrio alginolyticus chemovar. iophagus
C/Date: 24-Jun-1987 #sequence_revision 02-Jun-1988 #text_change 03-May-1994
C/Accession: A26093
R/Tong, N.T.; Taugita, A.; Keil-Dlouha, V.
Biochim. Biophys. Acta 874, 295-304, 1986
A/Reference number: A26093
A/Accession: A26093
A/Molecule type: protein
A/Residues: 1-12 <TON>
C/Keywords: hydrolase; metalloproteinase

Alignment Scores:
Pred. No.: 8.65e+04 Length: 12
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x A26093 (1-12)

Qy 3 TTGGCACTA 11
Db 9 LeuAlaLeu 11

RESULT 6
A55837
5-aminoimidazole ribonucleotide carboxylase/4-N-succinylamino carbonyl-5-aminoimidazole
C/Species: Gallus gallus (chicken)
C/Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 17-Mar-1999
C/Accession: A55837
R/Firestine, S.M.; Davisson, V.J.
Biochemistry 33, 11917-11926, 1994
A/Title: Carboxylases in de Novo purine biosynthesis. Characterization of the Gallus gallus
A/Reference number: A55837; MUID:95001903; PMID:7918410
A/Accession: A55837
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-12 <FIR>

Alignment Scores:
Pred. No.: 8.65e+04 Length: 12
Score: 3.00 Matches: 3

Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 2
Conservative: 0
Matches: 0
Indels: 0
Gaps: 0

US-10-070-588A-112 (1-11) x A55837 (1-12)

QY 3 TTGGCACTA 11
|||||
Db 6 LeuAlaLeu 8

RESULT 7

PA0098

ribosomal protein S3 - fungus (Fusarium sporotrichioides) (fragment)

C;Species: Fusarium sporotrichioides
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004

C;Accession: PA0098

R;Chow, L.P.; Fukaya, N.; Sugiyura, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.

submitted to JIPID, October 1994

A;Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrichioides

A;Reference number: PA0051

A;Accession: PA0098

A;Molecule type: protein

A;Residues: 1-12 <CHO>

A;Cross-references: UNIPROT:Q7M4X9

Alignment Scores:

Pred. No.: 8.65e+04 Length: 12
Score: 3.00 Matches: 3
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 2
Conservative: 0
Matches: 0
Indels: 0
Gaps: 0

US-10-070-588A-112 (1-11) x PA0098 (1-12)

QY 9 GTGCCAAAG 1
|||||
Db 6 ValProllys 8

RESULT 8

S07206

kassinin - Senegal running frog

C;Species: Kassina senegalensis (Senegal running frog)

C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 16-Aug-2004

C;Accession: S07206

R;Anastasi, A.; Montecucchi, P.; Erspamer, V.; Visser, J.

Experientia 33, 857-858, 1977

A;Title: Amino acid composition and sequence of kassinin, a tachykinin dodecapeptide from

A;Reference number: S07206; MUID:77246385; PMID:891753

A;Accession: S07206

A;Molecule type: protein

A;Residues: 1-12 <ANA>

A;Cross-references: UNIPROT:P08611

C;Keywords: amidated carboxyl end

P;12/Modified site: amidated carboxyl end (Met) #status experimental

Alignment Scores:

Pred. No.: 8.65e+04 Length: 12
Score: 3.00 Matches: 3
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 2
Conservative: 0
Matches: 0
Indels: 0
Gaps: 0

US-10-070-588A-112 (1-11) x S07206 (1-12)

QY 9 GTGCCAAAG 1
|||||
Db 2 ValProllys 4

RESULT 9

S03063

Ig lambda chain J region - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 11-Jan-2002

C;Accession: S03063

R;Udey, J.A.; Blomberg, B.B.

Nucleic Acids Res. 16, 2959-2969, 1988

A;Title: Intergenic exchange maintains identity between two human lambda light chain imm

A;Reference number: S03063; MUID:88217512; PMID:3130611

A;Accession: S03063

A;Molecule type: DNA

A;Residues: 1-13 <UDE>

A;Cross-references: EMBL:X06877; NID:g33357; PIDN:CAA29996.1; PID:g1335162

C;Keywords: heterotetramer; immunoglobulin

Alignment Scores:

Pred. No.: 8.42e+04 Length: 13
Score: 3.00 Matches: 3
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 2
Conservative: 0
Matches: 0
Indels: 0
Gaps: 0

US-10-070-588A-112 (1-11) x S03063 (1-13)

QY 2 TTGGCACT 10
|||||
Db 3 PheGlyThr 5

RESULT 10

PA0094

hyocyanine (6s)-dioxygenase II - fungus (Fusarium sporotrichioides) (fragment)

C;Species: Fusarium sporotrichioides

C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Mar-2001

C;Accession: PA0094

R;Chow, L.P.; Fukaya, N.; Sugiyura, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.

submitted to JIPID, October 1994

A;Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrichioides

A;Reference number: PA0051

A;Accession: PA0094

A;Molecule type: protein

A;Residues: 1-14 <CHO>

Alignment Scores:

Pred. No.: 8.21e+04 Length: 14
Score: 3.00 Matches: 3
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 2
Conservative: 0
Matches: 0
Indels: 0
Gaps: 0

US-10-070-588A-112 (1-11) x PA0094 (1-14)

QY 3 TTGGCACTA 11
|||||
Db 11 LeuAlaLeu 13

RESULT 11

B34135

DNA-binding protein q - Crithidia fasciculata mitochondrion (fragment)

C;Species: mitochondrion Crithidia fasciculata

C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 07-Dec-1999

C;Accession: B34135

R;Tittawella, I.

FEBS Lett. 260, 57-61, 1990

A;Title: Kinetoplast DNA-aggregating proteins from the parasitic protozoan Crithidia fasciculata

A;Reference number: A34135

A;Accession: B34135

A;Molecule type: protein

A;Residues: 1-14 <TIT>

C;Genetics:

A;Genome: mitochondrion

A;Genetic code: SGC6

C;Keywords: mitochondrion

Alignment Scores:
Pred. No.: 8.21e+04 14
Score: 3.00 3
Percent Similarity: 100.00% 0
Best Local Similarity: 100.00% 0
Query Match: 100.00% 0
DB: 2 0

US-10-070-588A-112 (1-11) x B34135 (1-14)

Qy 10 AGTGCCAAA 2

Db 5 SerAlalys 7

RESULT 12

PH0800

T-cell receptor alpha chain (J3) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C;Accession: PH0800

R;Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.

J. Exp. Med. 174, 1371-1383, 1991

A;Title: T cell receptor genes in a series of class I major histocompatibility complex-
allelic exclusion and antigen-specific repertoire.

A;Reference number: PH0746; MUID:92078846; PMID:1836010

A;Accession: PH0800

A;Molecule type: mRNA

A;Residues: 1-14 <CAS>

A;Cross-references: EMBL:X60907

A;Experimental source: T lymphocyte

C;Keywords: T-cell receptor

Alignment Scores:

Pred. No.: 8.21e+04 14
Score: 3.00 3
Percent Similarity: 100.00% 0
Best Local Similarity: 100.00% 0
Query Match: 100.00% 0
DB: 2 0

US-10-070-588A-112 (1-11) x PH0800 (1-14)

Qy 10 AGTGCCAAA 2

Db 8 SerAlalys 10

RESULT 13

PT0210

T-cell receptor alpha chain V-J region (4-1-K.1) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 30-May-1997

C;Accession: PT0210

R;Nakano, N.; Kikutani, H.; Nishimoto, H.; Kishimoto, T.

J. Exp. Med. 173, 1091-1097, 1991

A;Title: T cell receptor V gene usage of islet beta cell-reactive T cells is not restric

A;Reference number: PT0209; MUID:91217621; PMID:1902501

A;Accession: PT0210

A;Molecule type: mRNA

A;Residues: 1-14 <NAK>

C;Keywords: T-cell receptor

Alignment Scores:

Pred. No.: 8.21e+04 14
Score: 3.00 3
Percent Similarity: 100.00% 0
Best Local Similarity: 100.00% 0
Query Match: 100.00% 0
DB: 2 0

US-10-070-588A-112 (1-11) x PT0210 (1-14)

Qy 10 AGTGCCAAA 2

Db 12 SerAlalys 14

RESULT 14

S33801

Chaperone, TCP1-related - oat

C;Species: Avena sativa (oat)

C;Date: 02-Dec-1993 #sequence_revision 27-Feb-1997 #text_change 09-Jul-2004

C;Accession: S33801

R;Mummert, E.; Grimm, R.; Speth, V.; Eckerskorn, C.; Schiltz, E.; Schaefer

Nature 363, 644-648, 1993

A;Title: A TCP1-related molecular chaperone from plants refolds phytochrome to its photo

A;Reference number: S33800; MUID:93288140; PMID:8099715

A;Accession: S33801

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-14 <MUM>

A;Cross-references: UNIPROT:Q7M1G7

Alignment Scores:

Pred. No.: 8.21e+04 14
Score: 3.00 3
Percent Similarity: 100.00% 0
Best Local Similarity: 100.00% 0
Query Match: 100.00% 0
DB: 2 0

US-10-070-588A-112 (1-11) x S33801 (1-14)

Qy 10 AGTGCCAAA 2

Db 4 SerAlalys 6

RESULT 15

S33802

Chaperone, TCP1-related - oat

C;Species: Avena sativa (oat)

C;Date: 02-Dec-1993 #sequence_revision 27-Feb-1997 #text_change 09-Jul-2004

C;Accession: S33802

R;Mummert, E.; Grimm, R.; Speth, V.; Eckerskorn, C.; Schiltz, E.; Schaefer

Nature 363, 644-648, 1993

A;Title: A TCP1-related molecular chaperone from plants refolds phytochrome to its photo

A;Reference number: S33800; MUID:93288140; PMID:8099715

A;Accession: S33802

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-14 <MUM>

A;Cross-references: UNIPROT:Q7M1G6

Alignment Scores:

Pred. No.: 8.21e+04 14
Score: 3.00 3
Percent Similarity: 100.00% 0
Best Local Similarity: 100.00% 0
Query Match: 100.00% 0
DB: 2 0

US-10-070-588A-112 (1-11) x S33802 (1-14)

Qy 10 AGTGCCAAA 2

Db 4 SerAlalys 6

RESULT 16

PA0076

fructose-bisphosphate aldolase (EC 4.1.2.13) - fungus (Fusarium sporotrichioides) (fragm

C;Species: Fusarium sporotrichioides

C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Mar-2001

C;Accession: PA0076

R;Chow, L.P.; Fukaya, N.; Sugiyura, Y.; Ueno, Y.; Tabuchi, K.; Teugita, A.

submitted to JIPID, October 1994

A;Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrich

A;Reference number: PA0051

A;Accession: PA0076
A;Molecule type: protein
A;Residues: 1-15 <CHO>
C;Keywords: aldehyde-lyase; carbon-carbon lyase

Alignment Scores:
Pred. No.: 8.02e+04 Length: 15
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x PA0076 (1-15)

QY 10 AGTGCCAAA 2
Db 1 SerAlalys 3

RESULT 17

14K protein - California sea hare (fragment)
C;Species: Aplysia californica (California sea hare)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 03-Feb-1994
C;Accession: D60977
R;Sweatt, J.D.; Kennedy, T.E.; Wager-Smith, K.; Gawinowicz, M.A.; Barzilai, A.; Karl, K.
Electrophoresis 10, 152-157, 1989
A;Title: Development of a database of amino acid sequences for proteins identified and
A;Reference number: A60977; MUID:89276264; PMID:2731514
A;Accession: D60977
A;Molecule type: protein
A;Residues: 1-15 <SWE>

Alignment Scores:
Pred. No.: 8.02e+04 Length: 15
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x D60977 (1-15)

QY 3 TTGGCACTA 11
Db 2 LeuAlaleu 4

RESULT 18

formate dehydrogenase alpha chain - Alcaligenes eutrophus (fragment)
C;Species: Alcaligenes eutrophus
C;Date: 27-Apr-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: S59492
R;Friedebold, J.; Mayer, F.; Bill, E.; Trautwein, A.X.; Bowien, B.
Biol. Chem. Hoppe-Seyler 376, 561-568, 1995
A;Title: Structural and immunological studies on the soluble formate dehydrogenase from
A;Reference number: S59492; MUID:96145736; PMID:8561915
A;Accession: S59492
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-15 <PRI>
A;Cross-references: UNIPROT:O87815

Alignment Scores:
Pred. No.: 8.02e+04 Length: 15
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x S59492 (1-15)

QY 2 TTGGCACT 10
Db 9 PheGlyThr 11

RESULT 19

CQRT
cerebellin - rat
N;Contains: des-Ser-cerebellin
C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 09-Jul-2004
C;Accession: A03135
R;Slemmon, J.R.; Blacher, R.; Danho, W.; Hempstead, J.L.; Morgan, J.I.
Proc. Natl. Acad. Sci. U.S.A. 81, 6866-6870, 1984
A;Title: Isolation and sequencing of two cerebellum-specific peptides.
A;Reference number: A03135
A;Accession: A03135
A;Molecule type: protein
A;Residues: 1-16 <SLE>
A;Cross-references: UNIPROT:P23436
C;Comment: The sequence of des-Ser-cerebellin lacks 1-Ser.
C;Comment: The cerebellin is localized in the Purkinje cells of rat cerebellum.
C;Superfamily: complement subcomponent Clq chain A; complement Clq carboxyl-terminal hom
C;Keywords: brain

Alignment Scores:
Pred. No.: 7.85e+04 Length: 16
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x CQRT (1-16)

QY 10 AGTGCCAAA 2
Db 3 SerAlalys 5

RESULT 20

S66613
protein p12E - Friend murine leukemia virus (fragments)
C;Species: Friend murine leukemia virus
C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
C;Accession: S66613
R;Hensel, J.; Hintz, M.; Karas, M.; Linder, D.; Stahl, B.; Geyer, R.
Eur. J. Biochem. 232, 373-380, 1995
A;Title: Localization of the palmitoylation site in the transmembrane protein p12E of Fr
A;Reference number: S66613; MUID:96035869; PMID:7556184
A;Accession: S66613
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-9;10-16 <HEN>

Alignment Scores:
Pred. No.: 7.85e+04 Length: 16
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x S66613 (1-16)

QY 3 TTGGCACTA 11
Db 7 LeuAlaleu 9

RESULT 21

B60566
cytochrome P450m51a - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 28-Apr-1993 #sequence_revision 28-Apr-1993 #text_change 05-May-1993
C;Accession: B60566

R:Nagata, K.; Martin, B.M.; Gillette, J.R.; Sasame, H.A.
Drug Metab. Dispos. 18, 557-564, 1990
A:Title: Isozymes of cytochrome P-450 that metabolize naphthalene in liver and lung of
A:Reference number: A60566; MUID:91168724; PMID:1981702
A:Accession: B60566
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-16 <NAG>

Alignment Scores:
Pred. No.: 7.85e+04 Length: 16
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x B60566 (1-16)

Qy 3 TTGGCACTA 11
| | | | |
Db 7 LeuAlaLeu 9

RESULT 22

PH1476
T-cell receptor beta chain (clone 223/14) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 15-Mar-2004
C:Accession: PH1476
R:Casanova, J.L.; Martinon, F.; Gournier, H.; Barra, C.; Pannetier, C.; Regnault, A.; Ko
J. Exp. Med. 177, 811-820, 1993
A:Title: T cell receptor selection by and recognition of two class I major histocompatib
A:Reference number: PH1430; MUID:93171821; PMID:8436911
A:Accession: PH1476
A:Molecule type: mRNA
A:Residues: 1-16 <CAS>
A:Experimental source: cytolytic T-lymphocyte
C:Keywords: receptor; T-cell

Alignment Scores:
Pred. No.: 7.85e+04 Length: 16
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x PH1476 (1-16)

Qy 2 TTGGCACT 10
| | | | |
Db 5 PheGlyThr 7

RESULT 23

PH1474
T-cell receptor beta chain (clone A2/25) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 15-Mar-2004
C:Accession: PH1474
R:Casanova, J.L.; Martinon, F.; Gournier, H.; Barra, C.; Pannetier, C.; Regnault, A.; Ko
J. Exp. Med. 177, 811-820, 1993
A:Title: T cell receptor selection by and recognition of two class I major histocompatib
A:Reference number: PH1430; MUID:93171821; PMID:8436911
A:Accession: PH1474
A:Molecule type: mRNA
A:Residues: 1-16 <CAS>
A:Experimental source: cytolytic T-lymphocyte
C:Keywords: receptor; T-cell

Alignment Scores:
Pred. No.: 7.85e+04 Length: 16
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x PH1474 (1-16)

Qy 2 TTGGCACT 10
| | | | |
Db 5 PheGlyThr 7

RESULT 24

S11760
flgL protein - Caulobacter crescentus (fragment)
C:Species: Caulobacter crescentus
C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C:Accession: PQ0126; A25882; S11760
R:Schoenlein, P.V.; Gallman, L.S.; Winkler, M.E.; Ely, B.
Gene 93, 17-25, 1990
A:Title: Nucleotide sequence of the Caulobacter crescentus flaF and flbT genes and an an
A:Reference number: JQ0741; MUID:91033011; PMID:1699845
A:Accession: PQ0126
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-16 <SCH>
A:Cross-references: UNIPROT:P18914; GB:X15134; NID:G40418; PIDN:CAA33232.1; PID:G40422
R:Minnich, S.A.; Newton, A.
Proc. Natl. Acad. Sci. U.S.A. 84, 1142-1146, 1987
A:Title: Promoter mapping and cell cycle regulation of flagellin gene transcription in C
A:Reference number: A25882; MUID:87147229; PMID:3469658
A:Accession: A25882
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-12, 'V', 14-16 <MIN>
A:Cross-references: GB:M15688; NID:G144267; PIDN:AAA23050.1; PID:G144269
C:Genetics:
A:Gene: flgL

Alignment Scores:
Pred. No.: 7.85e+04 Length: 16
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x S11760 (1-16)

Qy 3 TTGGCACTA 11
| | | | |
Db 13 LeuAlaLeu 15

RESULT 25

A61268
cytochrome P450-thc - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 12-May-1994 #sequence_revision 12-May-1994 #text_change 05-Mar-1999
C:Accession: A61268
R:Bornheim, L.M.; Correia, M.A.
Mol. Pharmacol. 40, 228-234, 1991
A:Title: Purification and characterization of the major hepatic cannabinoid hydroxylase
A:Reference number: A61268; MUID:91342605; PMID:1875910
A:Accession: A61268
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-16 <BOR>
C:Genetics:
A:Gene: Cyp2c29
C:Superfamily: unassigned cytochrome P450; cytochrome P450 homology
C:Keywords: heme

Alignment Scores:
Pred. No.: 7.85e+04 Length: 16
Score: 3.00 Matches: 3

Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x A61268 (1-16)

Qy 3 TTGGCACTA 11

Db 7 LeuAlaLeu 9

RESULT 26

PL0124

Cerebellin - pig

C/Species: Sus scrofa domestica (domestic pig)

C/Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 16-Aug-2004

C/Accession: PL0124

R/Yianguo, Y.; Burnet, P.; Nikou, G.; Chrysanthou, B.J.; Bloom, S.R.

J. Neurochem. 53, 886-889, 1989

A/Title: Purification and characterisation of cerebellins from human and porcine cerebell

A/Reference number: PL0124; MUID:89341798; PMID:2760624

A/Accession: PL0124

A/Molecule type: protein

A/Residues: 1-16 <YIA>

A/Cross-references: UNIPROT:P23435; UNIPROT:P23436

A/Experimental source: brain

A/Note: the sequences of human and porcine cerebellin are identical to that of the rat

C/Comment: The peptide is identified in two molecular forms having 16 and 15 amino acid

Alignment Scores:

Pred. No.: 7.85e+04 Length: 16

Score: 3.00 Matches: 3

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x PL0124 (1-16)

Qy 10 AGTCCCAA 2

Db 3 SerAlaLys 5

RESULT 27

I51910

SP-A2 - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004

C/Accession: I51910

R/McCormick, S.M.; Boggaram, V.; Mendelson, C.R.

Am. J. Physiol. 266, L354-L366, 1994

A/Title: Characterization of mRNA transcripts and organization of human SP-A1 and SP-A2

A/Reference number: I51910; MUID:94234365; PMID:8179012

A/Accession: I51910

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-17 <RES>

A/Cross-references: UNIPROT:P78490; GB:S69679; NID:G546669; PIDN:AAB30729.1; PID:G546670

C/Genetics:

A/Gene: SP-A2

C/Superfamily: mannose-binding lectin; C-type lectin homology

Alignment Scores:

Pred. No.: 7.69e+04 Length: 17

Score: 3.00 Matches: 3

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x I51910 (1-17)

Qy 3 TTGGCACTA 11

Db 6 LeuAlaLeu 8

RESULT 28

S47201

T-cell receptor J-alpha wntv.3 - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 05-Nov-1999

C/Accession: S47201

R/Plaza, A.; Kono, D.H.; Theofilopoulos, A.N.

submitted to the EMBL Data Library, February 1993

A/Reference number: S40133

A/Accession: S47201

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-17 <PIA>

A/Cross-references: EMBL:X71048; NID:G506944; PIDN:CAA50365.1; PID:G510661

C/Keywords: T-cell receptor

Alignment Scores:

Pred. No.: 7.69e+04 Length: 17

Score: 3.00 Matches: 3

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x S47201 (1-17)

Qy 2 TTGGCACT 10

Db 7 PheGlyThr 9

RESULT 29

PH0778

T-cell receptor alpha chain (RA10.3.3) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C/Accession: PH0778

R/Casanova, J.L.; Romero, P.; Widmann, C.; Kourilesky, P.; Maryanski, J.L.

J. Exp. Med. 174, 1371-1383, 1991

A/Title: T cell receptor genes in a series of class I major histocompatibility complex-r

allelic exclusion and antigen-specific repertoire.

A/Reference number: PH0746; MUID:92078846; PMID:1836010

A/Accession: PH0778

A/Molecule type: mRNA

A/Residues: 1-17 <CAS>

A/Cross-references: EMBL:X60875

A/Experimental source: T lymphocyte

C/Keywords: T-cell receptor

Alignment Scores:

Pred. No.: 7.69e+04 Length: 17

Score: 3.00 Matches: 3

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x PH0778 (1-17)

Qy 10 AGTCCCAA 2

Db 11 SerAlaLys 13

RESULT 30

C56211

progesterone receptor-related protein p23 - rabbit (fragment)

C/Species: Oryctolagus cuniculus (domestic rabbit)

C/Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 20-Jun-2000

C/Accession: C56211

R/Johnson, J.L.; Beito, T.G.; Krco, C.J.; Toft, D.O.

Mol. Cell. Biol. 14, 1956-1963, 1994

A;Title: Characterization of a novel 23-kilodalton protein of unactive progesterone receptor
A;Reference number: A56211; MUID:94158868; PMID:8114727
A;Accession: C56211
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-18 <OH>
C;Superfamily: Caenorhabditis elegans hypothetical protein ZC395.10
C;Keywords: steroid hormone receptor

Alignment Scores:
Pred. No.: 7.54e+04 Length: 18
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x C56211 (1-18)

Qy 10 AGTGCCAAA 2
Db 5 SerAlaLys 7

RESULT 31
140062
shikimate 5-dehydrogenase (EC 1.1.1.25) - Buchnera aphidicola (fragment)
C;Species: Buchnera aphidicola
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 08-Oct-1999
C;Accession: I40062
R;Roubaksh, D.; Baumann, P.
Gene 155, 107-112, 1995
A;Title: Characterization of a putative 23S-5S rRNA operon of Buchnera aphidicola (endosymbiont)
A;Reference number: I40061; MUID:95212914; PMID:7535281
A;Accession: I40062
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-18 <RES>
A;Cross-references: EMBL:U10496; NID:9854711; PIDN:AAA79125.1; PID:9854712
C;Genetics:
A;Gene: aroB
C;Keywords: oxidoreductase

Alignment Scores:
Pred. No.: 7.54e+04 Length: 18
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x I40062 (1-18)

Qy 1 CTTGGGCAC 9
Db 4 LeuTrpHis 6

RESULT 32
S78767
ribosomal protein MRP-S29, mitochondrial - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: S78767
R;Graack, H.R.
submitted to the Protein Sequence Database, July 1999
A;Reference number: S78760
A;Accession: S78767
A;Molecule type: protein
A;Residues: 1-18 <GRA>
C;Keywords: mitochondrion
F;1-18/Product: ribosomal protein MRP-S29 (fragment) #status experimental <MAT>

Alignment Scores:
Pred. No.: 7.54e+04 Length: 18
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x S78767 (1-18)

Qy 3 TTGGCACTA 11
Db 3 LeuAlaLeu 5

RESULT 33
159649
human leukocyte antigen alpha chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I59649
R;Fogdell, A.; Olerup, O.
Tissue Antigens 44, 19-24, 1994
A;Title: The DOA1*0104 allele is carried by DRB1*1001- and DRB1*1401-positive haplotypes
A;Reference number: I59649; MUID:95064785; PMID:7974465
A;Accession: I59649
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-18 <RES>
A;Cross-references: UNIPROT:Q30216; GB:S75685; NID:g913771; PIDN:AAB32621.1; PID:g913772
C;Genetics:
A;Gene: GDB:H1A-DOA1
A;Cross-references: GDB:I20638; OMIM:146880
A;Map position: 6p21.3-6p21.3

Alignment Scores:
Pred. No.: 7.54e+04 Length: 18
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x I59649 (1-18)

Qy 3 TTGGCACTA 11
Db 3 LeuAlaLeu 5

RESULT 34
S70611
30K protein - Engelmannia pinnatifida (fragment)
C;Species: Engelmannia pinnatifida
C;Date: 14-Apr-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
C;Accession: S70611
R;Huynh, Q.K.; Borgmeyer, J.R.; Smith, C.E.; Bell, L.D.; Shah, D.M.
Biochem. J. 316, 723-727, 1996
A;Title: Isolation and characterization of a 30 kDa protein with antifungal activity from
A;Reference number: S70611; MUID:96265034; PMID:8670144
A;Accession: S70611
A;Molecule type: protein
A;Residues: 1-18 <HUV>
A;Cross-references: UNIPROT:Q10722
A;Experimental source: leaves
C;Keywords: antifungal

Alignment Scores:
Pred. No.: 7.54e+04 Length: 18
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x S70611 (1-18)

Qy 3 TTGGCACTA 11
Db 10 LeuAlaLeu 12

RESULT 35
I53673
amyloid protein - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 13-Aug-1999
C;Accession: I53673
R;Chernak, J.M.
Gene 133, 255-260, 1993
A;Title: Structural features of the 5' upstream regulatory region of the gene encoding
A;Reference number: I53673; MUID:94040820; PMID:8224912
A;Accession: I53673
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-19 <RES>
A;Cross-references: GB:L11926; NID:g949984; PIDN:AAA74458.1; PID:g202962
C;Genetics:
A;Gene: APP
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i

Alignment Scores:
Pred. No.: 7.41e+04 Length: 19
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x I53673 (1-19)

Qy 3 TTGGCACTA 11
Db 5 LeuAlaLeu 7

RESULT 36
beta-1,3-glucan-binding protein - signal crayfish (fragment)
C;Species: Pacifastacus leniusculus (signal crayfish)
C;Date: 17-Aug-1990 #sequence_revision 17-Aug-1990 #text_change 18-Jun-1993
C;Accession: A35301
R;Duvic, B.; Soederhaell, K.
J. Biol. Chem. 265, 9327-9332, 1990
A;Title: Purification and characterization of a beta-1,3-glucan binding protein from pla
A;Reference number: A35301; MUID:90264428; PMID:2111817
A;Accession: A35301
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-19 <DUV>

Alignment Scores:
Pred. No.: 7.41e+04 Length: 19
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x A35301 (1-19)

Qy 10 AGTGCCAAA 2
Db 13 SerAlaLys 15

RESULT 37
B46592
lactase-phlorizin hydrolase 140K isoform - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 01-Nov-1996
C;Accession: B46592
R;Dudley, M.A.; Hachey, D.L.; Quaroni, A.; Hutchens, T.W.; Nichols, B.L.; Rosenberger, J

J. Biol. Chem. 268, 13609-13616, 1993
A;Title: In vivo sucrose-isomaltase and lactase-phlorizin hydrolase turnover in the fed
A;Reference number: A46592; MUID:93293888; PMID:8514793
A;Accession: B46592
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-19 <DUV>
A;Note: sequence extracted from NCBI backbone (NCBIP:134560)
C;Keywords: carbohydrate digestion; intestine

Alignment Scores:
Pred. No.: 7.41e+04 Length: 19
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x B46592 (1-19)

Qy 9 GTGCCAAAG 1
Db 9 ValProLys 11

RESULT 38
A41077
protein-disulfide reductase (glutathione) (BC 1.8.4.2) Q-5 - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 12-Jun-1992 #sequence_revision 12-Jun-1992 #text_change 23-Jun-1993
C;Accession: A41077
R;Srivastava, S.P.; Chen, N.; Liu, Y.; Holtzman, J.L.
J. Biol. Chem. 266, 20337-20344, 1991
A;Title: Purification and characterization of a new isozyme of thiol:protein-disulfide o
fic phospholipase C form 1A.
A;Reference number: A41077; MUID:92041865; PMID:1657921
A;Accession: A41077
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-19 <SRI>
C;Keywords: oxidoreductase

Alignment Scores:
Pred. No.: 7.41e+04 Length: 19
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x A41077 (1-19)

Qy 3 TTGGCACTA 11
Db 1 LeuAlaLeu 3

RESULT 39
B60822
cytochrome P450 UT50 - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-2004
C;Accession: B60822
R;Ameliazad, Z.; Narbonne, J.F.; Wolf, C.R.; Robertson, L.W.; Oesch, F.
Biochem. Pharmacol. 37, 3245-3249, 1988
A;Title: Effect of nutritional imbalances on cytochrome P-450 isozymes in rat liver.
A;Reference number: A60822; MUID:88293549; PMID:3041969
A;Accession: B60822
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-19 <AME>
A;Cross-references: UNIPROT:Q7M068
C;Genetics:
A;Gene: CYP2C
C;Superfamily: cytochrome P450 homology

C;Keywords: heme

Alignment Scores:
Pred. No.: 7.41e+04 Length: 19
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x B60822 (1-19)

Qy 3 TTGGCACTA 11
| | | | |
Db 7 LeuAlaLeu 9

RESULT 40

S11471
A;Title: 25-hydroxyvitamin D(3) 25-monoxygenase (EC 1.14.14.-) cytochrome P450D2, kidney - pig
N;Alternate names: 25-hydroxyvitamin D(3) 25-hydroxylase; cytochrome P450(25)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 23-Apr-1993 #sequence_revision 23-Apr-1993 #text_change 05-Mar-1999
C;Accession: S11471

R;Bergman, T.; Postlind, H.
Biochem. J. 270, 345-350, 1990
A;Title: Characterization of pig kidney microsomal cytochrome P-450 catalysing 25-hydrox
A;Reference number: S11471; MUID:90380027; PMID:2169238
A;Accession: S11471
A;Molecule type: protein
A;Residues: 1-20 <BER>

C;Genetics:
A;Gene: CYP2D
C;Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology
C;Keywords: electron transfer; endoplasmic reticulum; heme; monooxygenase; oxidoreductase

Alignment Scores:
Pred. No.: 7.28e+04 Length: 20
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x S11471 (1-20)

Qy 3 TTGGCACTA 11
| | | | |
Db 11 LeuAlaLeu 13

RESULT 41

A23739
Cytochrome P450 MUT-2, hepatic - mouse (fragment)
N;Contains: oxidoreductase (EC 1.-.-.-)
C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 05-Mar-1999
C;Accession: A23739
R;Watanabe, K.; Narimatsu, S.; Yamamoto, I.; Yoshimura, H.
J. Biol. Chem. 266, 2709-2711, 1991

A;Title: Oxygenation mechanism in conversion of aldehyde to carboxylic acid catalyzed by
A;Reference number: A23739; MUID:91131554; PMID:1847130
A;Accession: A23739
A;Molecule type: protein
A;Residues: 1-20 <WAT>

C;Genetics:
A;Gene: Cyp2c
C;Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology
C;Keywords: electron transfer; heme; liver; monooxygenase; oxidoreductase; transmembrane

Alignment Scores:
Pred. No.: 7.28e+04 Length: 20
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x A23739 (1-20)

Qy 3 TTGGCACTA 11
| | | | |
Db 7 LeuAlaLeu 9

RESULT 42

A60822
Cytochrome P450 PB-3a - rat (fragment)
N;Contains: oxidoreductase (EC 1.-.-.-)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: A60822; I55191
R;Ameliazad, Z.; Narbonne, J.F.; Wolf, C.R.; Robertson, L.W.; Oesch, F.
Biochem. Pharmacol. 37, 3245-3249, 1988
A;Title: Effect of nutritional imbalances on cytochrome P-450 isozymes in rat liver.
A;Reference number: A60822; MUID:88293549; PMID:3041969
A;Accession: A60822

A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-20 <AME>
A;Cross-references: UNIPROT:P04167
R;Hashimoto, T.; Matsumoto, T.; Nishizawa, M.; Kawabata, S.
J. Biochem. 103, 487-492, 1988
A;Title: A mutant rat strain deficient in induction of a phenobarbital-inducible form o
A;Reference number: I55191; MUID:88273074; PMID:2839467
A;Accession: I55191
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-20 <RES>

A;Cross-references: GB:D00250; NID:Q220727; PIDN:BAA00181.1; PID:Q220728
C;Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology
C;Keywords: electron transfer; heme; monooxygenase; oxidoreductase; transmembrane protei

Alignment Scores:
Pred. No.: 7.28e+04 Length: 20
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x A60822 (1-20)

Qy 3 TTGGCACTA 11
| | | | |
Db 9 LeuAlaLeu 11

RESULT 43

S30381
Glutathione transferase (EC 2.5.1.18) class mu chain 7.2 - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 02-Dec-1993 #sequence_revision 08-Nov-1996 #text_change 09-Jul-2004
C;Accession: S30381
R;Primiano, T.; Novak, R.F.

Arch. Biochem. Biophys. 301, 404-410, 1993
A;Title: Purification and characterization of class mu glutathione S-transferase isozyme
A;Reference number: S30380; MUID:93213177; PMID:8460949
A;Accession: S30381

A;Molecule type: protein
A;Residues: 1-20 <PRI>
A;Cross-references: UNIPROT:Q9TQ08
C;Superfamily: Glutathione transferase
C;Keywords: dimer; transferase

Alignment Scores:
Pred. No.: 7.28e+04 Length: 20
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0
US-10-070-588A-112 (1-11) x S03081 (1-20)
Qy 3 TTGGCACTA 11
Db 12 LeuAlaLeu 14
RESULT 44
A60489
venombin A (EC 3.4.21.74) - cantil (fragment)
N;Alternate names: Agkistrodon bilineatus serine proteinase; alpha-fibrinogenase; ancro
C;Species: Agkistrodon bilineatus (cantil)
C;Date: 19-Mar-1993 #sequence_revision 19-Mar-1993 #text_change 09-Jul-2004
C;Accession: A60489
R;Nakagaki, T.; Kazim, A.L.; Kisiel, W.
Thromb. Res. 58, 593-602, 1990
A;Title: Isolation and characterization of a protein C activator from tropical moccasin
A;Reference number: A60489; MUID:90350102; PMID:2385829
A;Accession: A60489
A;Molecule type: protein
A;Residues: 1-20 <NA>
A;Cross-references: UNIPROT:P33588
C;Superfamily: trypsin; trypsin homology
C;Keywords: glycoprotein; hydrolase; serine proteinase; venom

Alignment Scores:
Pred. No.: 7.28e+04 Length: 20
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x A60489 (1-20)

Qy 3 TTGGCACTA 11
Db 15 LeuAlaLeu 17

RESULT 45
PN0133
pepsin (EC 3.4.23.-) 1 - horse (fragment)
N;Alternate names: pepsin (pI 1.8)
C;Species: Equus caballus (domestic horse)
C;Date: 07-May-1993 #sequence_revision 07-May-1993 #text_change 09-Jul-2004
C;Accession: PN0133
R;Gonchar, M.V.; Lavrenova, G.I.; Rudenskaya, G.N.; Gaide, A.V.; Stepanov, V.M.
Biochimia 49, 1026-1037, 1984
A;Title: Multiple forms of horse pepsin.
A;Reference number: PN0133; MUID:84281135; PMID:6432065
A;Accession: PN0133
A;Molecule type: protein
A;Residues: 1-20 <GON>
A;Cross-references: UNIPROT:Q7M3D6
A;Note: article in Russian with English abstract
C;Superfamily: pepsin
C;Keywords: aspartic proteinase; hydrolase; protein digestion

Alignment Scores:
Pred. No.: 7.28e+04 Length: 20
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x PN0133 (1-20)

Qy 2 TTGGCACT 10
Db 15 PheGlyThr 17

RESULT 46

PL0192
Ig lambda 2 chain - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 07-May-1999
C;Accession: PL0192
R;Alonso, A.; Chang, L.A.; Murialdo, H.
Mol. Immunol. 27, 115-127, 1990
A;Title: Analysis of the expression of murine lambda genes transfected into immunocompet
A;Reference number: PL0192; MUID:90205873; PMID:2108323
A;Accession: PL0192
A;Molecule type: DNA
A;Residues: 1-20 <ALO>
C;Genetics:
A;Introns: 16/2
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin

Alignment Scores:
Pred. No.: 7.28e+04 Length: 20
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x PL0192 (1-20)

Qy 3 TTGGCACTA 11
Db 11 LeuAlaLeu 13

RESULT 47

I38417
HLA-A11 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C;Accession: I38417
R;Balas, A.; Garcia-Sanchez, F.; Gomez-Reino, F.; Vicario, J.L.
Hum. Immunol. 41, 69-73, 1994
A;Title: HLA class I allele (HLA-A2) expression defect associated with a mutation in its
A;Reference number: I38417; MUID:95137784; PMID:7836067
A;Accession: I38417
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-20 <RES>
A;Cross-references: UNIPROT:O19618; EMBL:U02934; NID:9414543; PIDN:AAA76607.1; PID:94145
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology

Alignment Scores:
Pred. No.: 7.28e+04 Length: 20
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x I38417 (1-20)

Qy 3 TTGGCACTA 11
Db 17 LeuAlaLeu 19

RESULT 48

I38418
HLA-A2 - human (fragment)
N;Alternate names: HLA-A23
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C;Accession: I38418; I38419
R;Balas, A.; Garcia-Sanchez, F.; Gomez-Reino, F.; Vicario, J.L.
Hum. Immunol. 41, 69-73, 1994

A;Title: HLA class I allele (HLA-A2) expression defect associated with a mutation in its
A;Reference number: 138417; MUID:95137784; PMID:7836067
A;Accession: 138418
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-20 <RES>
A;Cross-references: UNIPROT:P01892; UNIPROT:O19620; EMBL:U02935; NID:g414545; PIDN:AAA76
A;Accession: 138419
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-20 <RE2>
A;Cross-references: EMBL:U02936; NID:g414547; PIDN:AAA76609.1; PID:g414548
C;Genetics:
A;Gene: HLA-2; HLA-23
A;Map position: 6p21.3
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology

Alignment Scores:
Pred. No.: 7.28e+04 Length: 20
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x I38418 (1-20)

Qy 3 TTGGCACTA 11
Db 17 LeuAlaLeu 19
|||||

RESULT 49
D49255
T-cell receptor beta chain V-D-J-C region (V beta 12, J beta 2.4) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 30-May-1997
C;Accession: D49255
R;Rosenberg, W.M.; Moss, P.A.; Bell, J.I.
Eur. J. Immunol. 22, 541-549, 1992
A;Title: Variation in human T cell receptor V beta and J beta repertoire: analysis using
A;Reference number: A49039; MUID:92164737; PMID:1311263
A;Accession: D49255
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-20 <ROS>
A;Note: sequence extracted from NCBI backbone (NCBIP:90725)
C;Keywords: T-cell receptor

Alignment Scores:
Pred. No.: 7.28e+04 Length: 20
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x D49255 (1-20)

Qy 10 AGTCCAAA 2
Db 12 SerAlaLys 14
|||||

RESULT 50
A54538
39k major outer membrane protein - Actinobacillus actinomycetemcomitans (strain Y4) (fra
C;Species: Actinobacillus actinomycetemcomitans
C;Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 09-Jul-2004
C;Accession: A54538
R;Koikeguchi, S.; Kato, K.; Nishimura, F.; Kurihara, H.; Murayama, Y.
FEMS Microbiol. Lett. 77, 85-90, 1991
A;Title: Isolation and partial characterization of a 39 kDa major outer membrane protein
A;Reference number: A54538
A;Accession: A54538

A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-20 <KOK>
A;Cross-references: UNIPROT:P20242

Alignment Scores:
Pred. No.: 7.28e+04 Length: 20
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x A54538 (1-20)

Qy 2 TTGGCACT 10
Db 7 PheGlyThr 9
|||||

Search completed: March 12, 2005, 11:08:11
Job time : 27.5 secs

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GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: March 12, 2005, 10:28:53 ; Search time 50.5 Seconds
(without alignments)
223.084 Million cell updates/sec

Title: US-10-070-588A-112

Perfect score: 3

Sequence: 1 cttgggacta 11

Scoring table:

OLIGO	60.0	Xgapext	60.0
Ygapop	60.0	Ygapext	60.0
Fgapop	6.0	Fgapext	7.0
Delop	6.0	Delext	7.0

Searched: 1612378 seqs, 512079187 residues

Word size: 1

Total number of hits satisfying chosen parameters: 3224203

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 500 summaries

Command line parameters:

-MODE=frame+n2p.model -DEV=xlh
-O=/cpn2_1/USPTO_spool/US10070588/runat_10032005_120705_15240/app_query.fasta_1.199
-DB=uniprot_03 -Qfmt=fastan -SUFFIX=olin2p.rup -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi
-LIST=500 -DOCALIGN=200 -THR SCORE=quality -THR_MIN=1 -ALIGN=50 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10070588 @CGN 1 1 140 @runat_10032005_120705_15240 -NCPU=3
-NO_WMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database :

1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	3	100.0	8	1 RS1_EWCH	P37985 erwina chr
C 2	3	100.0	8	2 Q6JC68	Q6JC68 glycine max
C 3	3	100.0	9	2 Q9MW43	Q9MW43 homo sapien
C 4	3	100.0	10	1 CX81_CANFA	P61904 canis famil
C 5	3	100.0	10	2 Q50843	Q50843 methanococ
C 6	3	100.0	10	2 Q78225	Q78225 neurospora
C 7	3	100.0	10	2 Q9SM70	Q9SM70 trichosurus
C 8	3	100.0	10	2 Q8SAC2	Q8SAC2 amblystegiu
C 9	3	100.0	10	2 Q9S905	Q9S905 glycine max
C 10	3	100.0	11	2 Q9C1R7	Q9C1R7 saccharomyc
C 11	3	100.0	11	2 Q7M374	Q7M374 bos taurus
C 12	3	100.0	11	2 Q9UEX7	Q9UEX7 homo sapien
C 13	3	100.0	11	2 Q68QV9	Q68QV9 escherichia
C 14	3	100.0	11	2 Q7MOD4	Q7MOD4 rattus norv
C 15	3	100.0	11	2 Q84247	Q84247 polyomaviru
C 16	3	100.0	12	1 TKN_KASSE	P08611 kassina sen

17	3	100.0	12	2 Q8J0A7	Q8J0A7 saccharomyc
C 18	3	100.0	12	2 Q7M4X9	Q7M4X9 fusarium sp
C 19	3	100.0	12	2 Q96PH0	Q96PH0 homo sapien
C 20	3	100.0	12	2 Q31851	Q31851 arabidopsis
C 21	3	100.0	12	2 Q6JC67	Q6JC67 glycine max
C 22	3	100.0	13	2 Q9UE87	Q9UE87 homo sapien
C 23	3	100.0	13	2 Q6SE60	Q6SE60 drosophila
C 24	3	100.0	13	2 Q7RAS8	Q7RAS8 plasmodium
C 25	3	100.0	13	2 Q93980	Q93980 brassica ol
C 26	3	100.0	13	2 Q6URV3	Q6URV3 sorghum bic
C 27	3	100.0	13	2 Q62352	Q62352 mus musculu
C 28	3	100.0	13	2 Q62354	Q62354 mus musculu
C 29	3	100.0	13	2 Q62355	Q62355 mus musculu
C 30	3	100.0	13	2 Q9FWP4	Q9FWP4 diosotichu
C 31	3	100.0	14	1 FERT_TOBAC	P82150 nicotiana t
C 32	3	100.0	14	1 UC34_MAIZE	P80640 zea mays (m
C 33	3	100.0	14	2 Q6JDV5	Q6JDV5 sus scrofa
C 34	3	100.0	14	2 Q9TRQ7	Q9TRQ7 bos taurus
C 35	3	100.0	14	2 Q714T6	Q714T6 prymnesium
C 36	3	100.0	14	2 Q9MRT8	Q9MRT8 alooe vera (
C 37	3	100.0	14	2 Q9MRV1	Q9MRV1 allium sati
C 38	3	100.0	14	2 Q9MRV4	Q9MRV4 allium porr
C 39	3	100.0	14	2 Q9MT61	Q9MT61 allium cepa
C 40	3	100.0	14	2 Q64224	Q64224 brachyheci
C 41	3	100.0	14	2 Q64225	Q64225 brachyheci
C 42	3	100.0	14	2 Q64228	Q64228 brachyheci
C 43	3	100.0	14	2 Q643A0	Q643A0 brachyheci
C 44	3	100.0	14	2 Q7M1G6	Q7M1G6 avena sativ
C 45	3	100.0	14	2 Q7M1G7	Q7M1G7 avena sativ
C 46	3	100.0	14	2 Q9FUX5	Q9FUX5 symphoricar
C 47	3	100.0	14	2 Q8VU21	Q8VU21 streptococ
C 48	3	100.0	14	2 Q711Z6	Q711Z6 lactobacill
C 49	3	100.0	15	2 Q9UR64	Q9UR64 pleurotus o
C 50	3	100.0	15	2 Q9MZRS	Q9MZRS oryctolagus
C 51	3	100.0	15	2 Q9TNQ5	Q9TNQ5 mus sp. maj
C 52	3	100.0	15	2 Q6XBM6	Q6XBM6 platylomell
C 53	3	100.0	15	2 Q76MM2	Q76MM2 eurypharynx
C 54	3	100.0	15	2 Q93LE6	Q93LE6 chloroflex
C 55	3	100.0	15	2 Q6QOR4	Q6QOR4 helicobacte
C 56	3	100.0	15	2 Q8R5G1	Q8R5G1 spermophili
C 57	3	100.0	16	1 CERB_PIG	P63181 sus scrofa
C 58	3	100.0	16	1 CERB_RAT	P63182 rattus norv
C 59	3	100.0	16	1 MMPX_SOLTU	P80501 solanum tub
C 60	3	100.0	16	2 Q9UWK4	Q9UWK4 methanobact
C 61	3	100.0	16	2 Q8J1R1	Q8J1R1 saccharomyc
C 62	3	100.0	16	2 Q6NSY3	Q6NSY3 homo sapien
C 63	3	100.0	16	2 Q7RJE1	Q7RJE1 plasmodium
C 64	3	100.0	16	2 Q6LCS7	Q6LCS7 bos taurus
C 65	3	100.0	16	2 Q92732	P92732 fejevarya
C 66	3	100.0	16	2 Q6XBM8	Q6XBM8 platylomell
C 67	3	100.0	16	2 Q680Q0	Q680Q0 arabidopsis
C 68	3	100.0	16	2 Q9S8H7	Q9S8H7 pinus conto
C 69	3	100.0	16	2 Q9R5S7	Q9R5S7 treponema d
C 70	3	100.0	16	2 Q9QV11	Q9QV11 rattus sp.
C 71	3	100.0	16	2 Q9PSL6	Q9PSL6 gallus gall
C 72	3	100.0	17	2 Q50842	Q50842 methanococ
C 73	3	100.0	17	2 Q78490	Q78490 homo sapien
C 74	3	100.0	17	2 Q96DJ6	Q96DJ6 homo sapien
C 75	3	100.0	17	2 Q6XBM7	Q6XBM7 platylomell
C 76	3	100.0	17	2 Q9S889	Q9S889 narcissus p
C 77	3	100.0	17	2 Q6LEF2	Q6LEF2 streptococ
C 78	3	100.0	17	2 Q8GJN9	Q8GJN9 lactococcus
C 79	3	100.0	17	2 Q98Y55	Q98Y55 newcastle d
C 80	3	100.0	17	2 Q90XE2	Q90XE2 gallus gall
C 81	3	100.0	18	2 Q789C7	Q789C7 neurospora
C 82	3	100.0	18	2 Q8SQ45	Q8SQ45 oryctolagus
C 83	3	100.0	18	2 Q30216	Q30216 homo sapien
C 84	3	100.0	18	2 Q9TNP1	Q9TNP1 mus sp. .m
C 85	3	100.0	18	2 Q37852	Q37852 bacterioph
C 86	3	100.0	18	2 Q10722	Q10722 engelmannia
C 87	3	100.0	18	2 Q6URV5	Q6URV5 sorghum bic
C 88	3	100.0	18	2 Q06514	Q06514 escherichia
C 89	3	100.0	18	2 Q53503	Q53503 lactobacill

90	3	100.0	18	2	Q9QW64	Q9qwg4 mus musculus	163	3	100.0	21	2	O25621	O25621 helicobacte
91	3	100.0	18	2	Q9WUQ6	Q9wug6 mus musculus	164	3	100.0	21	2	Q6RSN3	Q6rsn3 mus musculus
c 92	3	100.0	18	2	O13167	O13167 xiphias gla	165	3	100.0	21	2	Q9QUW4	Q9quw4 mus sp. a
c 93	3	100.0	19	1	TLB1_BONJA	P81882 bothrops ja	166	3	100.0	22	2	Q8NHD8	Q8nhd8 homo sapien
c 94	3	100.0	19	2	Q6PKG8	Q6pkg8 homo sapien	c 167	3	100.0	22	2	Q9UCE2	Q9uce2 homo sapien
c 95	3	100.0	19	2	Q9H2B3	Q9h2b3 homo sapien	168	3	100.0	22	2	Q9UN58	Q9un58 homo sapien
c 96	3	100.0	19	2	Q68M63	Q68m63 ciona intes	c 169	3	100.0	22	2	O04123	O04123 plaiemodum
97	3	100.0	19	2	Q9TWK9	Q9twk9 trypanosoma	c 170	3	100.0	22	2	Q8WSF0	Q8wsf0 trichinella
98	3	100.0	19	2	Q97584	Q97584 macaca mula	171	3	100.0	22	2	Q7PDX3	Q7pdx3 anopheles g
99	3	100.0	19	2	Q9TRR6	Q9trr6 oryctolagus	172	3	100.0	22	2	O8HZJ1	O8hzj1 sus scrofa
100	3	100.0	19	2	Q7X8N0	Q7x8n0 zea mays (m	c 173	3	100.0	22	2	Q7M3F1	Q7m3f1 bos taurus
101	3	100.0	19	2	Q9S8E9	Q9s8e9 zea mays (m	174	3	100.0	22	2	Q9GM95	Q9gm95 sus scrofa
102	3	100.0	19	2	Q7WVV3	Q7wvv3 streptococc	175	3	100.0	22	2	Q9TRC4	Q9trc4 canis famil
103	3	100.0	19	2	Q9R4T9	Q9r4t9 bacillus th	176	3	100.0	22	2	Q6XEN1	Q6xen1 pyrrhobartle
104	3	100.0	19	2	Q6LRE8	Q6le88 rattus norv	177	3	100.0	22	2	Q85G98	Q85g98 pyrrhobartle
105	3	100.0	19	2	Q7M068	Q7m068 rattus norv	178	3	100.0	22	2	Q9TC82	Q9tc82 centropomus
c 106	3	100.0	19	2	Q9QV70	Q9qv70 rattus sp.	179	3	100.0	22	2	Q9TC84	Q9tc84 centropomus
107	3	100.0	19	2	Q9PS70	Q9ps70 gallus gall	180	3	100.0	22	2	O42047	O42047 arabidopsis
c 108	3	100.0	19	2	Q905E4	Q905e4 human immun	181	3	100.0	22	2	Q7X8M9	Q7x8m9 zea mays (m
c 109	3	100.0	19	2	Q905F2	Q905f2 human immun	182	3	100.0	22	2	O56233	O56233 thermus aqu
c 110	3	100.0	19	2	Q905G0	Q905g0 human immun	c 183	3	100.0	22	2	Q9R4N9	Q9r4n9 brevudimon
c 111	3	100.0	19	2	Q905G8	Q905g8 human immun	c 184	3	100.0	22	2	O9R4Q3	O9r4q3 pseudomonas
c 112	3	100.0	19	2	Q905H2	Q905h2 human immun	c 185	3	100.0	22	2	O64970	O64970 alfalfa mos
c 113	3	100.0	19	2	Q905I4	Q905i4 human immun	186	3	100.0	22	2	Q87084	Q87084 suid herpes
c 114	3	100.0	19	2	Q905K4	Q905k4 human immun	187	3	100.0	22	2	O87085	Q87085 suid herpes
c 115	3	100.0	19	2	Q905K8	Q905k8 human immun	c 188	3	100.0	22	2	Q9PXB4	Q9pXB4 duck hepati
c 116	3	100.0	19	2	Q90R11	Q90r11 human immun	189	3	100.0	22	2	O91101	O91101 morone saxa
c 117	3	100.0	20	1	CPBX_CAVPO	P34033 cavia porce	190	3	100.0	23	2	P78489	P78489 homo sapien
c 118	3	100.0	20	1	CK81_THUOB	P80983 thunnus obe	191	3	100.0	23	2	Q9HCW9	Q9hcw9 homo sapien
c 119	3	100.0	20	1	OMP1_ACTAC	P20242 actinobacil	c 192	3	100.0	23	2	Q9UCE3	Q9uce3 homo sapien
120	3	100.0	20	1	VSPI_AGRBI	P33588 agkistrodon	193	3	100.0	23	2	O25137	O25137 haliotis ru
121	3	100.0	20	2	O8J1R0	O8j1r0 saccharomyc	194	3	100.0	23	2	Q86MM6	Q86mm6 pecten maxi
122	3	100.0	20	2	Q96A79	Q96a79 homo sapien	c 195	3	100.0	23	2	O8MIP9	O8mip9 ovis aries
123	3	100.0	20	2	Q7M4Q3	Q7m4q3 homo sapien	c 196	3	100.0	23	2	O28131	O28131 bos taurus
124	3	100.0	20	2	Q9UCB1	Q9ucb1 homo sapien	c 197	3	100.0	23	2	O9GLD1	O9glD1 bos taurus
c 125	3	100.0	20	2	Q9UCR9	Q9ucr9 homo sapien	198	3	100.0	23	2	Q6XBM9	Q6xbm9 vittia sali
c 126	3	100.0	20	2	O9UCR9	Q9ucr9 homo sapien	199	3	100.0	23	2	Q6XBN0	Q6xbn0 vittia sali
127	3	100.0	20	2	O41122	O41122 plasmodium	200	3	100.0	23	2	Q6XBN3	Q6xbn3 vittia pach
128	3	100.0	20	2	O6LBT5	O6lbt5 bos taurus	201	3	100.0	23	2	O8SAB8	O8sab8 vittia elim
129	3	100.0	20	2	Q7M3D6	Q7m3d6 equus cabal	202	3	100.0	23	2	O8SAC4	O8sac4 amblystegiu
130	3	100.0	20	2	Q9TQO8	Q9tqo8 oryctolagus	c 203	3	100.0	23	2	O6URS8	O6urs8 sorghum bic
131	3	100.0	20	2	Q9TRH8	Q9trh8 oryctolagus	c 204	3	100.0	23	2	Q71V79	Q71v79 arabidopsis
132	3	100.0	20	2	O19618	O19618 homo sapien	205	3	100.0	23	2	Q7X8T2	Q7x8t2 zea mays (m
133	3	100.0	20	2	O19620	O19620 homo sapien	206	3	100.0	23	2	Q9S893	Q9s893 arachis hyp
c 134	3	100.0	20	2	O6URV2	O6urv2 sorghum bic	207	3	100.0	23	2	O9S8G1	O9s8g1 populus tre
135	3	100.0	20	2	Q7X8M7	Q7x8m7 zea mays (m	208	3	100.0	23	2	O50301	O50301 bacillus st
c 136	3	100.0	20	2	Q9R4I9	Q9r4i9 vibrio chol	209	3	100.0	23	2	O6LEQ9	O6leq9 streptococc
137	3	100.0	20	2	Q8K4F4	Q8k4f4 mus musculus	210	3	100.0	23	2	O9AIL1	O9ail1 magnetospir
138	3	100.0	20	2	Q9R2A3	Q9r2a3 mus musculus	211	3	100.0	23	2	O91V21	O91v21 rattus norv
139	3	100.0	20	2	Q9IF53	Q9if53 newcastle d	212	3	100.0	23	2	Q91ZE2	Q91ze2 rattus norv
140	3	100.0	20	2	Q9PXE4	Q9pxe4 foot-and-mo	213	3	100.0	23	2	O62594	O62594 rattus leuc
141	3	100.0	21	1	GTE2_PSEPU	P82998 pseudomonas	214	3	100.0	23	2	O6LAD4	O6lad4 rattus norv
142	3	100.0	21	2	Q8TDP4	Q8tdp4 homo sapien	215	3	100.0	23	2	Q6S983	Q6s983 suid herpes
143	3	100.0	21	2	Q86UF6	Q86uf6 homo sapien	216	3	100.0	23	2	Q69391	Q69391 suid herpes
144	3	100.0	21	2	Q9P221	Q9p221 homo sapien	217	3	100.0	23	2	Q69392	Q69392 suid herpes
c 145	3	100.0	21	2	Q9TR71	Q9tr71 ursus arcto	218	3	100.0	23	2	Q69393	Q69393 suid herpes
146	3	100.0	21	2	Q9T2H2	Q9t2h2 dunaliella	219	3	100.0	23	2	Q69395	Q69395 suid herpes
c 147	3	100.0	21	2	Q41181	Q41181 nicotiana t	220	3	100.0	23	2	O87078	O87078 suid herpes
c 148	3	100.0	21	2	Q41559	Q41559 triticum ae	221	3	100.0	23	2	Q87079	Q87079 suid herpes
c 149	3	100.0	21	2	Q41564	Q41564 triticum ae	222	3	100.0	23	2	Q87080	Q87080 suid herpes
c 150	3	100.0	21	2	Q41565	Q41565 triticum ae	223	3	100.0	23	2	Q87081	Q87081 suid herpes
c 151	3	100.0	21	2	Q41566	Q41566 triticum ae	224	3	100.0	23	2	Q87082	Q87082 suid herpes
c 152	3	100.0	21	2	O42417	O42417 triticum ae	225	3	100.0	23	2	Q87083	Q87083 suid herpes
c 153	3	100.0	21	2	Q42501	Q42501 triticum ae	226	3	100.0	23	2	O87086	Q87086 suid herpes
c 154	3	100.0	21	2	Q6URT5	Q6urt5 sorghum bic	c 227	3	100.0	24	1	BOMN_BONVA	B01505 bombina var
c 155	3	100.0	21	2	Q7X8M8	Q7x8m8 zea mays (m	c 228	3	100.0	24	1	BRIA_RANLU	P82825 rana luteiv
c 156	3	100.0	21	2	Q9S786	Q9s786 triticum ae	c 229	3	100.0	24	1	BRIE_RANLU	P82826 rana luteiv
c 157	3	100.0	21	2	Q9S8P6	Q9s8p6 pisum sativ	c 230	3	100.0	24	1	CH60_ACICA	P81874 acinetobact
158	3	100.0	21	2	O44611	O44611 buchnera ap	231	3	100.0	24	1	GTE_PSEUF	P82997 pseudomonas
159	3	100.0	21	2	Q79DV3	Q79dv3 escherichia	232	3	100.0	24	2	O6LDJ0	O6ldj0 homo sapien
160	3	100.0	21	2	Q7M123	Q7m123 bacteroides	233	3	100.0	24	2	Q71UK6	Q71uk6 homo sapien
161	3	100.0	21	2	Q9L4S9	Q9l4s9 salmonella	234	3	100.0	24	2	Q7LDT3	Q7ldt3 homo sapien
162	3	100.0	21	2	Q9R4R7	Q9r4r7 streptomyce	235	3	100.0	24	2	Q7Z5M2	Q7z5m2 homo sapien

c 236	3	100.0	24	2	Q659N7	Q658n7 homo sapien	309	3	100.0	25	2	Q9TWN4	Q9twn4 theileria s
c 237	3	100.0	24	2	Q8WT34	Q8wt34 leishmania	310	3	100.0	25	2	Q64FD9	Q64fd9 toxoplasma
c 238	3	100.0	24	2	Q94368	Q94368 caenorhabdi	311	3	100.0	25	2	Q708G1	Q708g1 ovis aries
c 239	3	100.0	24	2	Q7M4H2	Q7m4h2 limulus pol	312	3	100.0	25	2	Q33292	Q33292 zea mays (m
c 240	3	100.0	24	2	Q19654	Q19654 homo sapien	313	3	100.0	25	2	Q76EK5	Q76ek5 auxis roche
c 241	3	100.0	24	2	Q70P01	Q70p01 homo sapien	314	3	100.0	25	2	Q8RV05	Q8rv05 amblystegiu
c 242	3	100.0	24	2	Q7J3FH7	Q7j3fh7 homo sapien	315	3	100.0	25	2	Q8SAC3	Q8sac3 amblystegiu
c 243	3	100.0	24	2	Q9MY32	Q9my32 homo sapien	316	3	100.0	25	2	Q8SAC6	Q8sac6 amblystegiu
c 244	3	100.0	24	2	Q9TNN9	Q9tnn9 homo sapien	317	3	100.0	25	2	Q8SAC8	Q8sac8 amblystegiu
c 245	3	100.0	24	2	Q9TP00	Q9tp00 homo sapien	c 318	3	100.0	25	2	Q6QVF4	Q6qv4 phaseolus v
c 246	3	100.0	24	2	Q9TQ80	Q9tq80 homo sapien	c 319	3	100.0	25	2	Q6QVG0	Q6qv0 phaseolus v
c 247	3	100.0	24	2	Q9UQU2	Q9uqu2 homo sapien	c 320	3	100.0	25	2	Q6QVG3	Q6qv3 phaseolus v
c 248	3	100.0	24	2	Q79910	Q79910 chamaeleo f	c 321	3	100.0	25	2	Q6QVG9	Q6qv9 phaseolus v
c 249	3	100.0	24	2	Q8SH84	Q8sh84 brookesia t	c 322	3	100.0	25	2	Q6QVH7	Q6qvh7 phaseolus v
c 250	3	100.0	24	2	Q8SH89	Q8sh89 brookesia t	c 323	3	100.0	25	2	Q6QVI2	Q6qvi2 phaseolus v
c 251	3	100.0	24	2	Q8SH95	Q8sh95 brookesia p	c 324	3	100.0	25	2	Q6QVI8	Q6qvi8 phaseolus v
c 252	3	100.0	24	2	Q8SHA1	Q8sha1 brookesia n	c 325	3	100.0	25	2	Q6QVJ9	Q6qv9 phaseolus v
c 253	3	100.0	24	2	Q8SHB0	Q8shb0 rhaphioleio	c 326	3	100.0	25	2	Q6QVK4	Q6qv4 phaseolus v
c 254	3	100.0	24	2	Q8SHB6	Q8shb6 furcifer ve	327	3	100.0	25	2	Q9AT69	Q9at69 coffea arab
c 255	3	100.0	24	2	Q8SHB9	Q8shb9 furcifer ou	328	3	100.0	25	2	Q44606	Q44606 buchnera ap
c 256	3	100.0	24	2	Q8SHC2	Q8shc2 furcifer la	329	3	100.0	25	2	Q6WVH1	Q6wvh1 actinomadar
c 257	3	100.0	24	2	Q8SHC5	Q8shc5 furcifer la	330	3	100.0	25	2	Q7DJ11	Q7dj11 salmonella
c 258	3	100.0	24	2	Q8SHC8	Q8shc8 furcifer be	331	3	100.0	25	2	Q7M0X0	Q7m0x0 streptomyc
c 259	3	100.0	24	2	Q8SHD1	Q8shd1 furcifer ba	332	3	100.0	25	2	Q840F9	Q840f9 chlamydia t
c 260	3	100.0	24	2	Q8SHD4	Q8shd4 chamaeleo w	333	3	100.0	25	2	Q9S0U6	Q9s0u6 shigella so
c 261	3	100.0	24	2	Q8SHE6	Q8she6 chamaeleo q	334	3	100.0	25	2	P72429	P72429 salmonella
c 262	3	100.0	24	2	Q8SHE9	Q8she9 chamaeleo p	335	3	100.0	25	2	Q7DAR1	Q7dar1 salmonella
c 263	3	100.0	24	2	Q8SHF2	Q8shf2 chamaeleo n	c 336	3	100.0	25	2	Q62533	Q62533 mus spretus
c 264	3	100.0	24	2	Q8SHF5	Q8shf5 chamaeleo m	337	3	100.0	25	2	Q71V84	Q71v84 mus musculu
c 265	3	100.0	24	2	Q8SHF8	Q8shf8 chamaeleo m	338	3	100.0	25	2	Q9JKY4	Q9jky4 mus musculu
c 266	3	100.0	24	2	Q8SHG1	Q8shg1 chamaeleo j	339	3	100.0	25	2	Q80J43	Q80j43 oyster noro
c 267	3	100.0	24	2	Q8SHG4	Q8shg4 chamaeleo j	340	3	100.0	25	2	Q80J44	Q80j44 oyster noro
c 268	3	100.0	24	2	Q8SHH3	Q8shh3 chamaeleo f	341	3	100.0	25	2	Q80J46	Q80j46 oyster noro
c 269	3	100.0	24	2	Q8SHH6	Q8shh6 chamaeleo f	c 342	3	100.0	26	2	Q9UWG7	Q9uwg7 sulfolobus
c 270	3	100.0	24	2	Q8SHI2	Q8shi2 chamaeleo d	343	3	100.0	26	2	Q8ZZV3	Q8zzv3 pyrobaculum
c 271	3	100.0	24	2	Q8SHI5	Q8shi5 chamaeleo c	344	3	100.0	26	2	Q9HFN6	Q9hfn6 candida rug
c 272	3	100.0	24	2	Q8SHJ7	Q8shj7 calumma par	345	3	100.0	26	2	Q6LDI0	Q6ldi0 homo sapien
c 273	3	100.0	24	2	Q8SHK0	Q8shk0 calumma osh	346	3	100.0	26	2	Q9NP34	Q9np34 homo sapien
c 274	3	100.0	24	2	Q8SHK3	Q8shk3 calumma nas	c 347	3	100.0	26	2	Q77226	Q77226 helix asper
c 275	3	100.0	24	2	Q8SHK6	Q8shk6 calumma hil	348	3	100.0	26	2	P90723	P90723 berce ovata
c 276	3	100.0	24	2	Q8SHK9	Q8shk9 calumma glo	c 349	3	100.0	26	2	Q9BLZ9	Q9blz9 macrotrache
c 277	3	100.0	24	2	Q8SHL5	Q8shl5 calumma fur	350	3	100.0	26	2	Q9NBB1	Q9nbb1 drosophila
c 278	3	100.0	24	2	Q8SHL8	Q8shl8 calumma cuc	351	3	100.0	26	2	Q64FE3	Q64fe3 toxoplasma
c 279	3	100.0	24	2	Q8SHM1	Q8shm1 calumma bre	c 352	3	100.0	26	2	Q8SP22	Q8sp22 macaca mula
c 280	3	100.0	24	2	Q8SHM4	Q8shm4 calumma boe	353	3	100.0	26	2	Q79883	Q79883 anolis pate
c 281	3	100.0	24	2	Q8SHM7	Q8shm7 bradypodion	354	3	100.0	26	2	P92614	P92614 aspidosceli
c 282	3	100.0	24	2	Q8SHN0	Q8shn0 bradypodion	355	3	100.0	26	2	P92652	P92652 euprepis au
c 283	3	100.0	24	2	Q8SHN3	Q8shn3 bradypodion	356	3	100.0	26	2	P92772	P92772 xantusia vi
c 284	3	100.0	24	2	Q8SHN6	Q8shn6 bradypodion	357	3	100.0	26	2	Q8SIU0	Q8siu0 xantusia ar
c 285	3	100.0	24	2	Q8SHN9	Q8shn9 bradypodion	358	3	100.0	26	2	Q8SIU3	Q8siu3 xantusia be
c 286	3	100.0	24	2	Q8SHP2	Q8shp2 bradypodion	359	3	100.0	26	2	Q8SIU6	Q8siu6 xantusia he
c 287	3	100.0	24	2	Q8SK10	Q8sk10 furcifer ca	360	3	100.0	26	2	Q6WBP2	Q6wbp2 scelopor
c 288	3	100.0	24	2	Q83270	Q83270 bacterioph	361	3	100.0	26	2	Q6WBS2	Q6wbs2 scelopor
c 289	3	100.0	24	2	Q8SAC1	Q8sac1 amblystegiu	362	3	100.0	26	2	Q6WBS3	Q6wbs3 phrynosoma
c 290	3	100.0	24	2	Q8SAC7	Q8sac7 amblystegiu	363	3	100.0	26	2	Q71DS0	Q71ds0 leioccephalu
c 291	3	100.0	24	2	Q6K426	Q6k426 oryza sativ	364	3	100.0	26	2	Q71DY3	Q71dy3 prietadacty
c 292	3	100.0	24	2	Q6URS9	Q6urs9 sorghum bic	365	3	100.0	26	2	Q71DZ2	Q71dz2 diplolaemus
c 293	3	100.0	24	2	Q9S8G2	Q9s8g2 maclura pom	366	3	100.0	26	2	Q71DZ5	Q71dz5 diplolaemus
c 294	3	100.0	24	2	Q8RIC0	Q8ric0 fusobacteri	367	3	100.0	26	2	Q71DZ8	Q71dz8 anolis sagr
c 295	3	100.0	24	2	Q9P899	Q9p899 mus musculu	368	3	100.0	26	2	Q71E04	Q71e04 anolis dist
c 296	3	100.0	24	2	Q7TQ64	Q7tq64 mus musculu	369	3	100.0	26	2	Q71E07	Q71e07 anolis cris
c 297	3	100.0	24	2	Q69137	Q69137 human herpe	370	3	100.0	26	2	Q71E10	Q71e10 anolis cybo
c 298	3	100.0	24	2	Q788Q0	Q788q0 xenopus lae	371	3	100.0	26	2	Q71E16	Q71e16 brachylophu
c 299	3	100.0	25	2	Q7M4X3	Q7m4x3 acromonium	372	3	100.0	26	2	Q71E25	Q71e25 corytophane
c 300	3	100.0	25	2	Q96Q67	Q96q67 homo sapien	373	3	100.0	26	2	Q71E34	Q71e34 phymaturus
c 301	3	100.0	25	2	Q9UCR8	Q9ucr8 homo sapien	374	3	100.0	26	2	Q71E37	Q71e37 phymaturus
c 302	3	100.0	25	2	Q9UL44	Q9ul44 homo sapien	375	3	100.0	26	2	Q76EJ9	Q76ej9 auxis roche
c 303	3	100.0	25	2	Q8IA15	Q8ia15 perionyx ex	376	3	100.0	26	2	Q85C11	Q85c11 pyrrhobryum
c 304	3	100.0	25	2	Q8MWU6	Q8mwu6 eisenia and	377	3	100.0	26	2	Q85C12	Q85c12 pyrrhobryum
c 305	3	100.0	25	2	Q8SZG6	Q8szg6 drosophila	378	3	100.0	26	2	Q85CJ7	Q85cj7 pyrrhobryum
c 306	3	100.0	25	2	Q9NM60	Q9nm60 sagitta sp.	379	3	100.0	26	2	Q85G89	Q85g89 pyrrhobryum
c 307	3	100.0	25	2	Q9TWE4	Q9twe4 lumbricus t	380	3	100.0	26	2	Q85G93	Q85g93 pyrrhobryum
c 308	3	100.0	25	2	Q9TWH1	Q9twh1 aplysia cal	381	3	100.0	26	2	Q9T8X9	Q9t8x9 phymaturus

382	3	100.0	26	2	Q9ZYS8	Q9ZYS8 stenocercus	455	3	100.0	27	2	O19703	O19703 homo sapien
383	3	100.0	26	2	Q9ZYT1	Q9ZYT1 phymaturus	456	3	100.0	27	2	O67A92	O67A92 homo sapien
384	3	100.0	26	2	Q9ZYT4	Q9ZYT4 leioccephalu	457	3	100.0	27	2	O67A93	O67A93 homo sapien
385	3	100.0	26	2	Q8RV97	Q8RV97 amblystegiu	458	3	100.0	27	2	O67A94	O67A94 homo sapien
386	3	100.0	26	2	O8SAC5	O8SAC5 amblystegiu	459	3	100.0	27	2	O67A95	O67A95 homo sapien
387	3	100.0	26	2	O8SAD0	O8SAD0 amblystegiu	460	3	100.0	27	2	O67A96	O67A96 homo sapien
388	3	100.0	26	2	O8SAD1	O8SAD1 amblystegiu	461	3	100.0	27	2	O67A97	O67A97 homo sapien
389	3	100.0	26	2	O8SAD5	O8SAD5 amblystegiu	462	3	100.0	27	2	O67A98	O67A98 homo sapien
390	3	100.0	26	2	Q9RSF2	Q9RSF2 thriobacillu	463	3	100.0	27	2	O67A99	O67A99 homo sapien
391	3	100.0	26	2	Q9Z424	Q9Z424 pseudomonas	464	3	100.0	27	2	O67AA0	O67AA0 homo sapien
392	3	100.0	26	2	O63408	O63408 rattus norv	465	3	100.0	27	2	O67AA1	O67AA1 homo sapien
393	3	100.0	26	2	O6LCB3	O6LCB3 mus musculu	466	3	100.0	27	2	O67AA2	O67AA2 homo sapien
394	3	100.0	26	2	O6LCE0	O6LCE0 mus musculu	467	3	100.0	27	2	O67AA3	O67AA3 homo sapien
395	3	100.0	26	2	O6LEI5	O6LEI5 rattus norv	468	3	100.0	27	2	O67AA4	O67AA4 homo sapien
C 396	3	100.0	26	2	Q9QVG9	Q9QVG9 rattus sp.	469	3	100.0	27	2	O67AA5	O67AA5 homo sapien
397	3	100.0	26	2	Q788Q1	Q788Q1 xenopus lae	470	3	100.0	27	2	O67AA6	O67AA6 homo sapien
C 398	3	100.0	26	2	O8AWR9	O8AWR9 stomatorhin	471	3	100.0	27	2	O67AA7	O67AA7 homo sapien
C 399	3	100.0	26	2	O8AWS0	O8AWS0 stomatorhin	472	3	100.0	27	2	O67AA8	O67AA8 homo sapien
C 400	3	100.0	26	2	O8AWS1	O8AWS1 stomatorhin	473	3	100.0	27	2	O67AA9	O67AA9 homo sapien
C 401	3	100.0	26	2	O8AWS2	O8AWS2 pollimyryus	474	3	100.0	27	2	O67AB0	O67AB0 homo sapien
C 402	3	100.0	26	2	O8AWS3	O8AWS3 pollimyryus	475	3	100.0	27	2	O67AB1	O67AB1 homo sapien
C 403	3	100.0	26	2	O8AWS4	O8AWS4 pollimyryus	476	3	100.0	27	2	O67AB2	O67AB2 homo sapien
C 404	3	100.0	26	2	O8AWS5	O8AWS5 pollimyryus	477	3	100.0	27	2	O67AB3	O67AB3 homo sapien
C 405	3	100.0	26	2	O8AWS6	O8AWS6 pollimyryus	478	3	100.0	27	2	O67AB4	O67AB4 homo sapien
C 406	3	100.0	26	2	O8AWS7	O8AWS7 paramormyro	479	3	100.0	27	2	O67AB5	O67AB5 homo sapien
C 407	3	100.0	26	2	O8AWS8	O8AWS8 myomyryus ma	480	3	100.0	27	2	O67AB6	O67AB6 homo sapien
C 408	3	100.0	26	2	O8AWS9	O8AWS9 mormyryus ru	481	3	100.0	27	2	O67AB7	O67AB7 homo sapien
C 409	3	100.0	26	2	O8AWT0	O8AWT0 mormyryus ov	482	3	100.0	27	2	O67AB8	O67AB8 homo sapien
C 410	3	100.0	26	2	O8AWT1	O8AWT1 mormyrops m	483	3	100.0	27	2	O67AB9	O67AB9 homo sapien
C 411	3	100.0	26	2	O8AWT2	O8AWT2 mormyrops z	484	3	100.0	27	2	O67AC0	O67AC0 homo sapien
C 412	3	100.0	26	2	O8AWT3	O8AWT3 mormyrops n	485	3	100.0	27	2	O67AC1	O67AC1 homo sapien
C 413	3	100.0	26	2	O8AWT4	O8AWT4 marcusenius	486	3	100.0	27	2	O67AC2	O67AC2 homo sapien
C 414	3	100.0	26	2	O8AWT5	O8AWT5 marcusenius	487	3	100.0	27	2	O67AC3	O67AC3 homo sapien
C 415	3	100.0	26	2	O8AWT6	O8AWT6 marcusenius	488	3	100.0	27	2	O67AC4	O67AC4 homo sapien
C 416	3	100.0	26	2	O8AWT7	O8AWT7 marcusenius	489	3	100.0	27	2	O79886	O79886 basiliscus
C 417	3	100.0	26	2	O8AWT8	O8AWT8 marcusenius	490	3	100.0	27	2	O79889	O79889 crotophytus
C 418	3	100.0	26	2	O8AWT9	O8AWT9 ivindomyryus	491	3	100.0	27	2	O79892	O79892 gambelia wi
C 419	3	100.0	26	2	O8AWU0	O8AWU0 isichtiys h	492	3	100.0	27	2	O79895	O79895 hoplocercus
C 420	3	100.0	26	2	O8AWU1	O8AWU1 hippopotamy	493	3	100.0	27	2	O79898	O79898 lioiaemus p
C 421	3	100.0	26	2	O8AWU2	O8AWU2 hyperopisus	494	3	100.0	27	2	O79901	O79901 oplurus cuv
C 422	3	100.0	26	2	O8AWU3	O8AWU3 hippopotamy	495	3	100.0	27	2	O79904	O79904 phrynosoma
C 423	3	100.0	26	2	O8AWU4	O8AWU4 hippopotamy	496	3	100.0	27	2	O79907	O79907 sauromalus
C 424	3	100.0	26	2	O8AWU5	O8AWU5 gnathonemus	497	3	100.0	27	2	P92574	P92574 bipes bipor
C 425	3	100.0	26	2	O8AWU6	O8AWU6 genyomyryus	498	3	100.0	27	2	P92630	P92630 eremias gra
C 426	3	100.0	26	2	O8AWU7	O8AWU7 campylomorm	499	3	100.0	27	2	P92705	P92705 platysaurus
C 427	3	100.0	26	2	O8AWU8	O8AWU8 campylomorm	500	3	100.0	27	2	Q8W7G5	Q8W7G5 lioiaemus m
C 428	3	100.0	26	2	O8AWU9	O8AWU9 campylomorm							
C 429	3	100.0	26	2	O8AWV0	O8AWV0 campylomorm							
C 430	3	100.0	26	2	O8AWV1	O8AWV1 brienomyryus							
C 431	3	100.0	26	2	O8AWV2	O8AWV2 brienomyryus							
C 432	3	100.0	26	2	O8AWV3	O8AWV3 brienomyryus							
C 433	3	100.0	26	2	O8AWV4	O8AWV4 brienomyryus							
C 434	3	100.0	26	2	O8AWV5	O8AWV5 brienomyryus							
C 435	3	100.0	26	2	O8AWV6	O8AWV6 boulengerom							
C 436	3	100.0	27	1	PSBY_FUCVE	Q9BAC7 fucus vesic							
C 437	3	100.0	27	1	SODM_DSSEDE	P11419 desulfovibr							
C 438	3	100.0	27	2	Q7SEU3	Q7SEU3 neurospora							
C 439	3	100.0	27	2	Q8WTR6	Q8WTR6 homo sapien							
C 440	3	100.0	27	2	Q96EQ2	Q96EQ2 homo sapien							
C 441	3	100.0	27	2	Q7Z700	Q7Z700 homo sapien							
C 442	3	100.0	27	2	Q9BS88	Q9BS88 homo sapien							
C 443	3	100.0	27	2	Q9UEF5	Q9UEF5 homo sapien							
C 444	3	100.0	27	2	Q96889	Q96889 sacculina c							
C 445	3	100.0	27	2	Q25584	Q25584 oikopleura							
C 446	3	100.0	27	2	Q8WTK5	Q8WTK5 aurelia aur							
C 447	3	100.0	27	2	Q94448	Q94448 chaetopteru							
C 448	3	100.0	27	2	Q69H26	Q69H26 symagittif							
C 449	3	100.0	27	2	Q7RBB1	Q7RBB1 plasmodium							
C 450	3	100.0	27	2	Q9BME3	Q9BME3 oxytricha t							
C 451	3	100.0	27	2	Q9Y181	Q9Y181 priapulius c							
C 452	3	100.0	27	2	Q29019	Q29019 sus scrofa							
C 453	3	100.0	27	2	Q9WZR2	Q9WZR2 oryctolagus							
C 454	3	100.0	27	2	O19501	O19501 homo sapien							

ALIGNMENTS

RESULT 1
 RS1_ERWCH
 ID RS1_ERWCH STANDARD; PRT; 8 AA.
 AC P37985;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE 30S ribosomal protein S1 (Fragment).
 GN Name=rpS1;
 OS Erwinia chrysanthemi.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Pectobacterium.
 OX NCBI_TaxID=556;
 RN [1]
 RP STRAIN=3937;
 RC Doullie A., Toussaint A., Faelen M.;
 RL Submitted (AUG-1993) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Binds mRNA; thus facilitating recognition of the
 CC initiation point. It is needed to translate mRNA with a short
 CC Shine-Dalgarno (SD) purine-rich sequence (By similarity).
 CC -!- SIMILARITY: Belongs to the ribosomal protein S1P family.
 CC -----

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).

DR EMBL; X74750; CAA52769.1; -;
DR PIR; S37141; S37141.
KW Repeat; Ribosomal protein; RNA-binding.
FT NON_TER 1
SQ SEQUENCE 8 AA; 837 MW; 9E18733DC5B339CD CRC64;

Alignment Scores:
Pred. No.: 1.28e+08 Length: 8
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-10-070-588a-112 (1-11) x RS1_ERWCH (1-8)

OY 10 ACTGCCAAA 2
Db 4 SerAlaLys 6
RESULT 2
Q6JC68 PRELIMINARY; PRT; 8 AA.
ID Q6JC68
AC Q6JC68;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Isoflavone synthase 1 (Fragment).
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX NCBI_TaxID=3847;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15356384;
RA Subramanian S., Hu X., Lu G., Odell J.T., Yu O.;
RT "The promoters of two isoflavone synthase genes respond differentially
RT to modulation and defense signals in transgenic soybean roots.";
RL Plant Mol. Biol. 54:623-639(2004).
DR EMBL; AY530096; AAT01227.1; -;
FT NON_TER 8
SQ SEQUENCE 8 AA; 859 MW; F1772DD72B172726 CRC64;

Alignment Scores:
Pred. No.: 1.28e+08 Length: 8
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-070-588a-112 (1-11) x Q6JC68 (1-8)

OY 3 TTGGCACTA 11
Db 5 LeuAlaLeu 7
RESULT 3
Q9MW43 PRELIMINARY; PRT; 9 AA.
ID Q9MW43
AC Q9MW43;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE MHC class I antigen (Fragment).
GN Name=HLA-B39061;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Blood;
RX MEDLINE=97246738; PubMed=9089103; DOI=10.1007/s002510050227;
RA Vargas-Alarcon G., Gomez-Casado E., Martinez-Laso J., Granados J.,
RA Layrisse Z., Alegre R., Arnalaz-Villena A.;
RT "Differences in intron 2 sequences between B*39061 and B*39062 in
RT Amerindians: comparison with those of B*3901, B*5101, and B*52012
RT alleles.";
RL Immunogenetics 45:436-439(1997).
DR EMBL; L76640; AAP86298.1; -;
DR GO; GO:0030106; F:MHC class I receptor activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
FT NON_TER 1
FT NON_TER 1
FT NON_TER 9
SQ SEQUENCE 9 AA; 975 MW; 51C661AB01A72DD7 CRC64;

Alignment Scores:
Pred. No.: 1.14e+08 Length: 9
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-070-588a-112 (1-11) x Q9MW43 (1-9)

OY 3 TTGGCACTA 11
Db 2 LeuAlaLeu 4
RESULT 4
CX81 CANFA
ID CX81 CANFA STANDARD; PRT; 10 AA.
AC P61504;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Cytochrome c oxidase polypeptide VIII-heart (EC 1.9.3.1) (Cytochrome c
DE oxidase subunit 8-1) (Fragment).
GN Name=COX8H;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE.
RX TISSUE=Heart, and Liver;
RX MEDLINE=8529022; DOI=10.1016/0305-0491(95)00093-3;
RA Linder D., Freund R., Kadenbach B.;
RT "Species-specific expression of cytochrome c oxidase isozymes.";
RL Comp. Biochem. Physiol. 112B:461-469(1995).
CC -!- FUNCTION: This protein is one of the nuclear-coded polypeptide
CC chains of cytochrome c oxidase, the terminal oxidase in
CC mitochondrial electron transport.
CC -!- CATALYTIC ACTIVITY: 4 ferrocycytochrome c + O(2) = 4 ferricytochrome
CC c + 2 H(2)O.
CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
CC -!- TISSUE SPECIFICITY: Heart specific isoform.
CC -!- SIMILARITY: Belongs to the cytochrome c oxidase VIII family.
KW Direct protein sequencing; Inner membrane; Mitochondrion;
KW Oxidoreductase.
FT NON_TER 10
FT NON_TER 10
SQ SEQUENCE 10 AA; 1027 MW; C22AFFB40DC7633D CRC64;
Alignment Scores:
Pred. No.: 4.93e+05 Length: 10

Score: 3.00 Matches: 3
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 1 Gaps: 0

US-10-070-588A-112 (1-11) x CX81_CANFA (1-10)

QY 10 AGTGCACAA 2
 Db 2 SerAlaLys 4

RESULT 5
 Q50843 PRELIMINARY; PRT; 10 AA.

ID Q50843
 AC Q50843
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last annotation update)
 DE RNA polymerase gene 3' flanking region with AT-rich DNA sequence (Fragment).
 DE (Fragment).
 OS Methanococcus voltae.
 OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
 OC Methanococcaceae; Methanococcus.
 OX NCBI_TaxID=2188;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85230552; PubMed=4006907;
 RA Bolischweiler C., Kuehn R., Klein A.;
 RT "Non-repetitive AT-rich sequences are found in intergenic regions of
 RT Methanococcus voltae DNA."
 RL EMBO J. 4:805-809 (1985).
 DR EMBL; X02517; CAA26353.1; --
 FT NON_TER 10
 SQ SEQUENCE 10 AA; 1149 MW; 27F22A2772CAA9C8 CRC64;

Alignment Scores:
 Pred. No.: 4.93e+05 Length: 10
 Score: 3.00 Matches: 3
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x Q50843 (1-10)

QY 9 GTGCCAAG 1
 Db 6 ValProLys 8

RESULT 6
 Q7S225 PRELIMINARY; PRT; 10 AA.

ID Q7S225
 AC Q7S225
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Predicted protein.
 GN Name=NCU09889.1;
 OS Neurospora crassa.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
 OX NCBI_TaxID=5141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=OR74A;
 RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
 RA Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehan B.,
 RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
 RA Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M.,
 RA Sellitrennikoff C.E., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
 RA Kotne G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
 RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,

RA Kamal M., Kamysseelis M., Mauceli E., Bielke C., Rudd S., Frishman D.,
 RA Kryatova S., Raemussen C., Metzberg R.L., Perkins D.D., Kroken S.,
 RA Cogoni C., Macino G., Catcheside D., Li W., Pratt R.J., Osmani S.A.,
 RA Desouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,
 RA Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
 RA Natvig D.O., Alex L.A., Manhaupt G., Ebbole D.J., Freitag M.,
 RA Paulsen I., Sachs M.S., Lander E.S., Nussbaum C., Birren B.,
 RT "The Genome Sequence of the Filamentous Fungus Neurospora crassa."
 RL Nature 0:0-0 (2003).
 CC CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AABX01000434; EAA29420.1; --
 SQ SEQUENCE 10 AA; 1071 MW; DA471E27272DD732 CRC64;

Alignment Scores:
 Pred. No.: 4.93e+05 Length: 10
 Score: 3.00 Matches: 3
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x Q7S225 (1-10)

QY 3 TTGGCACTA 11
 Db 4 LeuAlaLeu 6

RESULT 7
 Q95M70 PRELIMINARY; PRT; 10 AA.

ID Q95M70
 AC Q95M70
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Beta-2 microglobulin (Fragment).
 GN Name=B2MG;
 OS Trichosurus vulpecula (Brush-tailed possum).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Metatheria; Diprotodontia; Phalangeridae; Trichosurus.
 OX NCBI_TaxID=9337;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22419909; PubMed=12531282; DOI=10.1016/S0161-5890(02)00260-2;
 RA Western A.H., Eckery D.C., Demmer J., Juengel J.L., McNatty K.P.,
 RA Fidler A.E.;
 RT "Expression of the FcRn receptor (alpha and beta) gene homologues in
 RT the intestine of suckling brushtail possum (Trichosurus vulpecula)
 RT pouch young.";
 RL Mol. Immunol. 39:707-717 (2003).
 DR EMBL; AY033330; AAK57520.1; --
 FT NON_TER 10
 SQ SEQUENCE 10 AA; 1179 MW; CD4BBE2059C0440D CRC64;

Alignment Scores:
 Pred. No.: 4.93e+05 Length: 10
 Score: 3.00 Matches: 3
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x Q95M70 (1-10)

QY 3 TTGGCACTA 11
 Db 8 LeuAlaLeu 10

RESULT 8
 Q8SAC2 PRELIMINARY; PRT; 10 AA.
 ID Q8SAC2
 AC Q8SAC2;

DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE AtpB (Fragment).
OS Amblystegium varium.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
OC Bryopsida; Bryidae; Hypnales; Amblystegiaceae; Amblystegium.
OX NCBI_TaxID=111436;
RN (1)
RP SEQUENCE FROM N.A.
RX PubMed=15062791; DOI=10.1016/j.ympev.2003.09.020;
RA Vanderpoorten A., Shaw A.J., Cox C.J.;
RT "Evolution of multiple paralogous adenosine kinase genes in the moss
genus Hygroamblystegium: phylogenetic implications.";
RL Mol. Phylogenet. Evol. 31:505-516(2004).
DR EMBL; AF464972; AAL75469.1; -;
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1143 MW; 9D5040D1B415B8B1 CRC64;

Alignment Scores:
Pred. No.: 4.93e+05 Length: 10
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0
US-10-070-588A-112 (1-11) x Q8SAC2 (1-10)

QY 2 TTGGCACT 10
Db 8 PheGlyThr 10

RESULT 9
Q9S905 PRELIMINARY; PRT; 10 AA.
ID Q9S905
AC Q9S905;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE S3 peptide (Fragment).
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX NCBI_TaxID=3847;
RN (1)
RP SEQUENCE.
RX MEDLINE=92232221; PubMed=1368037; DOI=10.1016/0031-9422(92)80003-W;
RA Hirano H., Kagawa H., Okubo K.;
RL Phytochemistry 31:731-735(1992).
FT NON_TER 1 1
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 975 MW; 3C733271A879D1B7 CRC64;

Alignment Scores:
Pred. No.: 4.93e+05 Length: 10
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0
US-10-070-588A-112 (1-11) x Q9S905 (1-10)

QY 2 TTGGCACT 10
Db 5 PheGlyThr 7

RESULT 10
Q9C1R7 PRELIMINARY; PRT; 11 AA.
ID Q9C1R7
AC Q9C1R7;

DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Ssulp (Fragment).
GN Name=ssul;
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN (1)
RP SEQUENCE FROM N.A.
RX STRAIN=IT73;
RX MEDLINE=22253762; PubMed=12368245; DOI=10.1101/gr.436602;
RA Perez-Ortin J.E., Querol A., Puig S., Barrio E.;
RT "Molecular Characterization of a Chromosomal Rearrangement Involved in
the Adaptive Evolution of Yeast Strains.";
RL Genome Res. 12:1533-1539(2002).
DR EMBL; AF239758; AAK15080.1; -;
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1274 MW; 12567614D732D374 CRC64;

Alignment Scores:
Pred. No.: 4.79e+05 Length: 11
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0
US-10-070-588A-112 (1-11) x Q9C1R7 (1-11)

QY 3 TTGGCACT 11
Db 7 LeuAlaLeu 9

RESULT 11
Q7M374 PRELIMINARY; PRT; 11 AA.
ID Q7M374
AC Q7M374;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Ribosomal protein MRP-S24, mitochondrial (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN (1)
RP SEQUENCE.
RA Graack H.R.;
RL Submitted (JUL-1999) to the PIR data bank.
DR PIR; S78765; S78765.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1264 MW; 95F49156A32772CA CRC64;

Alignment Scores:
Pred. No.: 4.79e+05 Length: 11
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0
US-10-070-588A-112 (1-11) x Q7M374 (1-11)

QY 9 GTGCCAAAG 1
Db 5 ValProLys 7

RESULT 12
Q9UEX7

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ID Q9UEX7 PRELIMINARY; PRT; 11 AA.
AC Q9UEX7;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE Leucocyte antigen B (Fragment).
GN Name=HLA-A*03;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Fae I., Krika D., Cernava B., Fischer G.F.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY625283; CAB65736.1; -
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1118 MW; 5191BC69C1A72DD7 CRC64;

Alignment Scores:
Pred. No.: 4.79e+05 Length: 11
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-070-588a-112 (1-11) x Q9UEX7 (1-11)
QY 3 TTGGCACTA 11
Db 4 LeuAlaLeu 6

RESULT 13
Q68QV9 PRELIMINARY; PRT; 11 AA.
ID Q68QV9;
AC Q68QV9;
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Arginine biosynthesis repressor (Fragment).
GN Name=argR;
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15322001; DOI=10.1128/IAI.72.9.5080-5088.2004;
RA Lan R., Alles M.C., Donohoe K., Martinez M.B., Reeves P.R.;
RT "Molecular evolutionary relationships of enteroinvasive Escherichia
colli and Shigella spp.";
RL Infect. Immun. 72:5080-5088(2004).
DR EMBL; AY627168; AAU01857.1; -
DR EMBL; AY627169; AAU01859.1; -
DR EMBL; AY627170; AAU01861.1; -
DR EMBL; AY627171; AAU01863.1; -
DR EMBL; AY627172; AAU01865.1; -
DR EMBL; AY627173; AAU01867.1; -
DR EMBL; AY627174; AAU01869.1; -
DR EMBL; AY627175; AAU01871.1; -
DR EMBL; AY627176; AAU01873.1; -
DR EMBL; AY627177; AAU01875.1; -
DR EMBL; AY627178; AAU01877.1; -
DR EMBL; AY627244; AAU01795.1; -
DR EMBL; AY627245; AAU01797.1; -
DR EMBL; AY627246; AAU01799.1; -
DR EMBL; AY627247; AAU01801.1; -
DR EMBL; AY627248; AAU01803.1; -
DR EMBL; AY627249; AAU01805.1; -
DR EMBL; AY627250; AAU01807.1; -
DR EMBL; AY627251; AAU01809.1; -

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DR EMBL; AY627252; AAU01811.1; -
DR EMBL; AY627253; AAU01813.1; -
DR EMBL; AY627254; AAU01815.1; -
DR EMBL; AY627255; AAU01817.1; -
DR EMBL; AY627256; AAU01819.1; -
DR EMBL; AY627257; AAU01821.1; -
DR EMBL; AY627258; AAU01823.1; -
DR EMBL; AY627259; AAU01825.1; -
DR EMBL; AY627260; AAU01827.1; -
DR EMBL; AY627261; AAU01829.1; -
DR EMBL; AY627262; AAU01831.1; -
DR EMBL; AY627263; AAU01833.1; -
DR EMBL; AY627264; AAU01835.1; -
DR EMBL; AY627265; AAU01837.1; -
DR EMBL; AY627266; AAU01839.1; -
DR EMBL; AY627267; AAU01841.1; -
DR EMBL; AY627268; AAU01843.1; -
DR EMBL; AY627269; AAU01845.1; -
DR EMBL; AY627270; AAU01847.1; -
DR EMBL; AY627271; AAU01849.1; -
DR EMBL; AY627272; AAU01851.1; -
DR EMBL; AY627273; AAU01853.1; -
DR EMBL; AY627167; AAU01855.1; -
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1277 MW; 9B5PFE2206D33DC5 CRC64;

Alignment Scores:
Pred. No.: 4.79e+05 Length: 11
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-070-588a-112 (1-11) x Q68QV9 (1-11)
QY 10 AGTGCAAA 2
Db 4 SerAlaLys 6

RESULT 14
Q7MOD4 PRELIMINARY; PRT; 11 AA.
ID Q7MOD4;
AC Q7MOD4;
DT 01-MAR-2004 (TREMBlrel. 26, Created)
DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Cytochrome-c oxidase (EC 1.9.3.1) chain Via-H, cardiac
(Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE.
RA Schaeffer H., Noack H., Halangk W., Brandt U., von Jagow G.;
RT "Cytochrome-c oxidase in developing rat heart. Enzymic properties and
amino-terminal sequences suggest identity of the fetal heart and the
adult liver isoform.";
RL Eur. J. Biochem. 230:235-241(1995).
DR GO; GO:0004129; F:cytochrome-c oxidase activity; IEA.
DR PIR; S65377; S65377.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 927 MW; 4F3E577D71EAA873 CRC64;

Alignment Scores:
Pred. No.: 4.79e+05 Length: 11
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

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US-10-070-588A-112 (1-11) x Q7M0D4 (1-11)

QY 10 AGTGCCAAA 2

Db 2 SerAlaLys 4

RESULT 15

Q84247 PRELIMINARY; PRT; 11 AA.

AC Q84247;

DT 01-NOV-1996 (TRENBLrel. 01, Created)

DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)

DE 01-DEC-2001 (TRENBLrel. 19, Last annotation update)

OS Polymavirus BK (BKV).

OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.

OX NCBI_TaxID=10629;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Gardner;

RX MEDLINE=90324932; PubMed=21651132;

RA Moens U., Sundsfjord A., Flegstad T., Traavik T.;

RT "BK virus early RNA transcripts in stably transformed cells : enhanced

RT levels induced by dibutyl cAMP, forskolin and 12-O-

RT tetradecanoylphorbol-13-acetate treatment.";

RL J. Gen. Virol. 71:1461-1471(1990).

DR EMBL; D00678; BAA00585.1; -.

FT NON TER 11

SQ SEQUENCE 11 AA; 1044 MW; C2786C4E272DD72D CRC64;

Alignment Scores:

Pred. No.: 4.79e+05 Length: 11

Score: 3.00 Matches: 3

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x Q84247 (1-11)

QY 3 TTGGCACTA 11

Db 5 LeuAlaLeu 7

RESULT 16

TKN_KASSE

ID TKN_KASSE STANDARD; PRT; 12 AA.

AC P08611;

DT 01-AUG-1988 (Rel. 08, Created)

DT 01-AUG-1988 (Rel. 08, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE Kassinin.

OS Kassina senegalensis (Senegal running frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Hyperoliidae;

OC Kassina

OX NCBI_TaxID=8415;

RN [1]

RP SEQUENCE.

RC TISSUE=Skin secretion;

RX MEDLINE=77246385; PubMed=891753;

RA Anastasi A., Montecucci P.C., Erpamer V., Visser J.;

RT "Amino acid composition and sequence of kassinin, a tachykinin

RT dodecapeptide from the skin of the African frog Kassina

RT senegalensis.";

RL Experientia 33:857-858(1977).

CC -!- FUNCTION: Tachykinnins are active peptides which excite neurons,

CC evoke behavioral responses, are potent vasodilators and

CC secretagogues, and contract (directly or indirectly) many smooth

CC muscles.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- TISSUE SPECIFICITY: Skin.

CC -!- SIMILARITY: Belongs to the tachykinin family.

DR PIR; S07206; S07206.

DR PDB; 1MYU; NMR; A=1-12.

DR InterPro; IPR002040; Tachy_Neurokinin.

DR Pfam; PF02202; Tachykinin; 1.

DR PROSITE; PS00267; TACHYKININ; 1.

KW 3D-structure; Amidation; Amphibian defense peptide;

KW Direct protein sequencing; Neuropeptide; Tachykinin.

FT MOD_RES 12 12 Methionine amide.

SQ SEQUENCE 12 AA; 1336 MW; 91757AB9DD6DAB5 CRC64;

Alignment Scores:

Pred. No.: 4.67e+05 Length: 12

Score: 3.00 Matches: 3

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 1 Gaps: 0

US-10-070-588A-112 (1-11) x TKN_KASSE (1-12)

QY 9 GTGCCAAAG 1

Db 2 ValProLys 4

RESULT 17

Q8J0A7

ID Q8J0A7 PRELIMINARY; PRT; 12 AA.

AC Q8J0A7;

DT 01-MAR-2003 (TRENBLrel. 23, Created)

DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)

DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)

DE SSU1 protein (Fragment).

GN Name=SSU1;

OS Saccharomyces cerevisiae (Baker's yeast).

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.

OX NCBI_TaxID=4932;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=CECT 10557, and CECT 10120;

RX MEDLINE=22253762; PubMed=12368245; DOI=10.1101/gr.436602;

RA Perez-Ortin J.E., Querol A., Puig S., Barrio E.;

RT "Molecular Characterization of a Chromosomal Rearrangement Involved in

RT the Adaptive Evolution of Yeast Strains.";

RL Genome Res. 12:1533-1539(2002).

DR EMBL; AJ458364; CAD30222.1; -.

DR EMBL; AJ458366; CAD30224.1; -.

FT NON TER 12

SQ SEQUENCE 12 AA; 1402 MW; 3162567614D732D3 CRC64;

Alignment Scores:

Pred. No.: 4.67e+05 Length: 12

Score: 3.00 Matches: 3

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x Q8J0A7 (1-12)

QY 3 TTGGCACTA 11

Db 7 LeuAlaLeu 9

RESULT 18

Q7M4X9

ID Q7M4X9 PRELIMINARY; PRT; 12 AA.

AC Q7M4X9;

DT 01-MAR-2004 (TRENBLrel. 26, Created)

DT 01-MAR-2004 (TRENBLrel. 26, Last sequence update)

DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)

DE Ribosomal protein S3 (Fragment).

```

OS Fusarium sporotrichioides.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocremomycetidae; Hypocreales; Mitosporic Hypocreales; Fusarium.
OX NCBI_TaxID=5514;
RN [1]
RP SEQUENCE.
RA Chow L.P., Fukaya N., Sugiyama Y., Ueno Y., Tabuchi K., Teugita A.;
RL Submitted (OCT-1994) to the PIR data bank.
DR PIR; PA0098; PA0098.
FT NON_TER 1
FT NON_TER 12
SQ SEQUENCE 12 AA; 1242 MW; 227EFCBA7C2772D7 CRC64;

Alignment Scores:
Pred. No.: 4.67e+05 Length: 12
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x Q7M4X9 (1-12)

QY 9 GTGCCAAG 1
Db 6 ValProLys 8

RESULT 19
Q96PHO PRELIMINARY; PRT; 12 AA.
ID Q96PHO;
AC Q96PHO;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE H1028 protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=21474610; PubMed=11590366;
RA Demirci F.Y., White N.J., Rigatti B.W., Lewis K.F., Gorin M.B.;
RT "Identification, genomic structure, and screening of the vacuolar
RT proton-ATPase membrane sector-associated protein M8-9 gene within the
RT COD1 critical region (Xp11.4).";
RL Mol. Vision 7:234-239 (2001).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Demirci F.Y., White N.J., Rigatti B.W., Chun-Fang X., Gorin M.B.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF354120; AAL11062.1; -.
FT NON_TER 12
FT NON_TER 12
SQ SEQUENCE 12 AA; 1246 MW; D55E1977EE2732D2 CRC64;

Alignment Scores:
Pred. No.: 4.67e+05 Length: 12
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x Q96PHO (1-12)

QY 3 TTGGCACTA 11
Db 8 LeuAlaLeu 10

RESULT 20
Q31851 PRELIMINARY; PRT; 12 AA.
ID Q31851;
AC Q31851;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Glyceraldehyde-3-phosphate dehydrogenase (Fragment).
OS Arabidopsis thaliana (Mouse-ear cress).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Columbia; TISSUE=Leaf;
RX MEDLINE=94187724; PubMed=8139555;
RA Conley T.R., Park S.-C., Kwon H.-S., Peng H.-S., Shih M.-C.;
RT "Characterization of cis-acting elements in light regulation of the
RT nuclear gene encoding the A subunit of chloroplast isozymes
RT glyceraldehyde-3-phosphate dehydrogenase from Arabidopsis thaliana.";
RL Mol. Cell. Biol. 14:2525-2533 (1994).
DR EMBL; L14743; AAA31640.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
DR GO; GO:0005634; C:nucleus; IEA.
KW Chloroplast; Nuclear protein.
FT NON_TER 12
FT NON_TER 12
SQ SEQUENCE 12 AA; 1263 MW; 81BA4C7D4BD5B9D1 CRC64;

Alignment Scores:
Pred. No.: 4.67e+05 Length: 12
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x Q31851 (1-12)

QY 9 GTGCCAAG 1
Db 8 ValProLys 10

RESULT 21
Q6JC67 PRELIMINARY; PRT; 12 AA.
ID Q6JC67;
AC Q6JC67;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Isoflavone synthase 2 (Fragment).
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX NCBI_TaxID=3847;
RN [1]
RP SEQUENCE FROM N.A.
RC PubMed=15356384;
RA Subramanian S., Hu X., Lu G., Odell J.T., Yu O.;
RT "The promoters of two isoflavone synthase genes respond differentially
RT to modulation and defense signals in transgenic soybean roots.";
RL Plant Mol. Biol. 54:623-639 (2004).
DR EMBL; AY530097; AAT01228.1; -.
FT NON_TER 12
FT NON_TER 12
SQ SEQUENCE 12 AA; 1298 MW; 5E7DE50411772DD7 CRC64;

Alignment Scores:
Pred. No.: 4.67e+05 Length: 12
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

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US-10-070-588A-112 (1-11) x Q6JC67 (1-12)
QY 3 TTGGCACTA 11
DB 5 LeuAlaLeu 7

RESULT 22
Q9UE87
ID Q9UE87 PRELIMINARY; PRT; 13 AA.
AC Q9UE87;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Transforming growth factor alpha (Fragment).
GN Name:TFGA;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89219018; PubMed=2907605;
RA Jakobovits E.B., Schlokot U., Vannice J.L., Derynck R., Levinson A.D.;
RT "The human transforming growth factor alpha promoter directs
RT transcription initiation from a single site in the absence of a TATA
RT sequence."
RL Mol. Cell. Biol. 8:5549-5554(1988).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92168034; PubMed=1791840;
RA Saeki T., Cristiano A., Lynch M.J., Brattain M., Kim N., Normanno N.,
RA Kenney N., Ciardiello F., Salomon D.S.;
RT "Regulation by estrogen through the 5'-flanking region of the
RT transforming growth factor alpha gene."
RL Mol. Endocrinol. 5:1955-1963(1991).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=93364904; PubMed=8358733;
RA Lynch M.J., Pelosi L., Carboni J.M., Merwin J., Coleman K., Wang R.C.,
RA Lin P.F., Henry D.L., Brattain M.G.;
RT "Transforming growth factor-beta 1 induces transforming growth factor-
RT alpha promoter activity and transforming growth factor-alpha secretion
RT in the human colon adenocarcinoma cell line FET."
RL Cancer Res. 53:4041-4047(1993).
DR EMBL; M96868; AAA7958.1; -.
FT NON TER 13 13
SQ SEQUENCE 13 AA; 1318 MW; 2C6E4395FCE36D8 CRC64;

Alignment Scores:
Pred. No.: 4.57e+05 Length: 13
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x Q9UE87 (1-13)
QY 3 TTGGCACTA 11
DB 8 LeuAlaLeu 10

RESULT 23
Q6SE60
ID Q6SE60 PRELIMINARY; PRT; 13 AA.
AC Q6SE60;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Idgf3 (Fragment).
OS Drosophila simulans (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

US-10-070-588A-112 (1-11) x Q6JC67 (1-12)
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7240;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14762063; DOI=10.1101/gr.1329204;
RA Halligan D.L., Eyre-Walker A., Andolfatto P., Keightley P.D.;
RT "Patterns of evolutionary constraints in intronic and intergenic DNA
RT of Drosophila."
RL Genome Res. 14:273-279(2004).
DR EMBL; AY459538; AAR22997.1; -.
FT NON TER 13 13
SQ SEQUENCE 13 AA; 1392 MW; 220F3FF68C0CB733 CRC64;

Alignment Scores:
Pred. No.: 4.57e+05 Length: 13
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x Q6SE60 (1-13)
QY 3 TTGGCACTA 11
DB 9 LeuAlaLeu 11

RESULT 24
Q7RAS8
ID Q7RAS8 PRELIMINARY; PRT; 13 AA.
AC Q7RAS8;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN Name=PX06421;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73329;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=17XNL;
RX PubMed=12368865; DOI=10.1038/nature01099;
RA Carlton J.M., Angioli S.V., Suh B.B., Kooij T.W., Perte M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shalom S.J., van Aken S.E., Riedmuller S.B., Feidlyum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoalbi A., Cummings L.M.,
RA Florens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
RT parasite Plasmodium yoelii yoelii."
RL Nature 419:512-519(2002).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AABL01002172; EAA18636.1; -.
KW Hypothetical protein.
SQ SEQUENCE 13 AA; 1500 MW; D06789FF2AEBCEB9 CRC64;

Alignment Scores:
Pred. No.: 4.57e+05 Length: 13
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x Q7RAS8 (1-13)

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QY 3 TTGGCACTA 11
 |||||
 Db 2 LeuAlaLeu 4

RESULT 25

Q39380 PRELIMINARY; PRT; 13 AA.

ID Q39380;
 AC Q39380;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE IFA binding protein (ep10) (Fragment).
 OS Brassica oleracea (Cauliflower).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Brassica.
 OX NCBI_TaxID=3712;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Dok; TISSUE=Curd surface;
 RA Willis G.;
 RL Submitted (MAR-1996) to the EMBL/GenBank/DDJ databases.
 DR EMBL; X97678; CAA66268.1; --
 FT NON_TER 1
 SQ SEQUENCE 13 AA; 1413 MW; DID4EA3926B42772 CRC64;

Alignment Scores:

Pred. No.: 4.57e+05 Length: 13
 Score: 3.00 Matches: 3
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 2 Gaps: 0

US-10-070-588a-112 (1-11) x Q39380 (1-13)

QY 9 GTGCCAAG 1
 |||||
 Db 6 ValProlys 8

RESULT 26

Q6URV3 PRELIMINARY; PRT; 13 AA.

ID Q6URV3;
 AC Q6URV3;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE P-type R2R3 Myb protein (Fragment).
 GN Name=Myb18;
 OS Sorghum bicolor (Sorghum) (Sorghum vulgare).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC PACCAD clade; Panicoideae; Andropogoneae; Sorghum.
 OX NCBI_TaxID=4558;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC PubMed=14729259; DOI=10.1016/j.gene.2003.09.049;
 RA Jiang C., Gu J., Chopra S., Gu X., Peterson T.;
 RT "Ordered origin of the typical two- and three-repeat Myb genes.";
 RL Gene 326:13-22(2004).
 DR EMBL; AY363127; AAK54841.1; --
 FT NON_TER 1
 SQ SEQUENCE 13 AA; 1504 MW; 240AF718A7B0C413 CRC64;

Alignment Scores:

Pred. No.: 4.57e+05 Length: 13
 Score: 3.00 Matches: 3
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 2 Gaps: 0

US-10-070-588a-112 (1-11) x Q6URV3 (1-13)

QY 9 GTGCCAAG 1
 |||||
 Db 9 ValProlys 11

RESULT 27

Q62352 PRELIMINARY; PRT; 13 AA.

ID Q62352;
 AC Q62352;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Trypsin precursor (Fragment).
 GN Name=Prss3; Synonyms=Try3;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A/J;
 RX MEDLINE=87066713; PubMed=3641189;
 RA Stevenson B.J., Hagenbuechle O., Wellauer P.K.;
 RT "Sequence organisation and transcriptional regulation of the mouse
 elastase II and trypsin genes.";
 RL Nucleic Acids Res. 14:8307-8330(1986).
 DR EMBL; X04578; CAA28246.1; --
 KW Signal.
 FT NON_TER 1
 FT SIGNAL <1 13 Potential.
 SQ SEQUENCE 13 AA; 1270 MW; 1EFFF43B6E14D720 CRC64;

Alignment Scores:

Pred. No.: 4.57e+05 Length: 13
 Score: 3.00 Matches: 3
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 2 Gaps: 0

US-10-070-588a-112 (1-11) x Q62352 (1-13)

QY 3 TTGGCACTA 11
 |||||
 Db 7 LeuAlaLeu 9

RESULT 28

Q62354 PRELIMINARY; PRT; 13 AA.

ID Q62354;
 AC Q62354;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Trypsin precursor (Fragment).
 GN Name=Try4;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A/J;
 RX MEDLINE=87066713; PubMed=3641189;
 RA Stevenson B.J., Hagenbuechle O., Wellauer P.K.;
 RT "Sequence organisation and transcriptional regulation of the mouse
 elastase II and trypsin genes.";
 RL Nucleic Acids Res. 14:8307-8330(1986).
 DR EMBL; X04579; CAA28247.1; --
 DR MGD; MGI:102757; Try4.
 KW Signal.

FT NON_TER 1 1
FT SIGNAL <1 13 Potential.
SQ SEQUENCE 13 AA; 1320 MW; DDFFE2E16E14D729 CRC64;

Alignment Scores:
Pred. No.: 4.57e+05 Length: 13
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x Q62354 (1-13)

QY 3 TTGGGCACTA 11
Db 7 LeuAlaLeu 9

RESULT 29

Q62355
ID Q62355 PRELIMINARY; PRT; 13 AA.
AC Q62355;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Trypsin precursor (Fragment).
GN Name=Try4;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A/J;
RX MEDLINE=87066713; PubMed=3641189;
RA Stevenson B.J., Hegenbuchle O., Wellauer P.K.;
RT "Sequence organisation and transcriptional regulation of the mouse
elastase II and trypsin genes."
RL Nucleic Acids Res. 14:8307-8330(1986).
DR EMBL; X04580; CAA28248.1; --
DR MGD; MGI:102757; Try4.
KW Signal.
KW NON_TER 1 1
FT SIGNAL <1 13 Potential.
SQ SEQUENCE 13 AA; 1346 MW; DDFFF4200214D729 CRC64;

Alignment Scores:
Pred. No.: 4.57e+05 Length: 13
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x Q62355 (1-13)

QY 3 TTGGGCACTA 11
Db 7 LeuAlaLeu 9

RESULT 30

Q9PWP4
ID Q9PWP4 PRELIMINARY; PRT; 13 AA.
AC Q9PWP4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Chimeric AFGP/trypsinogen-like serine protease precursor
(Fragment).
OS Dissostichus mawsoni (Antarctic cod).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Perciformes; Perciformes;

OC Notothenioidae; Nototheniidae; Dissostichus.
OX NCBI_TaxID=36200;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99447034; PubMed=10519545; DOI=10.1038/46721;
RA Cheng C.H., Chen L.;
RT "Evolution of an antifreeze glycoprotein.";
RL Nature 401:443-444(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA Cheng C.-H.C.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF134320; AAD37246.1; --
DR GO; GO:0008233; F:peptidase activity; IEA.
KW Protease; Signal.
FT SIGNAL 1 >13 Potential.
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1340 MW; 5186FA54AF1E2727 CRC64;

Alignment Scores:

Pred. No.: 4.57e+05 Length: 13
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x Q9PWP4 (1-13)

QY 3 TTGGGCACTA 11
Db 4 LeuAlaLeu 6

RESULT 31

FERT_TOBAC
ID FERT_TOBAC STANDARD; PRT; 14 AA.
AC P82150;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Feruloyl-CoA thioesterase (EC 3.1.2.-) (Fragment).
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamiales; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE, CATALYTIC ACTIVITY, TISSUE SPECIFICITY, AND INDUCTION.
RC STRAIN=cv. Samsun NN; TISSUE=Stem;
RA Maury S., Geoffroy P., Legrand M.;
RL Submitted (NOV-1999) to Swiss-Prot.
CC -|- CATALYTIC ACTIVITY: Feruloyl-CoA + H(2)O = ferulate + CoA.
CC -|- PATHWAY: Phenylpropanoid metabolism.
CC -|- TISSUE SPECIFICITY: Expressed in stem, vascular tissues and
tobacco mosaic virus infected leaves.
CC -|- INDUCTION: By pathogen infection.
KW Direct protein sequencing; Hydrolase.
FT NON_TER 14 14
SQ SEQUENCE 14 AA; 1479 MW; 5F8B87AD9582AA7 CRC64;

Alignment Scores:
Pred. No.: 4.47e+05 Length: 14
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-10-070-588A-112 (1-11) x FERT_TOBAC (1-14)

QY 2 TTGGGCACT 10
Db 10 PheGlyThr 12

ID	UC34_MAIZE	STANDARD;	PRT;	14 AA.
AC	P80640;			
DT	01-OCT-1996	(Rel. 34, Created)		
DT	01-OCT-1996	(Rel. 34, Last sequence update)		
DT	03-JUL-2004	(Rel. 44, Last annotation update)		
DE	Unknown protein from 2D-PAGE of etiolated coleoptile (Spot 360)			
DE	(Fragments).			
OS	Zea mays (Maize).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;			
OC	PACCAD clade; Panicoideae; Andropogoneae; Zea.			
OX	NCBI_TaxID=4577;			
RN	[1]			
RP	SEQUENCE.			
RC	TISSUE=Coleoptile;			
RA	Touzert P., Riccardi F., Morin C., Damerval C., Huet J.-C.,			
RA	Pernollet J.-C., Zivy M., de Vienne D.;			
RT	"The maize two dimensional gel protein database: towards an integrated			
RT	genome analysis program."			
RL	Theor. Appl. Genet. 93:997-1005(1996).			
CC	-1- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown			
CC	protein is: 5.7, its MW is: 41.1 kDa.			
CC	-1- CAUTION: The order of the peptides shown is uncertain.			
DR	Maize-2DPAGE; P80640; COLEOPTILE.			
DR	MaizeDB; 123965; -.			
KW	Direct protein sequencing.			
FT	NON_TER	1	1	
FT	NON_CONS	8	9	
FT	NON_TER	14	14	
SQ	SEQUENCE	14 AA;	1527 MW;	DC525FF7B0BE682D CRC64;
Alignment Scores:				
Pred. No.:	4.47e+05			
Score:	3.00			
Length:	14			
Matches:	3			
Percent Similarity:	100.00%			
Conservative:	0			
Best Local Similarity:	100.00%			
Mismatches:	0			
Query Match:	100.00%			
Indels:	0			
Gaps:	0			
DB:	1			
US-10-070-588A-112 (1-11) x UC34_MAIZE (1-14)				
Qy	3 TTGGGACTA 11			
Db	6 LeuAlaLeu 8			
RESULT 33				
Q6JDV5	PRELIMINARY; PRT; 14 AA.			
ID	Q6JDV5;			
AC	05-JUL-2004 (TEMBLrel. 27, Created)			
DT	05-JUL-2004 (TEMBLrel. 27, Last sequence update)			
DT	05-JUL-2004 (TEMBLrel. 27, Last annotation update)			
DE	Janus kinase 2 (Fragment).			
GN	Names=JAK2;			
OS	Sus scrofa (Pig).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.			
OX	NCBI_TaxID=9823;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	PubMed=15147409; DOI=10.1111/j.1365-2052.2004.01128.x;			
RA	Wang H., Yu M., Liu B., Yerle M., Wang Y., Fan B., Zhu M.,			
RA	Li K.;			
RT	"Mapping of the porcine JAK2, JAK3 and TYK2 genes using somatic cell			
RT	and radiation hybrid panels."			
RL	Anim. Genet. 35:258-259(2004).			
DR	EMBL; AY509893; AAS79098.1; -.			
DR	GO; GO:0016			

RA Gueneau de Novoa P., Williams K.P.;
RT "The tRNA website: reductive evolution of tRNA in plastids and other
endosymbionts.";
RL Nucleic Acids Res. 32:D104-D108 (2004).
DR EMBL: AF550354; RAQ13670.1; --
FT NON_TER 1 1
SQ SEQUENCE 14 AA; 1490 MW; C5560BA69987A149 CRC64;

Alignment Scores:
Pred. No.: 4.47e+05 Length: 14
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x Q714T6 (1-14)

QY 3 TTGGGCACTA 11
Db 11 LeuAlaLeu 13

RESULT 36

Q9MRV8 ID Q9MRV8 PRELIMINARY; PRT; 14 AA.
AC Q9MRV8;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE PSI 9 kDa protein (Fragment).
GN Name=psaC;
OS Aloe vera (Aloe) (Aloe barbadensis).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Asphodelaceae;
OC Aloe.
OX NCBI_TaxID=34199;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Leaf;
RX MEDLINE=21109831; PubMed=11181728;
RA Lopez-Serrano M., del Campo E.M., Sabater B., Martin M.;
RT "Primary transcripts of ndhD of Liliaceae and Aloaceae require editing
of the start and 20th codons.";
RL J. Exp. Bot. 52:179-180 (2001).
DR EMBL: AJ278353; CAB96192.1; --
DR GO: GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER 1 1
SQ SEQUENCE 14 AA; 1744 MW; 8F14FD03E3B7D911 CRC64;

Alignment Scores:
Pred. No.: 4.47e+05 Length: 14
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x Q9MRV8 (1-14)

QY 1 CTTTGGGCAC 9
Db 2 LeuTrpHis 4

RESULT 37

Q9MRV1 ID Q9MRV1 PRELIMINARY; PRT; 14 AA.
AC Q9MRV1;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE PSI 9 kDa protein (Fragment).

GN Name=psaC;
OS Allium sativum (Garlic).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Alliaceae;
OC Allium.
OX NCBI_TaxID=4682;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Leaf;
RX MEDLINE=21109831; PubMed=11181728;
RA Lopez-Serrano M., del Campo E.M., Sabater B., Martin M.;
RT "Primary transcripts of ndhD of Liliaceae and Aloaceae require editing
of the start and 20th codons.";
RL J. Exp. Bot. 52:179-180 (2001).
DR EMBL: AJ278351; CAB96187.1; --
DR GO: GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER 1 1
SQ SEQUENCE 14 AA; 1744 MW; 8F14FD03E3B7D911 CRC64;

Alignment Scores:
Pred. No.: 4.47e+05 Length: 14
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x Q9MRV1 (1-14)

QY 1 CTTTGGGCAC 9
Db 2 LeuTrpHis 4

RESULT 38

Q9MRV4 ID Q9MRV4 PRELIMINARY; PRT; 14 AA.
AC Q9MRV4;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE PSI 9 kDa protein (Fragment).
GN Name=psaC;
OS Allium porrum (Leek).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Alliaceae;
OC Allium.
OX NCBI_TaxID=4681;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Leaf;
RX MEDLINE=21109831; PubMed=11181728;
RA Lopez-Serrano M., del Campo E.M., Sabater B., Martin M.;
RT "Primary transcripts of ndhD of Liliaceae and Aloaceae require editing
of the start and 20th codons.";
RL J. Exp. Bot. 52:179-180 (2001).
DR EMBL: AJ278352; CAB96185.1; --
DR GO: GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER 1 1
SQ SEQUENCE 14 AA; 1744 MW; 8F14FD03E3B7D911 CRC64;

Alignment Scores:
Pred. No.: 4.47e+05 Length: 14
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x Q9MRV4 (1-14)

```
QY 1 CTTGGCAC 9
Db 2 Leutirphis 4

RESULT 39
ID Q9MT61 PRELIMINARY; PRT; 14 AA.
AC Q9MT61;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE PSI 9 kDa protein (Fragment).
GN Name-psaC;
OS Allium cepa (Onion).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Alliaceae;
OC Allium.
OX NCBI_TaxID=4679;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Leaf;
RA MEDLINE=21109831; PubMed=11181728;
RX Lopez-Serrano M., del Campo E.M., Sabater B., Martin M.;
RT "Primary transcripts of ndhD of Liliaceae and Aloaceae require editing
RT of the start and 20th codons."
RL J. Exp. Bot. 52:179-180(2001).
DR EMBL; AJ278350; CAB96183.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER 1
SQ SEQUENCE 14 AA; 1744 MW; 8F14FD03E3B7D911 CRC64;

Alignment Scores:
Pred. No.: 4.47e+05 Length: 14
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-070-588a-112 (1-11) x Q9MT61 (1-14)

QY 1 CTTGGCAC 9
Db 2 Leutirphis 4

RESULT 40
ID Q642Z4 PRELIMINARY; PRT; 14 AA.
AC Q642Z4;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE AtpB (Fragment).
GN Name-atpB;
OS Brachytheciastrum venustum.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
OC Bryopsida; Bryidae; Hypnales; Brachytheciaceae; Brachytheciastrum.
OX NCBI_TaxID=292614;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Venustum1704, and Venustum1705;
RA Vanderpoorten A.;
RT "A molecular and morphological recircumscription of Brachytheciastrum
RT (Brachytheciaceae, Bryopsida).";
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY736270; AAU25912.1; -.
DR EMBL; AY736271; AAU25913.1; -.
KW Chloroplast.
FT NON_TER 14
SQ SEQUENCE 14 AA; 1544 MW; 811BBA1FD5040D1 CRC64;

Alignment Scores:
Pred. No.: 4.47e+05 Length: 14
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-070-588a-112 (1-11) x Q642Z4 (1-14)

QY 2 TTTGGCACT 10
Db 8 PheGlyThr 10

RESULT 41
ID Q642Z5 PRELIMINARY; PRT; 14 AA.
AC Q642Z5;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE AtpB (Fragment).
GN Name-atpB;
OS Brachytheciastrum velutinum.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
OC Bryopsida; Bryidae; Hypnales; Brachytheciaceae; Brachytheciastrum.
OX NCBI_TaxID=113273;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Velut1771;
RA Vanderpoorten A.;
RT "A molecular and morphological recircumscription of Brachytheciastrum
RT (Brachytheciaceae, Bryopsida).";
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY736269; AAU25911.1; -.
KW Chloroplast.
FT NON_TER 14
SQ SEQUENCE 14 AA; 1544 MW; 811BBA1FD5040D1 CRC64;

Alignment Scores:
Pred. No.: 4.47e+05 Length: 14
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-070-588a-112 (1-11) x Q642Z5 (1-14)

QY 2 TTTGGCACT 10
Db 8 PheGlyThr 10

RESULT 42
ID Q642Z8 PRELIMINARY; PRT; 14 AA.
AC Q642Z8;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE AtpB (Fragment).
GN Name-atpB;
OS Brachytheciastrum trachypodium.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
OC Bryopsida; Bryidae; Hypnales; Brachytheciaceae; Brachytheciastrum.
OX NCBI_TaxID=292612;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Trachypol1762, Trachypol1766, and Trachypol1770;
FT NON_TER 14
SQ SEQUENCE 14 AA; 1544 MW; 811BBA1FD5040D1 CRC64;
```

```
RA Vanderpoorten A.;
RT "A molecular and morphological recircumscription of Brachytheciastrum
   (Brachytheciaceae, Bryopsida).";
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY736266; AAU25908.1; -
DR EMBL; AY736267; AAU25909.1; -
DR EMBL; AY736268; AAU25910.1; -
KW Chloroplast.
FT NON TER 14 14
SQ SEQUENCE 14 AA; 1544 MW; 811BBAA1FD5040D1 CRC64;

Alignment Scores:
Pred. No.: 4.47e+05 Length: 14
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x Q64228 (1-14)
QY 2 TTTGGCACT 10
Db 8 PheGlyThr 10
RESULT 43
Q643A0 PRELIMINARY; PRT; 14 AA.
AC Q643A0;
DT 25-OCT-2004 (TReMBLrel. 28, Created)
DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
DE AtpB (Fragment).
GN Name=atpB;
OS Brachytheciastrum collinum.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
OC Bryopsida; Bryidae; Hypnales; Brachytheciaceae; Brachytheciastrum.
OX NCBI_TaxID=219719;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Collinum1767, Collinum1769, and Collinum1765;
RA Vanderpoorten A.;
RT "A molecular and morphological recircumscription of Brachytheciastrum
   (Brachytheciaceae, Bryopsida).";
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY736264; AAU25906.1; -
DR EMBL; AY736265; AAU25907.1; -
DR EMBL; AY736263; AAU25905.1; -
KW Chloroplast.
FT NON TER 14 14
SQ SEQUENCE 14 AA; 1544 MW; 811BBAA1FD5040D1 CRC64;

Alignment Scores:
Pred. No.: 4.47e+05 Length: 14
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x Q643A0 (1-14)
QY 2 TTTGGCACT 10
Db 8 PheGlyThr 10
RESULT 44
Q7M1G6 PRELIMINARY; PRT; 14 AA.
AC Q7M1G6;
DT 01-MAR-2004 (TReMBLrel. 26, Created)
DT 01-MAR-2004 (TReMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE AtpB (Fragment).
GN Name=atpB;
OS Brachytheciastrum collinum.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
OC Bryopsida; Bryidae; Hypnales; Brachytheciaceae; Brachytheciastrum.
OX NCBI_TaxID=219719;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Collinum1767, Collinum1769, and Collinum1765;
RA Vanderpoorten A.;
RT "A molecular and morphological recircumscription of Brachytheciastrum
   (Brachytheciaceae, Bryopsida).";
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY736264; AAU25906.1; -
DR EMBL; AY736265; AAU25907.1; -
DR EMBL; AY736263; AAU25905.1; -
KW Chloroplast.
FT NON TER 14 14
SQ SEQUENCE 14 AA; 1544 MW; 811BBAA1FD5040D1 CRC64;

Alignment Scores:
Pred. No.: 4.47e+05 Length: 14
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x Q643A0 (1-14)
QY 2 TTTGGCACT 10
Db 8 PheGlyThr 10
RESULT 45
Q7M1G7 PRELIMINARY; PRT; 14 AA.
AC Q7M1G7;
DT 01-MAR-2004 (TReMBLrel. 26, Created)
DT 01-MAR-2004 (TReMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE AtpB (Fragment).
GN Name=atpB;
OS Brachytheciastrum collinum.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
OC Bryopsida; Bryidae; Hypnales; Brachytheciaceae; Brachytheciastrum.
OX NCBI_TaxID=219719;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Collinum1767, Collinum1769, and Collinum1765;
RA Vanderpoorten A.;
RT "A molecular and morphological recircumscription of Brachytheciastrum
   (Brachytheciaceae, Bryopsida).";
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY736264; AAU25906.1; -
DR EMBL; AY736265; AAU25907.1; -
DR EMBL; AY736263; AAU25905.1; -
KW Chloroplast.
FT NON TER 14 14
SQ SEQUENCE 14 AA; 1544 MW; 811BBAA1FD5040D1 CRC64;

Alignment Scores:
Pred. No.: 4.47e+05 Length: 14
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x Q7M1G6 (1-14)
QY 10 AGTGCCAAA 2
Db 4 SerAlaLys 6
RESULT 46
Q9FUX5 PRELIMINARY; PRT; 14 AA.
ID Q9FUX5
```

```
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Chaperone, TCPI-related.
OS Avena sativa (Oat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Aveneae; Avena.
OX NCBI_TaxID=4498;
RN [1]
RP SEQUENCE.
RX MEDLINE=93288140; PubMed=8099715; DOI=10.1038/363644a0;
RA Mummert E., Grimm R., Speth V., Eckerskorn C., Schiltz E.,
RA Gatenby A.A., Schaefer E.;
RT "A TCPI-related molecular chaperone from plants refolds phytochrome to
   its photoreversible form.";
RL Nature 363:644-648(1993).
DR PIR; S33802; S33802.
SQ SEQUENCE 14 AA; 1525 MW; 439F33C92C4B6D77 CRC64;

Alignment Scores:
Pred. No.: 4.47e+05 Length: 14
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x Q7M1G6 (1-14)
QY 10 AGTGCCAAA 2
Db 4 SerAlaLys 6
RESULT 45
Q7M1G7 PRELIMINARY; PRT; 14 AA.
AC Q7M1G7;
DT 01-MAR-2004 (TReMBLrel. 26, Created)
DT 01-MAR-2004 (TReMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Chaperone, TCPI-related.
OS Avena sativa (Oat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Aveneae; Avena.
OX NCBI_TaxID=4498;
RN [1]
RP SEQUENCE.
RX MEDLINE=93288140; PubMed=8099715; DOI=10.1038/363644a0;
RA Mummert E., Grimm R., Speth V., Eckerskorn C., Schiltz E.,
RA Gatenby A.A., Schaefer E.;
RT "A TCPI-related molecular chaperone from plants refolds phytochrome to
   its photoreversible form.";
RL Nature 363:644-648(1993).
DR PIR; S33801; S33801.
SQ SEQUENCE 14 AA; 1607 MW; 438023C92C4B77C7 CRC64;

Alignment Scores:
Pred. No.: 4.47e+05 Length: 14
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x Q7M1G7 (1-14)
QY 10 AGTGCCAAA 2
Db 4 SerAlaLys 6
RESULT 46
Q9FUX5 PRELIMINARY; PRT; 14 AA.
ID Q9FUX5
```

AC Q9FUX5;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Waxy (Fragment).
OS Symphoricarpos albus (Common snowberry).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Campanulids; Dipsacales; Caprifoliaceae; Symphoricarpos.
OX NCBI_TaxID=13702;
RN [1]
RP SEQUENCE FROM N.A.
RA Gould K.R., Donoghue M.J.;
RL "Phylogeny and biogeography of Triosteum (Caprifoliaceae).";
RL Harv. Pap. Bot. 5:157-166(2000).
DR EMBL; AF277633; AAG31453.1; -.
FT NON_TER 1 1
SQ SEQUENCE 14 AA; 1485 MW; D08E206E5B7F8E5D CRC64;

Alignment Scores:
Pred. No.: 4.47e+05 Length: 14
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x Q9FUX5 (1-14)

QY 10 AGTGCCAAA 2
Db |||||

RESULT 47
Q8VU21 PRELIMINARY; PRT; 14 AA.
AC Q8VU21;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Oligopeptide transporter (Fragment).
GN Name=alia;
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RA Griffiths D.B., Hall L.M.C.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF246897; AAL68419.1; -.
FT NON_TER 14 14
SQ SEQUENCE 14 AA; 1450 MW; 455351FA2F4BEE27 CRC64;

Alignment Scores:
Pred. No.: 4.47e+05 Length: 14
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x Q8VU21 (1-14)

QY 3 TTGGCACTA 11
Db |||||

RESULT 48
Q711Z6 PRELIMINARY; PRT; 14 AA.
ID Q711Z6
AC Q711Z6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE 50S ribosomal protein L16 (Fragment).
OS Lactobacillus delbrueckii (subsp. lactis).
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=29397;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 4797;
RA Langenheim J.F., Ulrich R.L.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF496131; AAO6791.1; -.
DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
KW Ribosomal protein.
FT NON_TER 14 14
SQ SEQUENCE 14 AA; 1793 MW; 6B2956C438AC1BD4 CRC64;

Alignment Scores:
Pred. No.: 4.47e+05 Length: 14
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x Q711Z6 (1-14)

QY 9 GTGCCAAAG 1
Db |||||

RESULT 49
Q9UR64 PRELIMINARY; PRT; 15 AA.
ID Q9UR64;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE 46 kDa heme-containing ascorbate oxidase (Fragment).
OS Pleurotus ostreatus (Oyster mushroom) (White-rot fungus).
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OC Agaricales; Pleurotaceae; Pleurotus.
OX NCBI_TaxID=5322;
RN [1]
RP SEQUENCE.
RX MEDLINE=96216386; PubMed=8621708; DOI=10.1074/jbc.271.36.22052;
RA Kim Y.R., Yu S.W., Lee S.R., Hwang Y.Y., Kang S.O.;
RT "A heme-containing ascorbate oxidase from Pleurotus ostreatus.";
RL J. Biol. Chem. 271:3105-3111(1996).
SQ SEQUENCE 15 AA; 1738 MW; FF939C118BD30D75 CRC64;

Alignment Scores:
Pred. No.: 4.38e+05 Length: 15
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x Q9UR64 (1-15)

QY 3 TTGGCACTA 11
Db |||||

RESULT 50
Q9WZR5 PRELIMINARY; PRT; 15 AA.
ID Q9WZR5
AC Q9WZR5;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)

DE Interleukin 4 variant IL-4int2A (Fragment).
GN Name=IL-4;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=20304414; PubMed=10843729; DOI=10.1006/cyto.1999.0658;
RA Perkins H.D., van Leeuwen B.H., Hardy C.M., Kerr P.J.;
RT "The complete cDNA sequences of IL-2, IL-4, IL-6 AND IL-10 from the
RT European rabbit (Oryctolagus cuniculus).";
RL Cytokine 12:555-565(2000).
DR EMBL; AF169172; AAF86656.1; -.
FT NON TER 1 1
SQ SEQUENCE 15 AA; 1586 MW; 876C550E85307B55 CRC64;

Alignment Scores:
Pred. No.: 4.38e+05 Length: 15
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x Q9M2R5 (1-15)

QY 9 GTGCCAAG 1
Db |||||
12 ValProLys 14

Search completed: March 12, 2005, 11:07:34
Job time : 61.5 secs

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GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: March 12, 2005, 10:59:19 ; Search time 17 Seconds
(without alignments)
96.605 Million cell updates/sec

Title: US-10-070-588a-112

Perfect score: 3

Sequence: 1 ctttgcacta 11

Scoring table:

OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 513545 seqs, 74649064 residues

Word size: 1

Total number of hits satisfying chosen parameters: 895877

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 500 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DEV=xlh
-Q=/cgn2_1/USPTO.spool/US10070588/runat_10032005_120706_15259/app_query.fasta.1.199
-DB=issued Patents AA -QMT=fastan -SUFFIX=olin2p.ra1 -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi
-LIST=500 -DOALIGN=200 -THR SCORE=quality -THR MIN=1 -ALIGN=50 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10070588 @CGN 1 1 30 @runat_10032005_120706_15259 -NCPU=6 -ICPU=3
-NO_MMAP -LARGESQUERY -NEG_SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database :

Issued Patents AA:*
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2: /cgn2_6/ptodata/1/iaa/5B.COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A.COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS.COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	3	100.0	8	1	US-07-752-101A-4
2	3	100.0	8	1	US-08-204-656B-13
3	3	100.0	8	1	US-08-079-741A-101
4	3	100.0	8	1	US-07-939-085A-101
5	3	100.0	8	1	US-08-470-702-13
6	3	100.0	8	1	US-08-467-831-13
7	3	100.0	8	1	US-08-331-657-3
8	3	100.0	8	1	US-08-571-985-16
C 9	3	100.0	8	1	US-08-408-604A-181
10	3	100.0	8	1	US-08-408-604A-207
11	3	100.0	8	1	US-08-633-760-3
12	3	100.0	8	2	US-08-668-871-9
C 13	3	100.0	8	1	US-07-752-101A-4
14	3	100.0	8	1	US-08-204-656B-13
15	3	100.0	8	1	US-08-079-741A-101
16	3	100.0	8	1	US-07-939-085A-101
17	3	100.0	8	1	US-08-470-702-13
18	3	100.0	8	1	US-08-467-831-13
19	3	100.0	8	1	US-08-331-657-3
20	3	100.0	8	1	US-08-571-985-16
21	3	100.0	8	1	US-08-408-604A-181
22	3	100.0	8	1	US-08-408-604A-207
23	3	100.0	8	1	US-08-633-760-3
24	3	100.0	8	2	US-08-668-871-9
C 25	3	100.0	8	1	US-07-752-101A-4
26	3	100.0	8	1	US-08-204-656B-13
27	3	100.0	8	1	US-08-079-741A-101
28	3	100.0	8	1	US-07-939-085A-101
29	3	100.0	8	1	US-08-470-702-13
30	3	100.0	8	1	US-08-467-831-13
31	3	100.0	8	1	US-08-331-657-3
32	3	100.0	8	1	US-08-571-985-16
33	3	100.0	8	1	US-08-408-604A-181
34	3	100.0	8	1	US-08-408-604A-207
35	3	100.0	8	1	US-08-633-760-3
36	3	100.0	8	2	US-08-668-871-9
C 37	3	100.0	8	1	US-07-752-101A-4
38	3	100.0	8	1	US-08-204-656B-13
39	3	100.0	8	1	US-08-079-741A-101
40	3	100.0	8	1	US-07-939-085A-101
41	3	100.0	8	1	US-08-470-702-13
42	3	100.0	8	1	US-08-467-831-13
43	3	100.0	8	1	US-08-331-657-3
44	3	100.0	8	1	US-08-571-985-16
45	3	100.0	8	1	US-08-408-604A-181
46	3	100.0	8	1	US-08-408-604A-207
47	3	100.0	8	1	US-08-633-760-3
48	3	100.0	8	2	US-08-668-871-9
C 49	3	100.0	8	1	US-07-752-101A-4
50	3	100.0	8	1	US-08-204-656B-13
51	3	100.0	8	1	US-08-079-741A-101
52	3	100.0	8	1	US-07-939-085A-101
53	3	100.0	8	1	US-08-470-702-13
54	3	100.0	8	1	US-08-467-831-13
55	3	100.0	8	1	US-08-331-657-3
56	3	100.0	8	1	US-08-571-985-16
57	3	100.0	8	1	US-08-408-604A-181
58	3	100.0	8	1	US-08-408-604A-207
59	3	100.0	8	1	US-08-633-760-3
60	3	100.0	8	2	US-08-668-871-9
61	3	100.0	8	1	US-07-752-101A-4
62	3	100.0	8	1	US-08-204-656B-13
63	3	100.0	8	1	US-08-079-741A-101
64	3	100.0	8	1	US-07-939-085A-101
65	3	100.0	8	1	US-08-470-702-13
66	3	100.0	8	1	US-08-467-831-13
67	3	100.0	8	1	US-08-331-657-3
68	3	100.0	8	1	US-08-571-985-16
69	3	100.0	8	1	US-08-408-604A-181
70	3	100.0	8	1	US-08-408-604A-207
71	3	100.0	8	1	US-08-633-760-3
72	3	100.0	8	2	US-08-668-871-9
73	3	100.0	8	1	US-07-752-101A-4
74	3	100.0	8	1	US-08-204-656B-13
75	3	100.0	8	1	US-08-079-741A-101
76	3	100.0	8	1	US-07-939-085A-101
77	3	100.0	8	1	US-08-470-702-13
78	3	100.0	8	1	US-08-467-831-13
79	3	100.0	8	1	US-08-331-657-3
80	3	100.0	8	1	US-08-571-985-16
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82	3	100.0	8	1	US-08-408-604A-207
83	3	100.0	8	1	US-08-633-760-3
84	3	100.0	8	2	US-08-668-871-9
85	3	100.0	8	1	US-07-752-101A-4

Sequence 9, Appli
Sequence 51, Appli
Sequence 163, App
Sequence 53, Appli
Sequence 16, Appli
Sequence 123, App
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Sequence 366, App
Sequence 367, App
Sequence 368, App
Sequence 369, App
Sequence 387, App
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Sequence 54, Appli
Sequence 188, App
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Sequence 188, App
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Sequence 39, Appli

86	3	100.0	9	1	US-08-454-207A-40	Sequence 40, Appl	159	3	100.0	9	3	US-09-518-046-60	Sequence 60, Appl
87	3	100.0	9	1	US-08-454-207A-41	Sequence 41, Appl	160	3	100.0	9	3	US-09-567-995-9	Sequence 9, Appl
88	3	100.0	9	1	US-08-454-207A-48	Sequence 48, Appl	161	3	100.0	9	3	US-09-406-781-19	Sequence 19, Appl
89	3	100.0	9	1	US-08-454-207A-49	Sequence 49, Appl	162	3	100.0	9	3	US-09-492-543-33	Sequence 33, Appl
90	3	100.0	9	1	US-08-454-207A-51	Sequence 50, Appl	163	3	100.0	9	3	US-09-492-543-53	Sequence 53, Appl
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92	3	100.0	9	1	US-08-454-207A-52	Sequence 52, Appl	165	3	100.0	9	3	US-09-492-543-96	Sequence 96, Appl
93	3	100.0	9	1	US-08-454-207A-53	Sequence 53, Appl	166	3	100.0	9	3	US-09-492-543-106	Sequence 106, Appl
94	3	100.0	9	1	US-08-454-207A-54	Sequence 54, Appl	167	3	100.0	9	3	US-09-492-543-111	Sequence 111, Appl
95	3	100.0	9	1	US-08-454-207A-57	Sequence 57, Appl	168	3	100.0	9	3	US-09-492-543-123	Sequence 123, Appl
96	3	100.0	9	1	US-08-454-207A-58	Sequence 58, Appl	169	3	100.0	9	3	US-09-492-543-138	Sequence 138, Appl
97	3	100.0	9	1	US-08-454-207A-59	Sequence 59, Appl	170	3	100.0	9	3	US-09-492-543-142	Sequence 142, Appl
98	3	100.0	9	1	US-08-454-207A-60	Sequence 60, Appl	171	3	100.0	9	3	US-09-241-268-1	Sequence 1, Appl
99	3	100.0	9	1	US-08-454-207A-61	Sequence 61, Appl	172	3	100.0	9	3	US-08-292-492B-5	Sequence 5, Appl
100	3	100.0	9	1	US-08-454-207A-62	Sequence 62, Appl	173	3	100.0	9	3	US-09-705-160-39	Sequence 39, Appl
101	3	100.0	9	1	US-08-454-207A-63	Sequence 63, Appl	174	3	100.0	9	3	US-09-256-194-14	Sequence 14, Appl
102	3	100.0	9	1	US-08-454-207A-64	Sequence 64, Appl	175	3	100.0	9	4	US-09-165-863-6	Sequence 6, Appl
103	3	100.0	9	1	US-08-454-207A-65	Sequence 65, Appl	176	3	100.0	9	4	US-09-160-513-13	Sequence 13, Appl
104	3	100.0	9	1	US-08-454-207A-66	Sequence 66, Appl	177	3	100.0	9	4	US-09-160-513-40	Sequence 40, Appl
105	3	100.0	9	1	US-08-454-207A-67	Sequence 67, Appl	178	3	100.0	9	4	US-09-697-884-50	Sequence 50, Appl
106	3	100.0	9	1	US-08-454-207A-68	Sequence 68, Appl	179	3	100.0	9	4	US-09-495-562-1	Sequence 1, Appl
107	3	100.0	9	1	US-08-454-207A-69	Sequence 69, Appl	180	3	100.0	9	4	US-09-435-524-3	Sequence 3, Appl
108	3	100.0	9	1	US-08-454-207A-70	Sequence 70, Appl	181	3	100.0	9	4	US-09-435-524-4	Sequence 4, Appl
109	3	100.0	9	1	US-08-709-173-8	Sequence 8, Appl	182	3	100.0	9	4	US-09-847-185-25	Sequence 25, Appl
110	3	100.0	9	1	US-08-709-173-11	Sequence 11, Appl	183	3	100.0	9	4	US-09-213-383-19	Sequence 19, Appl
111	3	100.0	9	1	US-08-709-173-14	Sequence 14, Appl	184	3	100.0	9	4	US-08-403-459-49	Sequence 49, Appl
112	3	100.0	9	1	US-08-638-911A-15	Sequence 15, Appl	185	3	100.0	9	4	US-08-403-459-50	Sequence 50, Appl
113	3	100.0	9	1	US-08-638-911A-18	Sequence 18, Appl	186	3	100.0	9	4	US-09-289-350-6	Sequence 6, Appl
114	3	100.0	9	1	US-08-638-911A-21	Sequence 21, Appl	187	3	100.0	9	4	US-09-574-749B-8	Sequence 8, Appl
115	3	100.0	9	1	US-08-363-691-3	Sequence 3, Appl	188	3	100.0	9	4	US-09-341-982-92	Sequence 92, Appl
116	3	100.0	9	1	US-08-787-547-7	Sequence 47, Appl	189	3	100.0	9	4	US-09-880-132-19	Sequence 19, Appl
117	3	100.0	9	2	US-08-468-819-19	Sequence 19, Appl	190	3	100.0	9	4	US-09-318-141-6	Sequence 6, Appl
118	3	100.0	9	2	US-08-482-651-10	Sequence 10, Appl	191	3	100.0	9	4	US-09-318-243-38	Sequence 38, Appl
119	3	100.0	9	2	US-08-482-651-37	Sequence 37, Appl	192	3	100.0	9	4	US-09-918-243-43	Sequence 43, Appl
120	3	100.0	9	2	US-08-389-360-3	Sequence 3, Appl	193	3	100.0	9	4	US-09-918-243-46	Sequence 46, Appl
121	3	100.0	9	2	US-08-389-360-4	Sequence 4, Appl	194	3	100.0	9	4	US-09-604-958-8	Sequence 8, Appl
122	3	100.0	9	2	US-08-709-177-8	Sequence 8, Appl	195	3	100.0	9	4	US-09-382-497-3	Sequence 3, Appl
123	3	100.0	9	2	US-08-709-177-11	Sequence 11, Appl	196	3	100.0	9	4	US-09-382-497-4	Sequence 4, Appl
124	3	100.0	9	2	US-08-902-516-25	Sequence 25, Appl	197	3	100.0	9	4	US-09-750-876-6	Sequence 6, Appl
125	3	100.0	9	2	US-08-968-676-13	Sequence 13, Appl	198	3	100.0	9	4	US-09-750-876-8	Sequence 8, Appl
126	3	100.0	9	2	US-08-968-676-49	Sequence 49, Appl	199	3	100.0	9	4	US-09-454-204A-10	Sequence 10, Appl
127	3	100.0	9	2	US-08-993-738A-1	Sequence 1, Appl	200	3	100.0	9	4	US-09-721-108-185	Sequence 185, Appl
128	3	100.0	9	2	US-09-036-582-6	Sequence 6, Appl	201	3	100.0	9	4	US-09-169-717B-12	Sequence 12, Appl
129	3	100.0	9	2	US-08-318-856A-5	Sequence 5, Appl	202	3	100.0	9	4	US-09-647-372B-8	Sequence 8, Appl
130	3	100.0	9	2	US-08-318-856A-53	Sequence 53, Appl	203	3	100.0	9	4	US-09-647-372B-10	Sequence 10, Appl
131	3	100.0	9	2	US-08-986-234-65	Sequence 65, Appl	204	3	100.0	9	4	US-09-633-994-5	Sequence 5, Appl
132	3	100.0	9	2	US-08-986-234-66	Sequence 66, Appl	205	3	100.0	9	4	US-09-806-769-6	Sequence 6, Appl
133	3	100.0	9	2	US-08-986-234-99	Sequence 99, Appl	206	3	100.0	9	4	US-09-396-315-50	Sequence 50, Appl
134	3	100.0	9	2	US-08-986-234-100	Sequence 100, Appl	207	3	100.0	9	4	US-09-462-453-2	Sequence 2, Appl
135	3	100.0	9	2	US-08-159-339A-182	Sequence 182, Appl	208	3	100.0	9	4	US-09-995-587A-8	Sequence 8, Appl
136	3	100.0	9	3	US-08-159-339A-769	Sequence 769, Appl	209	3	100.0	9	4	US-09-171-553B-15	Sequence 15, Appl
137	3	100.0	9	3	US-08-159-339A-1008	Sequence 1008, Appl	210	3	100.0	9	4	US-09-124-398-15	Sequence 15, Appl
138	3	100.0	9	3	US-08-159-339A-1009	Sequence 1009, Appl	211	3	100.0	9	4	US-09-408-036B-38	Sequence 38, Appl
139	3	100.0	9	3	US-08-159-339A-1010	Sequence 1010, Appl	212	3	100.0	9	4	US-09-631-863A-95	Sequence 95, Appl
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142	3	100.0	9	3	US-08-037-679-1	Sequence 1, Appl	215	3	100.0	9	4	US-09-693-746-118	Sequence 118, Appl
143	3	100.0	9	3	US-08-314-742-6	Sequence 6, Appl	216	3	100.0	9	4	US-09-980-177A-1	Sequence 1, Appl
144	3	100.0	9	3	US-08-660-092-13	Sequence 13, Appl	217	3	100.0	9	4	PCT-US94-09143-20	Sequence 20, Appl
145	3	100.0	9	3	US-08-660-092-40	Sequence 40, Appl	218	3	100.0	9	4	PCT-US95-04121-36	Sequence 36, Appl
146	3	100.0	9	3	US-09-183-931-39	Sequence 39, Appl	219	3	100.0	9	5	US-08-164-839-41	Sequence 41, Appl
147	3	100.0	9	3	US-09-551-510-6	Sequence 6, Appl	220	3	100.0	10	1	US-08-371-930-11	Sequence 11, Appl
148	3	100.0	9	3	US-09-551-510-7	Sequence 7, Appl	221	3	100.0	10	1	US-08-462-949-23	Sequence 23, Appl
149	3	100.0	9	3	US-09-551-510-8	Sequence 8, Appl	222	3	100.0	10	1	US-08-583-799-41	Sequence 41, Appl
150	3	100.0	9	3	US-09-183-706-9	Sequence 9, Appl	223	3	100.0	10	1	US-08-239-854-7	Sequence 7, Appl
151	3	100.0	9	3	US-09-171-878-14	Sequence 14, Appl	224	3	100.0	10	1	US-08-330-163-45	Sequence 45, Appl
152	3	100.0	9	3	US-08-713-354C-1	Sequence 1, Appl	225	3	100.0	10	1	US-08-023-764B-23	Sequence 23, Appl
153	3	100.0	9	3	US-09-166-448-50	Sequence 50, Appl	226	3	100.0	10	1	US-08-214-650-2	Sequence 2, Appl
154	3	100.0	9	3	US-09-502-600-38	Sequence 38, Appl	227	3	100.0	10	1	US-08-454-207A-2	Sequence 2, Appl
155	3	100.0	9	3	US-09-502-600-43	Sequence 43, Appl	228	3	100.0	10	1	US-08-454-207A-5	Sequence 5, Appl
156	3	100.0	9	3	US-09-502-600-46	Sequence 46, Appl	229	3	100.0	10	1	US-08-482-111-45	Sequence 45, Appl
157	3	100.0	9	3	US-09-518-046-48	Sequence 48, Appl	230	3	100.0	10	1		
158	3	100.0	9	3			231	3	100.0	10	1		

232	3	100.0	10	2	US-08-482-651-59	Sequence 59, Appl	c 305	3	100.0	10	4	US-09-261-894A-16	Sequence 16, Appl
c 233	3	100.0	10	2	US-08-685-589A-132	Sequence 132, App	c 306	3	100.0	10	4	US-09-261-894A-17	Sequence 17, Appl
c 234	3	100.0	10	2	US-08-968-676-16	Sequence 16, Appl	c 307	3	100.0	10	4	US-09-261-894A-45	Sequence 45, Appl
c 235	3	100.0	10	2	US-08-968-676-17	Sequence 17, Appl	c 308	3	100.0	10	4	US-09-261-894A-47	Sequence 47, Appl
c 236	3	100.0	10	2	US-08-968-676-45	Sequence 45, Appl	c 309	3	100.0	10	4	US-09-261-894A-50	Sequence 50, Appl
c 237	3	100.0	10	2	US-08-968-676-47	Sequence 47, Appl	c 310	3	100.0	10	4	US-09-261-894A-51	Sequence 51, Appl
c 238	3	100.0	10	2	US-08-968-676-50	Sequence 50, Appl	c 311	3	100.0	10	4	US-09-261-894A-52	Sequence 52, Appl
c 239	3	100.0	10	2	US-08-968-676-51	Sequence 51, Appl	c 312	3	100.0	10	4	US-09-261-894A-53	Sequence 53, Appl
c 240	3	100.0	10	2	US-08-968-676-52	Sequence 52, Appl	c 313	3	100.0	10	4	US-09-261-894A-54	Sequence 54, Appl
c 241	3	100.0	10	2	US-08-968-676-53	Sequence 53, Appl	c 314	3	100.0	10	4	US-09-261-894A-55	Sequence 55, Appl
c 242	3	100.0	10	2	US-08-968-676-54	Sequence 54, Appl	c 315	3	100.0	10	4	US-09-261-894A-56	Sequence 56, Appl
c 243	3	100.0	10	2	US-08-968-676-55	Sequence 55, Appl	c 316	3	100.0	10	4	US-09-261-894A-57	Sequence 57, Appl
c 244	3	100.0	10	2	US-08-968-676-56	Sequence 56, Appl	c 317	3	100.0	10	4	US-09-261-894A-58	Sequence 58, Appl
c 245	3	100.0	10	2	US-08-968-676-57	Sequence 57, Appl	c 318	3	100.0	10	4	US-09-261-894A-94	Sequence 94, Appl
c 246	3	100.0	10	2	US-08-968-676-58	Sequence 58, Appl	c 319	3	100.0	10	4	US-09-261-894A-107	Sequence 107, App
c 247	3	100.0	10	2	US-08-968-676-94	Sequence 94, Appl	c 320	3	100.0	10	4	US-09-261-894A-108	Sequence 108, App
c 248	3	100.0	10	2	US-08-968-676-107	Sequence 107, App	c 321	3	100.0	10	4	US-09-261-894A-109	Sequence 109, App
c 249	3	100.0	10	2	US-08-968-676-108	Sequence 108, App	c 322	3	100.0	10	4	US-09-261-894A-110	Sequence 110, App
c 250	3	100.0	10	2	US-08-968-676-109	Sequence 109, App	c 323	3	100.0	10	4	US-09-261-894A-111	Sequence 111, App
c 251	3	100.0	10	2	US-08-968-676-110	Sequence 110, App	c 324	3	100.0	10	4	US-09-261-894A-112	Sequence 112, App
c 252	3	100.0	10	2	US-08-968-676-111	Sequence 111, App	c 325	3	100.0	10	4	US-09-261-894A-113	Sequence 113, App
c 253	3	100.0	10	2	US-08-968-676-112	Sequence 112, App	c 326	3	100.0	10	4	US-09-693-746-55	Sequence 55, Appl
c 254	3	100.0	10	2	US-08-968-676-113	Sequence 113, App	c 327	3	100.0	10	4	US-09-693-746-75	Sequence 75, Appl
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c 256	3	100.0	10	2	US-08-350-260A-514	Sequence 514, App	c 329	3	100.0	10	5	PCT-US95-02121-47	Sequence 47, Appl
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c 258	3	100.0	10	3	US-08-822-586-2	Sequence 2, Appl	c 331	3	100.0	10	5	PCT-US95-02121-126	Sequence 126, App
c 259	3	100.0	10	3	US-08-822-586-6	Sequence 6, Appl	c 332	3	100.0	10	5	PCT-US95-02121-133	Sequence 133, App
c 260	3	100.0	10	3	US-08-822-586-10	Sequence 10, Appl	c 333	3	100.0	10	5	PCT-US95-06157-14	Sequence 14, Appl
c 261	3	100.0	10	3	US-08-822-586-30	Sequence 30, Appl	c 334	3	100.0	11	1	US-08-134-211A-2	Sequence 2, Appl
c 262	3	100.0	10	3	US-08-822-586-34	Sequence 34, Appl	c 335	3	100.0	11	1	US-08-388-267C-11	Sequence 11, Appl
c 263	3	100.0	10	3	US-08-822-586-38	Sequence 38, Appl	c 336	3	100.0	11	1	US-08-347-198A-5	Sequence 5, Appl
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c 265	3	100.0	10	3	US-08-159-339A-962	Sequence 962, App	c 338	3	100.0	11	1	US-08-408-604A-70	Sequence 70, Appl
c 266	3	100.0	10	3	US-08-159-339A-993	Sequence 993, App	c 339	3	100.0	11	2	US-08-705-660-41	Sequence 41, Appl
c 267	3	100.0	10	3	US-08-159-339A-1031	Sequence 1031, Ap	c 340	3	100.0	11	2	US-08-968-676-12	Sequence 12, Appl
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c 269	3	100.0	10	3	US-08-767-820A-14	Sequence 14, Appl	c 342	3	100.0	11	2	US-08-968-676-46	Sequence 46, Appl
c 270	3	100.0	10	3	US-09-385-442-19	Sequence 19, Appl	c 343	3	100.0	11	2	US-08-433-133-26	Sequence 26, Appl
c 271	3	100.0	10	3	US-08-660-092-212	Sequence 212, App	c 344	3	100.0	11	2	US-08-433-133-40	Sequence 40, Appl
c 272	3	100.0	10	3	US-08-441-507-52	Sequence 52, Appl	c 345	3	100.0	11	2	US-09-005-397-28	Sequence 28, Appl
c 273	3	100.0	10	3	US-09-461-697-283	Sequence 283, App	c 346	3	100.0	11	3	US-08-552-500-12	Sequence 12, Appl
c 274	3	100.0	10	3	US-08-590-563-24	Sequence 24, Appl	c 347	3	100.0	11	3	US-08-833-553-3	Sequence 3, Appl
c 275	3	100.0	10	3	US-08-938-085A-59	Sequence 59, Appl	c 348	3	100.0	11	3	US-08-989-045-41	Sequence 41, Appl
c 276	3	100.0	10	3	US-09-468-265-6	Sequence 6, Appl	c 349	3	100.0	11	3	US-08-335-844A-29	Sequence 29, Appl
c 277	3	100.0	10	3	US-09-044-718-62	Sequence 62, Appl	c 350	3	100.0	11	3	US-08-195-006-12	Sequence 12, Appl
c 278	3	100.0	10	4	US-09-160-513-212	Sequence 212, App	c 351	3	100.0	11	3	US-08-836-075A-149	Sequence 149, App
c 279	3	100.0	10	4	US-09-160-513-222	Sequence 222, App	c 352	3	100.0	11	3	US-09-418-222-3	Sequence 3, Appl
c 280	3	100.0	10	4	US-08-197-484-47	Sequence 47, Appl	c 353	3	100.0	11	3	US-08-456-748B-2	Sequence 2, Appl
c 281	3	100.0	10	4	US-08-197-484-54	Sequence 54, Appl	c 354	3	100.0	11	3	US-08-492-411A-33	Sequence 33, Appl
c 282	3	100.0	10	4	US-08-197-484-126	Sequence 126, App	c 355	3	100.0	11	3	US-09-277-720-11	Sequence 11, Appl
c 283	3	100.0	10	4	US-08-197-484-133	Sequence 133, App	c 356	3	100.0	11	3	US-09-063-733A-30	Sequence 30, Appl
c 284	3	100.0	10	4	US-09-396-813-12	Sequence 12, Appl	c 357	3	100.0	11	4	US-09-336-813-6	Sequence 6, Appl
c 285	3	100.0	10	4	US-08-520-373D-25	Sequence 25, Appl	c 358	3	100.0	11	4	US-09-129-366-29	Sequence 29, Appl
c 286	3	100.0	10	4	US-09-106-568E-26	Sequence 26, Appl	c 359	3	100.0	11	4	US-09-538-873-9	Sequence 9, Appl
c 287	3	100.0	10	4	US-09-106-568E-46	Sequence 46, Appl	c 360	3	100.0	11	4	US-09-538-873-11	Sequence 11, Appl
c 288	3	100.0	10	4	US-09-106-568E-63	Sequence 63, Appl	c 361	3	100.0	11	4	US-09-538-873-12	Sequence 12, Appl
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c 293	3	100.0	10	4	US-09-490-702B-38	Sequence 38, Appl	c 366	3	100.0	11	4	US-09-350-641C-1693	Sequence 1693, App
c 294	3	100.0	10	4	US-10-072-844-59	Sequence 59, Appl	c 367	3	100.0	11	4	US-09-721-108-183	Sequence 183, App
c 295	3	100.0	10	4	US-08-983-157B-7	Sequence 7, Appl	c 368	3	100.0	11	4	US-09-350-841A-1892	Sequence 1892, Ap
c 296	3	100.0	10	4	US-09-721-870-97	Sequence 97, Appl	c 369	3	100.0	11	4	US-09-403-269-3	Sequence 3, Appl
c 297	3	100.0	10	4	US-10-072-841A-59	Sequence 59, Appl	c 370	3	100.0	11	4	US-09-315-355A-41	Sequence 41, Appl
c 298	3	100.0	10	4	US-09-721-108-184	Sequence 184, App	c 371	3	100.0	11	4	US-09-743-225-4	Sequence 4, Appl
c 299	3	100.0	10	4	US-09-235-832-24	Sequence 24, Appl	c 372	3	100.0	11	4	US-09-261-894A-12	Sequence 12, Appl
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c 302	3	100.0	10	4	US-09-974-992B-26	Sequence 26, Appl	c 375	3	100.0	11	5	PCT-US92-03432-10	Sequence 10, Appl
c 303	3	100.0	10	4	US-10-062-848-62	Sequence 62, Appl	c 376	3	100.0	11	5	PCT-US94-07644A-12	Sequence 12, Appl
c 304	3	100.0	10	4	US-10-219-631A-59	Sequence 59, Appl	c 377	3	100.0	11	6	5171684-10	Patent No. 5171684

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379 Patent No. 5210075-35 11 6 5210075-35 3 100.0
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421 Patent No. 5210075-35 11 6 5210075-35 3 100.0
422 Patent No. 5210075-35 11 6 5210075-35 3 100.0
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424 Patent No. 5210075-35 11 6 5210075-35 3 100.0
425 Patent No. 5210075-35 11 6 5210075-35 3 100.0
426 Patent No. 5210075-35 11 6 5210075-35 3 100.0
427 Patent No. 5210075-35 11 6 5210075-35 3 100.0
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430 Patent No. 5210075-35 11 6 5210075-35 3 100.0
431 Patent No. 5210075-35 11 6 5210075-35 3 100.0
432 Patent No. 5210075-35 11 6 5210075-35 3 100.0
433 Patent No. 5210075-35 11 6 5210075-35 3 100.0
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435 Patent No. 5210075-35 11 6 5210075-35 3 100.0
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450 Patent No. 5210075-35 11 6 5210075-35 3 100.0

451 Patent No. 5210075-2 11 6 5210075-2 3 100.0
452 Patent No. 5210075-35 11 6 5210075-35 3 100.0
453 Patent No. 5171684 11 6 5171684-10 3 100.0
454 Patent No. 5210075-2 11 6 5210075-2 3 100.0
455 Patent No. 5210075-35 11 6 5210075-35 3 100.0
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477 Patent No. 5210075-35 11 6 5210075-35 3 100.0
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482 Patent No. 5210075-35 11 6 5210075-35 3 100.0
483 Patent No. 5210075-35 11 6 5210075-35 3 100.0
484 Patent No. 5210075-35 11 6 5210075-35 3 100.0
485 Patent No. 5210075-35 11 6 5210075-35 3 100.0
486 Patent No. 5210075-35 11 6 5210075-35 3 100.0
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488 Patent No. 5210075-35 11 6 5210075-35 3 100.0
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494 Patent No. 5210075-35 11 6 5210075-35 3 100.0
495 Patent No. 5210075-35 11 6 5210075-35 3 100.0
496 Patent No. 5210075-35 11 6 5210075-35 3 100.0
497 Patent No. 5210075-35 11 6 5210075-35 3 100.0
498 Patent No. 5210075-35 11 6 5210075-35 3 100.0
499 Patent No. 5210075-35 11 6 5210075-35 3 100.0
500 Patent No. 5210075-35 11 6 5210075-35 3 100.0

ALIGNMENTS

RESULT 1

US-07-752-101A-4
; Sequence 4, Application US/07752101A
; Patent No. 5326857
; GENERAL INFORMATION:
; APPLICANT: Yamamoto, Fumi-ichiro
; APPLICANT: White, Thayer
; APPLICANT: Hakomori, Sen-itiroh
; APPLICANT: Clausen, Henrik
; TITLE OF INVENTION: ABO GENOTYPING
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: U.S.
; ZIP: 98104
; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/752,101A
FILING DATE: 19910829
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 150036.406C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-622-4900
TELEFAX: 206-682-6031
TELEX: 3723836
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
US-07-752-101A-4

Alignment Scores:
Pred. No.: 1.85e+07
Score: 3.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 1
Gaps: 0

US-10-070-588A-112 (1-11) x US-07-752-101A-4 (1-8)

QY 9 GTGCCAAG 1
Db 6 ValProlys 8

RESULT 2
US-08-204-656B-13
Sequence 13, Application US/08204656B
Patent No. 5538882
GENERAL INFORMATION:
APPLICANT: Matsui, Ikuo
APPLICANT: Ishikawa, Kazuhiko
APPLICANT: Miyairi, Sachio
APPLICANT: Honda, Koichi
TITLE OF INVENTION: Variant-Type Carbohydrate Hydrolase,
TITLE OF INVENTION: Variant Gene Of The Enzyme And Method For Producing
TITLE OF INVENTION: Oligosaccharide Using The Enzyme
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP
STREET: 8110 Gatehouse Road, Suite 500 East
CITY: Falls Church
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22042
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/204,656B
FILING DATE: 02-MAR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Weiner, Marc S.

REGISTRATION NUMBER: 32,181
REFERENCE/DOCKET NUMBER: 234-252P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
TELEX: 248345
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
US-08-204-656B-13

Alignment Scores:
Pred. No.: 1.85e+07
Score: 3.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 1
Gaps: 0

US-10-070-588A-112 (1-11) x US-08-204-656B-13 (1-8)

QY 2 TTTGGCACT 10
Db 3 PheGlyThr 5

RESULT 3
US-08-079-741A-101
Sequence 101, Application US/08079741A
Patent No. 5585275
GENERAL INFORMATION:
APPLICANT: SURNAME, OTHER NAMES and/or INITIALS
APPLICANT: Johnson, Charles R.
APPLICANT: Giebel, Lutz B.
TITLE OF INVENTION: Pilot Apparatus For Peptide
TITLE OF INVENTION: Synthesis and Screening
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS: Inventors'/Assignee's Counsel
ADDRESSEE: ROSENBLUM, PARISH & ISAACS
STREET: 160 W. Santa Clara Street, Suite 1500
CITY: San Jose
STATE: California
COUNTRY: USA
ZIP: 95113
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3-1/2 inch, 1.44M byte
MEDIUM TYPE: storage
COMPUTER: IBM Clone
OPERATING SYSTEM: MS-DOS 5.00
SOFTWARE: WordPerfect 5.1, ASCII format (DOS text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/079,741A
FILING DATE: 18-June-1993
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/939,065
FILING DATE: 02-Sept-1992
ATTORNEY/AGENT INFORMATION:
NAME: DULIN, JACQUES M.
REGISTRATION NUMBER: 24,067
REFERENCE/DOCKET NUMBER: 5303-8
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 977-0120
TELEFAX: (408) 977-0129
INFORMATION FOR SEQ ID NO: 101:
SEQUENCE CHARACTERISTICS:
LENGTH: 8

```

; TYPE: Amino Acids
; STRANDEDNESS:
; TOPOLOGY: Linear
; MOLECULE TYPE: Peptide
; DESCRIPTION:
; FEATURE:
; NAME/KEY: Pepsyn-K Bead Test Peptide
; LOCATION:
; IDENTIFICATION METHOD: Constructed using a
; IDENTIFICATION METHOD: Milligen/Bioscience Model 9600 peptide synthesizer.
; OTHER INFORMATION: Biological activity not
; PUBLICATION INFORMATION:
; AUTHORS:
; TITLE:
; JOURNAL:
; VOLUME:
; ISSUE:
; PAGES:
; DATE:
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO: 101: From 1 to 8
US-08-079-741A-101

Alignment Scores:
Pred No.: 1.85e+07 Length: 8
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-10-070-588A-112 (1-11) x US-08-079-741A-101 (1-8)

Qy 3 TTGGCACTA 11
Db 4 LeuAlaLeu 6

RESULT 4
US-07-939-065A-101
; Sequence 101, Application US/07939065A
; Patent No. 5591646
; GENERAL INFORMATION:
; APPLICANT: SURNAME, OTHER NAMES and/or INITIALS
; APPLICANT: Johnson, Charles R.
; APPLICANT: Giebel, Lutz B.
; TITLE OF INVENTION: Method and Apparatus For Peptide
; TITLE OF INVENTION: Synthesis and Screening
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS: Inventors'/Assignee's Counsel
; ADDRESSEE: PILLSBURY MADISON & SUTRO
; STREET: Ten Almaden Boulevard, Suite 800
; CITY: San Jose
; STATE: California
; COUNTRY: USA
; ZIP: 95113
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3-1/2 inch, 1.44M byte
; MEDIUM TYPE: storage
; COMPUTER: IBM Clone
; OPERATING SYSTEM: MS-DOS 5.0
; SOFTWARE: WordPerfect 5.2, ASCII format (DOS text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/939,065A
; FILING DATE: 02-Sept-1992
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: NA
; FILING DATE: NA
; ATTORNEY/AGENT INFORMATION:
; NAME: DULIN, JACQUES M.
; REGISTRATION NUMBER: 24,067

; TYPE: Amino Acids
; STRANDEDNESS:
; TELEPHONE: (408) 947-4000
; TELEFAX: (408) 287-8341
; INFORMATION FOR SEQ ID NO: 101:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8
; TYPE: Amino Acids
; STRANDEDNESS:
; TOPOLOGY: Linear
; MOLECULE TYPE: Peptide
; DESCRIPTION:
; FEATURE:
; NAME/KEY: Pepsyn-K Bead Test Peptide
; LOCATION:
; IDENTIFICATION METHOD: Constructed using a
; IDENTIFICATION METHOD: Milligen/Bioscience Model 9600 peptide synthesizer.
; OTHER INFORMATION: Biological activity not
; OTHER INFORMATION: determined. Xaa represents a random amino acid
; OTHER INFORMATION: selected from mixtures of the following 10 amino
; OTHER INFORMATION: acids to give equal incorporation: Nle, His, Pro,
; OTHER INFORMATION: Gln, Tyr, Gly, Phe, Arg, Glu, Ala. Where Leu or
; OTHER INFORMATION: Ala is specified at any position in the sequence,
; OTHER INFORMATION: then Leu refers to Nle (or normal-leucine) and Ala
; OTHER INFORMATION: refers to Ala (or beta-alanine).
; PUBLICATION INFORMATION:
; AUTHORS:
; TITLE:
; JOURNAL:
; VOLUME:
; ISSUE:
; PAGES:
; DATE:
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO: 101: 1 to 8
US-07-939-065A-101

Alignment Scores:
Pred No.: 1.85e+07 Length: 8
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-10-070-588A-112 (1-11) x US-07-939-065A-101 (1-8)

Qy 3 TTGGCACTA 11
Db 4 LeuAlaLeu 6

RESULT 5
US-08-470-702-13
; Sequence 13, Application US/08470702
; Patent No. 5631149
; GENERAL INFORMATION:
; APPLICANT: MATSUI, IKUO
; APPLICANT: ISHIKAWA, KAZUHIKO
; APPLICANT: MIYAIRI, SACHIO
; APPLICANT: HONDA, KOICHI
; TITLE OF INVENTION: VARIANT-TYPE CARBOHYDRATE HYDROLASE,
; TITLE OF INVENTION: VARIANT GENE OF THE ENZYME AND METHOD FOR PRODUCING
; TITLE OF INVENTION: OLIGOSACCHARIDE USING THE ENZYME
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
; STREET: 8110 Gatehouse Road, Suite 500 East
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22042
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/470,702
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/204,656

FILING DATE: 02-MAR-1994

ATTORNEY/AGENT INFORMATION:

NAME: WEINER, MARC S.

REGISTRATION NUMBER: 32,181

REFERENCE/DOCKET NUMBER: 234-252P

TELEPHONE: (703) 205-8000

TELEFAX: (703) 205-8050

TELEX: 248345

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: N-terminal

US-08-470-702-13

Alignment Scores:

Pred. No.:	1.85e+07	Length:	8
Score:	3.00	Matches:	3
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	1	Gaps:	0

US-10-070-588A-112 (1-11) x US-08-470-702-13 (1-8)

Qy 2 TTGGCACT 10

Db 3 PheGlyThr 5

RESULT 6

US-08-467-831-13

Sequence 13, Application US/08467831

Patent No. 5635378

GENERAL INFORMATION:

APPLICANT: MATSUI, IKUO

APPLICANT: ISHIKAWA, KAZUHIKO

APPLICANT: MIYAIRI, SACHIO

APPLICANT: HONDA, KOICHI

TITLE OF INVENTION: VARIANT-TYPE CARBOHYDRATE HYDROLASE.

TITLE OF INVENTION: VARIANT GENE OF THE ENZYME AND METHOD FOR PRODUCING

TITLE OF INVENTION: OLIGOSACCHARIDE USING THE ENZYME

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH

STREET: 8110 Gatehouse Road, Suite 500 East

CITY: Falls Church

STATE: Virginia

COUNTRY: U.S.A.

ZIP: 22042

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/467,831

FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/204,656

FILING DATE: 02-MAR-1994

ATTORNEY/AGENT INFORMATION:

NAME: WEINER, MARC S.

REGISTRATION NUMBER: 32,181

REFERENCE/DOCKET NUMBER: 234-252P

TELEPHONE: (703) 205-8000

TELEFAX: (703) 205-8050

TELEX: 248345

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: N-terminal

US-08-467-831-13

Alignment Scores:

Pred. No.:	1.85e+07	Length:	8
Score:	3.00	Matches:	3
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	1	Gaps:	0

US-10-070-588A-112 (1-11) x US-08-467-831-13 (1-8)

Qy 2 TTGGCACT 10

Db 3 PheGlyThr 5

RESULT 7

US-08-331-657-3

Sequence 3, Application US/08331657

Patent No. 5783183

GENERAL INFORMATION:

APPLICANT: Langeveld, Pieter C.

APPLICANT: Van Solingen, Pieter

APPLICANT: Stark, Jacobus

APPLICANT: Vollebregt, Adrianus W.H.

TITLE OF INVENTION: Cloning of the zymocin gene and use of

TITLE OF INVENTION: zymocin in beverages

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: Morrison & Foerster

STREET: 2000 Pennsylvania Avenue, NW

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20006-1812

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/331,657

FILING DATE: 22-FEB-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Murashige, Kate H.

REGISTRATION NUMBER: 29,959

REFERENCE/DOCKET NUMBER: 4615-0049.00

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 887-1500

TELEFAX: (202) 887-0763
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: Williopsis mrakii
; STRAIN: IFO 895
; IMMEDIATE SOURCE:
; CLONE: Peptide2
US-08-331-657-3

Alignment Scores:
Pred. No.: 1.85e+07 Length: 8
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-10-070-588A-112 (1-11) x US-08-331-657-3 (1-8)

Qy 2 TTGGCACT 10
| | | | | | | |
Db 2 PheGlyThr 4

RESULT 8
US-08-571-985-16
; Sequence 16, Application US/08571985
; Patent No. 5783557
; GENERAL INFORMATION:
; APPLICANT: Burstein, Yigal
; APPLICANT: Trainin, Nathan
; APPLICANT: Rycus, Avigail
; TITLE OF INVENTION: THF-gamma2 Analogs and Pharmaceutical
; TITLE OF INVENTION: Compositions Comprising Them
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kohn & Associates
; STREET: 30500 No. 5783557thwestern Hwy., Suite 410
; CITY: Farmington Hills
; STATE: Michigan
; COUNTRY: USA
; ZIP: 48334
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/571,985
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 106214
; FILING DATE: 01-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohn, Kenneth I
; REGISTRATION NUMBER: 30,955
; REFERENCE/DOCKET NUMBER: 2163.00048
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (810) 539-5050
; TELEFAX: (810) 539-5055
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid

TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-571-985-16

Alignment Scores:
Pred. No.: 1.85e+07 Length: 8
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-10-070-588A-112 (1-11) x US-08-571-985-16 (1-8)

Qy 9 GTGCCAAG 1
| | | | | | | |
Db 4 ValProlys 6

RESULT 9
US-08-408-604A-181
; Sequence 181, Application US/08408604A
; Patent No. 5801149
; GENERAL INFORMATION:
; APPLICANT: Shoelson, Steven
; TITLE OF INVENTION: INHIBITION OF SIGNAL TRANSDUCTION MOLECULES
; NUMBER OF SEQUENCES: 211
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/408,604A
; FILING DATE: 21-MAR-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/134,558
; FILING DATE: 08-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/959,949
; FILING DATE: 09-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/722,359
; FILING DATE: 19-JUNE-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Myers, Louis
; REGISTRATION NUMBER: 35,965
; REFERENCE/DOCKET NUMBER: JDP-014CP3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 181:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-408-604A-181

Alignment Scores:
Pred. No.: 1.85e+07 Length: 8
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0

DB: 1 Gaps: 0
US-10-070-588A-112 (1-11) x US-08-408-604A-181 (1-8)
Qy 10 AGTGCCAA 2
Db 5 SerAlaLys 7
RESULT 10
US-08-408-604A-207
; Sequence 207, Application US/08408604A
; Patent No. 5801149
; GENERAL INFORMATION:
; APPLICANT: Shoelson, Steven
; TITLE OF INVENTION: INHIBITION OF SIGNAL TRANSDUCTION MOLECULES
; NUMBER OF SEQUENCES: 211
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/408,604A
; FILING DATE: 21-MAR-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/134,558
; FILING DATE: 08-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/959,949
; FILING DATE: 09-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/722,359
; FILING DATE: 19-JUNE-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Myers, Louis
; REGISTRATION NUMBER: 35,965
; REFERENCE/DOCKET NUMBER: JDP-014CP3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 207:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-408-604A-207
Alignment Scores:
Pred. No.: 1.85e+07 Length: 8
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0
US-10-070-588A-112 (1-11) x US-08-408-604A-207 (1-8)
Qy 10 AGTGCCAA 2
Db 5 SerAlaLys 7
RESULT 11
US-08-633-760-3
; Sequence 3, Application US/08633760
; Patent No. 5804429
; GENERAL INFORMATION:
; APPLICANT: NIWA, MINEO
; APPLICANT: SAITO, YOSHIMASA
; APPLICANT: FUJIMURA, TAKAO
; APPLICANT: ISHII, YOSHINORI
; APPLICANT: NOGUCHI, YUJI
; TITLE OF INVENTION: A NEW CEPHALOSPORIN C ACYLASE
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/633,760
; FILING DATE: 01-MAY-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 18-929-0 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-633-760-3
Alignment Scores:
Pred. No.: 1.85e+07 Length: 8
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0
US-10-070-588A-112 (1-11) x US-08-633-760-3 (1-8)
Qy 3 TTGGCACTA 11
Db 5 LeuAlaLeu 7
RESULT 12
US-08-668-871-9
; Sequence 9, Application US/08668871
; Patent No. 5811389
; GENERAL INFORMATION:
; APPLICANT: Bannwarth, Wilhelm
; APPLICANT: Gerber, Fernand
; APPLICANT: Grieder, Alfred
; APPLICANT: Knieringer, Andreas
; APPLICANT: Mueller, Klaus
; APPLICANT: Obrecht, Daniel
; APPLICANT: Trzeciak, Arnold
; TITLE OF INVENTION: TRI- AND TETRACYCLIC COMPOUNDS
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: New Jersey
COUNTRY: United States of America
ZIP: 07110-1199
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/668,871
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/106,508
FILING DATE:
APPLICATION NUMBER: CH 2725/92
FILING DATE: 31-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: Kass, Alan P
REGISTRATION NUMBER: 32142
REFERENCE/DOCKET NUMBER: RAN 4781/1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-4205
TELEFAX: (201) 235-3500
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-668-871-9

Alignment Scores:
Pred. No.: 1.85e+07 Length: 8
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x US-08-668-871-9 (1-8)

Qy 3 TTGGCACTA 11
Db 5 LeuAlaLeu 7

RESULT 13
US-08-669-683-9
Sequence 9, Application US/08669683
Patent No. 5811548
GENERAL INFORMATION:
APPLICANT: Bannwarth, Wilhelm
APPLICANT: Gerber, Fernand
APPLICANT: Grieder, Alfred
APPLICANT: Knierringer, Andreas
APPLICANT: Mueller, Klaus
APPLICANT: Obrecht, Daniel
APPLICANT: Trzeciak, Arnold
TITLE OF INVENTION: TRI- AND TETRACYCLIC COMPOUNDS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: New Jersey
COUNTRY: United States of America
ZIP: 07110-1199
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/669,683
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/106,508
FILING DATE:
APPLICATION NUMBER: CH 2725/92
FILING DATE: 31-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: Kass, Alan P
REGISTRATION NUMBER: 32142
REFERENCE/DOCKET NUMBER: RAN 4781/1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-4205
TELEFAX: (201) 235-3500
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-669-683-9

Alignment Scores:
Pred. No.: 1.85e+07 Length: 8
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x US-08-669-683-9 (1-8)

Qy 3 TTGGCACTA 11
Db 5 LeuAlaLeu 7

RESULT 14
US-08-482-651-51
Sequence 51, Application US/08482651
Patent No. 5874409
GENERAL INFORMATION:
APPLICANT: Victoria, Edward J.
APPLICANT: Marquis, David M.
TITLE OF INVENTION: APL IMMUNOREACTIVE PEPTIDES, CONJUGATES
TITLE OF INVENTION: THEREOF AND METHODS OF TREATMENT FOR APL ANTIBODY-MEDIATED
TITLE OF INVENTION: PATHOLOGIES
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,651
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Park, Freddie K.
REGISTRATION NUMBER: 35,636
REFERENCE/DOCKET NUMBER: 25231-20061.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600

TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-482-651-51

Alignment Scores:
Pred. No.: 1.85e+07
Score: 3.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x US-08-482-651-51 (1-8)

Qy 3 TTGGCACTA 11
| | | | | | | |
Db 3 LeuAlaLeu 5

RESULT 15
US-08-968-676-163
Sequence 163, Application US/08968676
Patent No. 5919639
GENERAL INFORMATION:
APPLICANT: Humphreys, Robert E
APPLICANT: Adams, Sharlene
APPLICANT: Xu, Minzhen
TITLE OF INVENTION: IMMUNOTHERAPY BY MODULATION OF ANTIGEN
NUMBER OF SEQUENCES: 165
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kevin M. Farrell, P.C.
STREET: P.O. Box 999
CITY: York Harbor
STATE: ME
COUNTRY: USA
ZIP: 03911
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/968,676
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Farrell, Kevin M
REGISTRATION NUMBER: 35,505
REFERENCE/DOCKET NUMBER: REH-9601
TELEPHONE: (207) 363-0558
TELEFAX: (207) 363-0528
INFORMATION FOR SEQ ID NO: 163:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-968-676-163

Alignment Scores:
Pred. No.: 1.85e+07
Score: 3.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x US-08-968-676-163 (1-8)

Qy 10 AGTGCCAA 2
| | | | | | | |
Db 4 SerAlaLys 6

RESULT 16
US-09-016-366A-53
Sequence 53, Application US/09016366A
Patent No. 5955431
GENERAL INFORMATION:
APPLICANT: Stevens, Richard L.
APPLICANT: Huang, Chifu
TITLE OF INVENTION: MAST CELL PROTEASE PEPTIDE
TITLE OF INVENTION: INHIBITORS
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
STREET: 600 Atlantic Avenue
CITY: Boston
STATE: MA
COUNTRY: U.S.A.
ZIP: 02210-2211
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,366A
FILING DATE: January 30, 1998
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/037,090
FILING DATE: 05-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Plumer, Elizabeth R.
REGISTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: B0801/7093
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFAX: 617-720-2441
TELEX:
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-016-366A-53

Alignment Scores:
Pred. No.: 1.85e+07
Score: 3.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x US-09-016-366A-53 (1-8)

Qy 3 TTGGCACTA 11
| | | | | | | |
Db 2 LeuAlaLeu 4

RESULT 17
US-09-116-766-16
Sequence 16, Application US/09116766
Patent No. 5968898
GENERAL INFORMATION:
APPLICANT: Burstein, Yigal

APPLICANT: Trainin, Nathan
APPLICANT: Rycus, AviGail
TITLE OF INVENTION: THF-gamma2 Analogs and Pharmaceutical
TITLE OF INVENTION: Compositions Comprising Them
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kohn & Associates
STREET: 30500 No. 596898thwestern Hwy., Suite 410
CITY: Farmington Hills
STATE: Michigan
COUNTRY: USA
ZIP: 48334
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/09/116,766
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 106214
FILING DATE: 01-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Montgomery, Ilene N.
REGISTRATION NUMBER: 38,972
REFERENCE/DOCKET NUMBER: 2163.00050
TELEPHONE: (248) 539-5050
TELEFAX: (248) 539-5055
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-116-766-16

Alignment Scores:
Pred. No.: 1.85e+07 Length: 8
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x US-09-116-766-16 (1-8)

Qy 9 GTGCCAAAG 1
Db 4 ValProllys 6

RESULT 18
US-08-310-912A-123
Sequence 123, Application US/08310912A
Patent No. 5981730
GENERAL INFORMATION:
APPLICANT: Ausubel, Frederick M.
APPLICANT: Staakawicz, Brian J.
APPLICANT: Brent, Andrew F.
APPLICANT: Dahlbeck, Douglas
APPLICANT: Katagiri, Fumiaki
APPLICANT: Kunkel, Barbara N.
APPLICANT: Mindrinos, Michael N.
APPLICANT: Yu, Guo-Liang
TITLE OF INVENTION: RPS2 GENE FAMILY, PRIMERS, PROBES, AND DETECTION
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 208
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston

STATE: MA
COUNTRY: USA
ZIP: 02110-2904
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30B
CURRENT APPLICATION NUMBER: US/08/310,912A
FILING DATE: September 22, 1994
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/227,360
FILING DATE: April 13, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Lech, Karen F.
REGISTRATION NUMBER: 35,238
REFERENCE/DOCKET NUMBER: 00786/254001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 100254
INFORMATION FOR SEQ ID NO: 123:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-310-912A-123

Alignment Scores:
Pred. No.: 1.85e+07 Length: 8
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x US-08-310-912A-123 (1-8)

Qy 3 TTGGCACTA 11
Db 4 LeuAlaLeu 6

RESULT 19
US-08-310-912A-125
Sequence 125, Application US/08310912A
Patent No. 5981730
GENERAL INFORMATION:
APPLICANT: Ausubel, Frederick M.
APPLICANT: Staakawicz, Brian J.
APPLICANT: Brent, Andrew F.
APPLICANT: Dahlbeck, Douglas
APPLICANT: Katagiri, Fumiaki
APPLICANT: Kunkel, Barbara N.
APPLICANT: Mindrinos, Michael N.
APPLICANT: Yu, Guo-Liang
TITLE OF INVENTION: RPS2 GENE FAMILY, PRIMERS, PROBES, AND DETECTION
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 208
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2904
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30B

;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/310.912A
;; FILING DATE: September 22, 1994
;; CLASSIFICATION: 536
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/227.360
;; FILING DATE: April 13, 1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Lech, Karen F.
;; REGISTRATION NUMBER: 35,238
;; REFERENCE/DOCKET NUMBER: 00786/254001
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (617) 542-5070
;; TELEFAX: (617) 542-8906
;; TELEX: 100254
;; INFORMATION FOR SEQ ID NO: 125:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 8 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-310-912A-125

Alignment Scores:
Pred. No.: 1.85e+07 Length: 8
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-070-588A-112 (1-11) x US-08-310-912A-125 (1-8)

Qy 3 TTGGCACTA 11
Db 4 Leulalaleu 6

RESULT 20
US-08-444-818-366
; Sequence 366, Application US/08444818
; Patent No. 6150087
; GENERAL INFORMATION:
; APPLICANT: Chien, David Y.
; APPLICANT: Rutter, William J.
; TITLE OF INVENTION: NANBV Diagnostics and Vaccines
; NUMBER OF SEQUENCES: 777
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608-2916
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444.818
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/403.590
; FILING DATE: 14-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Harbin, Alisa A.
; REGISTRATION NUMBER: 33,895
; REFERENCE/DOCKET NUMBER: 0110.002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (508)359-3876
; TELEFAX: (508)359-3885
; INFORMATION FOR SEQ ID NO: 366:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-444-818-367

Alignment Scores:
Pred. No.: 1.85e+07 Length: 8
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 8 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-444-818-366

Alignment Scores:
Pred. No.: 1.85e+07 Length: 8
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-070-588A-112 (1-11) x US-08-444-818-366 (1-8)

Qy 1 CTTTGGCAC 9
Db 6 LeuTriphis 8

RESULT 21
US-08-444-818-367
; Sequence 367, Application US/08444818
; Patent No. 6150087
; GENERAL INFORMATION:
; APPLICANT: Chien, David Y.
; APPLICANT: Rutter, William J.
; TITLE OF INVENTION: NANBV Diagnostics and Vaccines
; NUMBER OF SEQUENCES: 777
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608-2916
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444.818
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/403.590
; FILING DATE: 14-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Harbin, Alisa A.
; REGISTRATION NUMBER: 33,895
; REFERENCE/DOCKET NUMBER: 0110.002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (508)359-3876
; TELEFAX: (508)359-3885
; INFORMATION FOR SEQ ID NO: 367:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-444-818-367

Alignment Scores:
Pred. No.: 1.85e+07 Length: 8
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-070-588A-112 (1-11) x US-08-444-818-367 (1-8)

Qy 1 CTTTGGCAC 9
Db 5 LeuTrpHis 7

RESULT 22

US-08-444-818-368
; Sequence 368, Application US/08444818
; Patent No. 6150087
; GENERAL INFORMATION:
; APPLICANT: Chien, David Y.
; APPLICANT: Rutter, William J.
; TITLE OF INVENTION: NANBV Diagnostics and Vaccines
; NUMBER OF SEQUENCES: 777
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; City: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608-2916
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,818
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/403,590
; FILING DATE: 14-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Harbin, Alisa A.
; REGISTRATION NUMBER: 33,895
; REFERENCE/DOCKET NUMBER: 0110.002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (508)359-3876
; TELEFAX: (508)359-3885
; INFORMATION FOR SEQ ID NO: 368:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-444-818-368

Alignment Scores:
Pred. No.: 1.85e+07 Length: 8
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-070-588A-112 (1-11) x US-08-444-818-368 (1-8)

Qy 1 CTTTGGCAC 9
Db 4 LeuTrpHis 6

RESULT 23

US-08-444-818-369
; Sequence 369, Application US/08444818
; Patent No. 6150087
; GENERAL INFORMATION:
; APPLICANT: Chien, David Y.
; APPLICANT: Rutter, William J.
; TITLE OF INVENTION: NANBV Diagnostics and Vaccines

; NUMBER OF SEQUENCES: 777
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; City: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608-2916
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,818
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/403,590
; FILING DATE: 14-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Harbin, Alisa A.
; REGISTRATION NUMBER: 33,895
; REFERENCE/DOCKET NUMBER: 0110.002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (508)359-3876
; TELEFAX: (508)359-3885
; INFORMATION FOR SEQ ID NO: 369:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-444-818-369

Alignment Scores:
Pred. No.: 1.85e+07 Length: 8
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-070-588A-112 (1-11) x US-08-444-818-369 (1-8)

Qy 1 CTTTGGCAC 9
Db 3 LeuTrpHis 5

RESULT 24

US-08-444-818-387
; Sequence 387, Application US/08444818
; Patent No. 6150087
; GENERAL INFORMATION:
; APPLICANT: Chien, David Y.
; APPLICANT: Rutter, William J.
; TITLE OF INVENTION: NANBV Diagnostics and Vaccines
; NUMBER OF SEQUENCES: 777
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; City: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608-2916
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,818

FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/403,590
FILING DATE: 14-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Harbin, Alisa A.
REGISTRATION NUMBER: 33,895
REFERENCE/DOCKET NUMBER: 0110.002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (508)359-3876
TELEFAX: (508)359-3885
INFORMATION FOR SEQ ID NO: 387:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-444-818-387

Alignment Scores:
Pred. No.: 1.85e+07 Length: 8
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-070-588A-112 (1-11) x US-08-444-818-387 (1-8)

Qy 3 TTGGCACTA 11
| | | | | | | |
Db 1 LeuAlaLeu 3

RESULT 25

US-09-296-284-14
Sequence 14, Application US/09296284A
Patent No. 6204040
GENERAL INFORMATION:
APPLICANT: Choi, Eui-Sung
APPLICANT: Rhee, Sang-Ki
APPLICANT: Lee, Eun-Hae
TITLE OF INVENTION: Gluconobacter Suboxydians Sorbitol Dehydrogenase, Genes
TITLE OF INVENTION: and Methods of Use Thereof
FILE REFERENCE: 1533.0870000
CURRENT APPLICATION NUMBER: US/09/296,284A
CURRENT FILING DATE: 1999-04-22
NUMBER OF SEQ ID NOS: 87
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 14
LENGTH: 8
TYPE: PPT
ORGANISM: Gluconobacter suboxydians
US-09-296-284-14

Alignment Scores:
Pred. No.: 1.85e+07 Length: 8
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-070-588A-112 (1-11) x US-09-296-284-14 (1-8)

Qy 9 GTGCCAAG 1
| | | | | | | |
Db 6 ValProlys 8

RESULT 26

US-08-660-092-54
Sequence 54, Application US/08660092

Patent No. 6207160
GENERAL INFORMATION:
APPLICANT: Victoria, Edward J.
APPLICANT: Marquis, David M.
APPLICANT: Jones, David S.
APPLICANT: Yu, Lin
TITLE OF INVENTION: aPL IMMUNOREACTIVE PEPTIDES, CONJUGATES
TITLE OF INVENTION: THEREOF AND METHODS OF TREATMENT FOR aPL ANTIBODY-MEDIATED
NUMBER OF INVENTION: PATHOLOGIES
NUMBER OF SEQUENCES: 216
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/660,092
FILING DATE: 06-JUN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Park, Freddie K.
REGISTRATION NUMBER: 35,636
REFERENCE/DOCKET NUMBER: 25231-20061.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-660-092-54
Alignment Scores:
Pred. No.: 1.85e+07 Length: 8
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0
US-10-070-588A-112 (1-11) x US-08-660-092-54 (1-8)
Qy 3 TTGGCACTA 11
| | | | | | | |
Db 3 LeuAlaLeu 5
RESULT 27
US-08-660-092-188
Sequence 188, Application US/08660092
Patent No. 6207160
GENERAL INFORMATION:
APPLICANT: Victoria, Edward J.
APPLICANT: Marquis, David M.
APPLICANT: Jones, David S.
APPLICANT: Yu, Lin
TITLE OF INVENTION: aPL IMMUNOREACTIVE PEPTIDES, CONJUGATES
TITLE OF INVENTION: THEREOF AND METHODS OF TREATMENT FOR aPL ANTIBODY-MEDIATED
NUMBER OF INVENTION: PATHOLOGIES
NUMBER OF SEQUENCES: 216
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO

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; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/660,092
; FILING DATE: 06-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Park, Freddie K.
; REGISTRATION NUMBER: 35,636
; REFERENCE/DOCKET NUMBER: 25231-20061.20
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 188:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /product="OTHER"
; OTHER INFORMATION: /label=Hc
; OTHER INFORMATION: /note="homocysteine"
US-08-660-092-188

Alignment Scores:
Pred. No.: 1.85e+07 Length: 8
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-070-588A-112 (1-11) x US-08-660-092-188 (1-8)

Qy 3 TTGGCACTA 11
| | | | |
Db 5 LeuAlaLeu 7

RESULT 28
US-09-301-085-123
; Sequence 123, Application US/09301085
; Patent No. 6262248
; GENERAL INFORMATION:
; APPLICANT: Ausubel, Frederick M.
; APPLICANT: Staskawicz, Brian J.
; APPLICANT: Brent, Andrew F.
; APPLICANT: Dahlbeck, Douglas
; APPLICANT: Katagiri, Fumiaki
; APPLICANT: Kunkel, Barbara N.
; APPLICANT: Mindrinos, Michael N.
; APPLICANT: Yu, Guo-Liang
; TITLE OF INVENTION: RPS2 GENE FAMILY, PRIMERS, PROBES, AND
; FILE REFERENCE: 00786/254002
; CURRENT FILING DATE: 1999-04-28
; EARLIER APPLICATION NUMBER: US/09/301,085
; EARLIER FILING DATE: 1999-04-28
; EARLIER APPLICATION NUMBER: 08/310,912
; EARLIER FILING DATE: 1994-09-22
; EARLIER APPLICATION NUMBER: 08/227,360
; EARLIER FILING DATE: 1994-04-13
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 123
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-301-085-125

Alignment Scores:
Pred. No.: 1.85e+07 Length: 8
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-070-588A-112 (1-11) x US-09-301-085-125 (1-8)

Qy 3 TTGGCACTA 11
| | | | |
Db 5 LeuAlaLeu 7

RESULT 29
US-09-301-085-125
; Sequence 125, Application US/09301085
; Patent No. 6262248
; GENERAL INFORMATION:
; APPLICANT: Ausubel, Frederick M.
; APPLICANT: Staskawicz, Brian J.
; APPLICANT: Brent, Andrew F.
; APPLICANT: Dahlbeck, Douglas
; APPLICANT: Katagiri, Fumiaki
; APPLICANT: Kunkel, Barbara N.
; APPLICANT: Mindrinos, Michael N.
; APPLICANT: Yu, Guo-Liang
; TITLE OF INVENTION: RPS2 GENE FAMILY, PRIMERS, PROBES, AND
; FILE REFERENCE: 00786/254002
; CURRENT FILING DATE: 1999-04-28
; EARLIER APPLICATION NUMBER: US/09/301,085
; EARLIER FILING DATE: 1999-04-28
; EARLIER APPLICATION NUMBER: 08/310,912
; EARLIER FILING DATE: 1994-09-22
; EARLIER APPLICATION NUMBER: 08/227,360
; EARLIER FILING DATE: 1994-04-13
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 125
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-301-085-125

Alignment Scores:
Pred. No.: 1.85e+07 Length: 8
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-070-588A-112 (1-11) x US-09-301-085-125 (1-8)

Qy 3 TTGGCACTA 11
| | | | |
Db 4 LeuAlaLeu 6

RESULT 30
US-09-394-630-19
; Sequence 19, Application US/09394630
; Patent No. 6395306
; GENERAL INFORMATION:
; APPLICANT: Cui, Xiangmin
; APPLICANT: Lu, Yuefeng
; APPLICANT: Pan Pacific Pharmaceutical, Inc.
; TITLE OF INVENTION: Useful Properties of a Bee Venom Protein and Gene
```

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; SEQ ID NO 123
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-301-085-123

Alignment Scores:
Pred. No.: 1.85e+07 Length: 8
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-070-588A-112 (1-11) x US-09-301-085-123 (1-8)

Qy 3 TTGGCACTA 11
| | | | |
Db 4 LeuAlaLeu 6

RESULT 29
US-09-301-085-125
; Sequence 125, Application US/09301085
; Patent No. 6262248
; GENERAL INFORMATION:
; APPLICANT: Ausubel, Frederick M.
; APPLICANT: Staskawicz, Brian J.
; APPLICANT: Brent, Andrew F.
; APPLICANT: Dahlbeck, Douglas
; APPLICANT: Katagiri, Fumiaki
; APPLICANT: Kunkel, Barbara N.
; APPLICANT: Mindrinos, Michael N.
; APPLICANT: Yu, Guo-Liang
; TITLE OF INVENTION: RPS2 GENE FAMILY, PRIMERS, PROBES, AND
; FILE REFERENCE: 00786/254002
; CURRENT FILING DATE: 1999-04-28
; EARLIER APPLICATION NUMBER: US/09/301,085
; EARLIER FILING DATE: 1999-04-28
; EARLIER APPLICATION NUMBER: 08/310,912
; EARLIER FILING DATE: 1994-09-22
; EARLIER APPLICATION NUMBER: 08/227,360
; EARLIER FILING DATE: 1994-04-13
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 125
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-301-085-125

Alignment Scores:
Pred. No.: 1.85e+07 Length: 8
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-070-588A-112 (1-11) x US-09-301-085-125 (1-8)

Qy 3 TTGGCACTA 11
| | | | |
Db 4 LeuAlaLeu 6

RESULT 30
US-09-394-630-19
; Sequence 19, Application US/09394630
; Patent No. 6395306
; GENERAL INFORMATION:
; APPLICANT: Cui, Xiangmin
; APPLICANT: Lu, Yuefeng
; APPLICANT: Pan Pacific Pharmaceutical, Inc.
; TITLE OF INVENTION: Useful Properties of a Bee Venom Protein and Gene
```


;; TITLE OF INVENTION: Encoding Same
;; FILE REFERENCE: 019049-000200US
;; CURRENT APPLICATION NUMBER: US/09/394,630
;; CURRENT FILING DATE: 1999-09-13
;; PRIOR APPLICATION NUMBER: US 60/100,172
;; PRIOR FILING DATE: 1998-09-14
;; NUMBER OF SEQ ID NOS: 22
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 19
;; LENGTH: 8
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence:peptide
;; OTHER INFORMATION: fragment #88 from in-gel trypsin digestion
;; NAME/KEY: MOD RES
;; LOCATION: (1)-(2)
;; OTHER INFORMATION: Xaa = unsure amino acid
US-09-394-630-19

Alignment Scores: Length: 8
Pred. No.: 1.85e+07 3
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-070-588A-112 (1-11) x US-09-394-630-19 (1-8)

Qy 9 GTGCCAAG 1
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Db 6 ValProLys 8

RESULT 31

US-09-160-513-54
; Sequence 54, Application US/09160513
; Patent No. 6410775
; GENERAL INFORMATION:
; APPLICANT: Victoria, Edward J.
; APPLICANT: Marquis, David M.
; APPLICANT: Jones, David S.
; APPLICANT: Yu, Lin
; TITLE OF INVENTION: aPL IMMUNOREACTIVE PEPTIDES, CONJUGATES THEREOF AND METHODS O
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/09/160,513
; APPLICATION NUMBER: US/09/160,513
; FILING DATE: 1998-DEC-24
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: CATHERINE M. POLIZZI
; REGISTRATION NUMBER: 40,130
; REFERENCE/DOCKET NUMBER: 25231-20061.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 813-5600
; TELEFAX: (650) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid

;; STRANDEDNESS: single
;; TOPOLOGY: linear
US-09-160-513-54
Alignment Scores: Length: 8
Pred. No.: 1.85e+07 3
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-070-588A-112 (1-11) x US-09-160-513-54 (1-8)

Qy 3 TTGCACTA 11
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Db 3 LeuAlaLeu 5

RESULT 32

US-09-160-513-188
; Sequence 188, Application US/09160513
; Patent No. 6410775
; GENERAL INFORMATION:
; APPLICANT: Victoria, Edward J.
; APPLICANT: Marquis, David M.
; APPLICANT: Jones, David S.
; APPLICANT: Yu, Lin
; TITLE OF INVENTION: aPL IMMUNOREACTIVE PEPTIDES, CONJUGATES THEREOF AND METHODS O
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/09/160,513
; APPLICATION NUMBER: US/09/160,513
; FILING DATE: 1998-DEC-24
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: CATHERINE M. POLIZZI
; REGISTRATION NUMBER: 40,130
; REFERENCE/DOCKET NUMBER: 25231-20061.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 813-5600
; TELEFAX: (650) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 188:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /product= "OTHER"
; OTHER INFORMATION: /label= Hc
; OTHER INFORMATION: /note= "homocysteine"
US-09-160-513-188
Alignment Scores: Length: 8
Pred. No.: 1.85e+07 3
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-070-588A-112 (1-11) x US-09-160-513-188 (1-8)

Qy 3 TTGGCACTA 11
Db 5 LeuAlaLeu 7

RESULT 33

US-09-675-922-22
; Sequence 22, Application US/09675922
; Patent No. 6468731
; GENERAL INFORMATION:
; APPLICANT: Hubbell A., Jeffrey
; APPLICANT: Schense C., Jason
; APPLICANT: Sakiyama E., Shelley
; TITLE OF INVENTION: Enzyme-Mediated Modification of Fibrin for Tissue
; FILE REFERENCE: ETH 107 DIV
; CURRENT APPLICATION NUMBER: US/09/675,922
; CURRENT FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 22
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: ACETYLTATION Acetylated Glycine
; OTHER INFORMATION: Description of Artificial Sequence: substrate
; OTHER INFORMATION: sequence for protease
US-09-675-922-22

Alignment Scores:
Pred. No.: 1.85e+07 Length: 8
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-070-588A-112 (1-11) x US-09-675-922-22 (1-8)

Qy 3 TTGGCACTA 11
Db 3 LeuAlaLeu 5

RESULT 34

US-09-704-251-15
; Sequence 15, Application US/09704251
; Patent No. 6548477
; GENERAL INFORMATION:
; APPLICANT: Olson, Gary L.
; APPLICANT: Self, Christopher
; APPLICANT: Lee, Lily
; APPLICANT: Cook, Charles M.
; TITLE OF INVENTION: THERAPEUTIC AGENTS AND METHODS OF USE THEREOF FOR THE
; FILE REFERENCE: PPI-106
; CURRENT APPLICATION NUMBER: US/09/704,251
; CURRENT FILING DATE: 2000-11-01
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 15
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Motifs
US-09-704-251-15

Alignment Scores:
Pred. No.: 1.85e+07 Length: 8
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-070-588A-112 (1-11) x US-09-704-251-15 (1-8)

Qy 3 TTGGCACTA 11
Db 3 LeuAlaLeu 5

RESULT 35

US-08-635-886C-124
; Sequence 124, Application US/08635886C
; Patent No. 6555114
; GENERAL INFORMATION:
; APPLICANT: LEROUX-ROELS, Geert
; APPLICANT: DELEYS, Robert
; APPLICANT: MAERTENS, Geert
; TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
; FILE REFERENCE: 2752-18
; CURRENT APPLICATION NUMBER: US/08/635,886C
; CURRENT FILING DATE: 1996-04-25
; PRIOR APPLICATION NUMBER: PCT/EP94/03555
; PRIOR FILING DATE: 1994-10-28
; PRIOR APPLICATION NUMBER: EP 93402718.6
; PRIOR FILING DATE: 1993-11-04
; NUMBER OF SEQ ID NOS: 286
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 124
; LENGTH: 8
; TYPE: PRT
; ORGANISM: hepatitis C virus
US-08-635-886C-124

Alignment Scores:
Pred. No.: 1.85e+07 Length: 8
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-070-588A-112 (1-11) x US-08-635-886C-124 (1-8)

Qy 1 CTTTGGCAC 9
Db 5 Leutrphis 7

RESULT 36

US-08-635-886C-125
; Sequence 125, Application US/08635886C
; Patent No. 6555114
; GENERAL INFORMATION:
; APPLICANT: LEROUX-ROELS, Geert
; APPLICANT: DELEYS, Robert
; APPLICANT: MAERTENS, Geert
; TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
; FILE REFERENCE: 2752-18
; CURRENT APPLICATION NUMBER: US/08/635,886C
; CURRENT FILING DATE: 1996-04-25
; PRIOR APPLICATION NUMBER: PCT/EP94/03555
; PRIOR FILING DATE: 1994-10-28
; PRIOR APPLICATION NUMBER: EP 93402718.6
; PRIOR FILING DATE: 1993-11-04
; NUMBER OF SEQ ID NOS: 286
; SOFTWARE: Patent in version 3.1
US-08-635-886C-125

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; SEQ ID NO 125
; LENGTH: 8
; TYPE: PRT
; ORGANISM: hepatitis C virus
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (8)..(8)
; OTHER INFORMATION: Xaa is Ile, Val, Phe or Leu
US-08-635-886C-125

Alignment Scores:
Pred. No.: 1.85e+07 Length: 8
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-070-588A-112 (1-11) x US-08-635-886C-125 (1-8)

Qy 1 CTTTGGCAC 9
Db 1 Leutirphis 3

RESULT 37
US-08-964-747-8
; Sequence 8, Application US/08964747
; Patent No. 659664
; GENERAL INFORMATION:
; APPLICANT: Gatanaga, Tetsuya
; APPLICANT: Granger, Gale A.
; TITLE OF INVENTION: Isolated Tumor Necrosis Factor Receptor
; TITLE OF INVENTION: Releasing Enzyme, Compositions Comprising the Enzyme and
; TITLE OF INVENTION: Methods of the Use Thereof
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CAMPBELL AND FLORES LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/964,747
; FILING DATE: 05-NOV-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/030,761
; FILING DATE: 06-NOV-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UC 3666
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (858)535-9001
; TELEFAX: (858)535-8949
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: /note= "Xaa is Gln or Ile (Q/I)"
; FEATURE:
```

```
; NAME/KEY: Modified-site
; LOCATION: 8
; OTHER INFORMATION: /note= "Xaa is Ser or Pro (S/P)"
US-08-964-747-8

Alignment Scores:
Pred. No.: 1.85e+07 Length: 8
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-070-588A-112 (1-11) x US-08-964-747-8 (1-8)

Qy 3 TTGGCACTA 11
Db 1 LeuAlaLeu 3

RESULT 38
US-09-562-913-8
; Sequence 8, Application US/09562913
; Patent No. 6573062
; GENERAL INFORMATION:
; APPLICANT: Gatanaga, Tetsuya
; APPLICANT: Granger, Gale A.
; TITLE OF INVENTION: Isolated Tumor Necrosis Factor Receptor
; TITLE OF INVENTION: Releasing Enzyme, Compositions Comprising the Enzyme and
; TITLE OF INVENTION: Methods of the Use Thereof
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CAMPBELL AND FLORES LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/562,913
; FILING DATE: 02-May-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/964,747
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UC 3666
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (858)535-9001
; TELEFAX: (858)535-8949
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: /note= "Xaa is Gln or Ile (Q/I)"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 8
; OTHER INFORMATION: /note= "Xaa is Ser or Pro (S/P)"
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-562-913-8
```

Alignment Scores:
Pred. No.: 1.85e+07 Length: 8
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-070-588A-112 (1-11) x US-09-562-913-8 (1-8)

Qy 3 TTGGCACTA 11
Db 1 LeuAlaLeu 3
|||||

RESULT 39

US-09-269-439-12
; Sequence 12, Application US/09269439
; Patent No. 6610649
; GENERAL INFORMATION:
; APPLICANT: Johansson, Bo-Lennart
; APPLICANT: Jorvall, Hans
; FILE OF INVENTION: INSULIN C-PEPTIDES
; CURRENT APPLICATION NUMBER: US/09/269,439
; CURRENT FILING DATE: 1999-07-08
; EARLIER APPLICATION NUMBER: PCT/GB97/02627
; EARLIER FILING DATE: 1997-09-26
; EARLIER APPLICATION NUMBER: SE96/03533-2
; EARLIER FILING DATE: 1996-09-27
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-269-439-12

Alignment Scores:
Pred. No.: 1.85e+07 Length: 8
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-070-588A-112 (1-11) x US-09-269-439-12 (1-8)

Qy 3 TTGGCACTA 11
Db 1 LeuAlaLeu 3
|||||

RESULT 40

US-08-974-690C-124
; Sequence 124, Application US/08974690C
; Patent No. 6613333
; GENERAL INFORMATION:
; APPLICANT: LEROUX-ROELS, Geert
; APPLICANT: DELEYS, Robert
; APPLICANT: MAERTENS, Geert
; TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
; FILE OF INVENTION: VIRUS
; FILE REFERENCE: 2551-94
; CURRENT APPLICATION NUMBER: US/08/974,690C
; CURRENT FILING DATE: 1997-11-19
; PRIOR APPLICATION NUMBER: PCT/EP94/03555
; PRIOR FILING DATE: 1994-10-28
; PRIOR APPLICATION NUMBER: EP 93402718.6
; PRIOR FILING DATE: 1993-11-04
; NUMBER OF SEQ ID NOS: 286
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 124

; LENGTH: 8
; TYPE: PRT
; ORGANISM: hepatitis C virus
US-08-974-690C-124
Alignment Scores:
Pred. No.: 1.85e+07 Length: 8
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0
US-10-070-588A-112 (1-11) x US-08-974-690C-124 (1-8)

Qy 1 CTTTGGCAC 9
Db 5 LeuTriHis 7
|||||

RESULT 41

US-08-974-690C-125
; Sequence 125, Application US/08974690C
; Patent No. 6613333
; GENERAL INFORMATION:
; APPLICANT: LEROUX-ROELS, Geert
; APPLICANT: DELEYS, Robert
; APPLICANT: MAERTENS, Geert
; TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
; FILE OF INVENTION: VIRUS
; FILE REFERENCE: 2551-94
; CURRENT APPLICATION NUMBER: US/08/974,690C
; CURRENT FILING DATE: 1997-11-19
; PRIOR APPLICATION NUMBER: PCT/EP94/03555
; PRIOR FILING DATE: 1994-10-28
; PRIOR APPLICATION NUMBER: EP 93402718.6
; PRIOR FILING DATE: 1993-11-04
; NUMBER OF SEQ ID NOS: 286
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 125
; LENGTH: 8
; TYPE: PRT
; ORGANISM: hepatitis C virus
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (8)-(8)
; OTHER INFORMATION: Xaa is Ile, Val, Phe or Leu
US-08-974-690C-125

Alignment Scores:
Pred. No.: 1.85e+07 Length: 8
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0
US-10-070-588A-112 (1-11) x US-08-974-690C-125 (1-8)

Qy 1 CTTTGGCAC 9
Db 1 LeuTriHis 3
|||||

RESULT 42

US-09-721-108-186
; Sequence 186, Application US/09721108
; Patent No. 6664374
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES COMPRISING IL-6 LIGAND-BINDING RECEPTOR
; TITLE OF INVENTION: DOMAINS AND RELATED NUCLEIC ACIDS, ANTIBODIES,
; TITLE OF INVENTION: COMPOSITIONS, AND METHODS OF USE
; FILE REFERENCE: 207474
; CURRENT APPLICATION NUMBER: US/09/721,108

;; CURRENT FILING DATE: 2000-11-22
;; PRIOR APPLICATION NUMBER: PCT/US00/23490
;; PRIOR FILING DATE: 2000-08-25
;; PRIOR APPLICATION NUMBER: US 60/151,277
;; PRIOR FILING DATE: 1999-08-27
;; NUMBER OF SEQ ID NOS: 309
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 186
;; LENGTH: 8
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Binding peptide
US-09-721-108-186

Alignment Scores:
Pred. No.: 1.85e+07 Length: 8
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-070-588A-112 (1-11) x US-09-721-108-186 (1-8)

Qy 2 TTGGCACT 10
Db 6 PheGlyThr 8

RESULT 43

US-08-974-685-124
; Sequence 124, Application US/08974685
; Patent No. 6689368
; GENERAL INFORMATION:

APPLICANT: LEROUX-ROELS, GEERT
DELEYS, ROBERT
MAERTENS, GEERT

TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF
HEPATITIS C VIRUS STRUCTURAL PROTEINS, PROPHYLACTIC AND
THERAPEUTIC COMPOSITIONS CONTAINING THE SAME

NUMBER OF SEQUENCES: 181

CORRESPONDENCE ADDRESS:

ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/974,685
FILING DATE: 19-NO. 6689368-1997
CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 1487-11
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100

INFORMATION FOR SEQ ID NO: 124:

SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 124:

US-08-974-685-124

Alignment Scores:

Pred. No.: 1.85e+07 Length: 8
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-070-588A-112 (1-11) x US-08-974-685-124 (1-8)

Qy 1 CTTGGCAC 9
Db 5 LeuTrpHis 7

RESULT 44

US-08-974-685-125
; Sequence 125, Application US/08974685
; Patent No. 6689368
; GENERAL INFORMATION:

APPLICANT: LEROUX-ROELS, GEERT
DELEYS, ROBERT
MAERTENS, GEERT

TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF
HEPATITIS C VIRUS STRUCTURAL PROTEINS, PROPHYLACTIC AND
THERAPEUTIC COMPOSITIONS CONTAINING THE SAME

NUMBER OF SEQUENCES: 181

CORRESPONDENCE ADDRESS:

ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/974,685
FILING DATE: 19-NO. 6689368-1997
CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 1487-11
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100

INFORMATION FOR SEQ ID NO: 125:

SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

FEATURE:

NAME/KEY: misc-feature

LOCATION: 8

OTHER INFORMATION: Xaa is Ile or Val or Phe or Leu
SEQUENCE DESCRIPTION: SEQ ID NO: 125:

US-08-974-685-125

Alignment Scores:

Pred. No.: 1.85e+07 Length: 8
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-070-588A-112 (1-11) x US-08-974-685-125 (1-8)

QY 1 CTTTGCAC 9
Db 1 LeuTprHis 3

RESULT 45

US-09-707-263A-10
; Sequence 10, Application US/09707263A
; Patent No. 6696546

; GENERAL INFORMATION:
; APPLICANT: Bond, Gareth L

; APPLICANT: Manley, James L
; APPLICANT: Prives, Carol

; TITLE OF INVENTION: A Peptide That Kills Growing But No. 6696546 Stationary Cells
; FILE REFERENCE: 63331

; CURRENT APPLICATION NUMBER: US/09/707,263A
; CURRENT FILING DATE: 2000-11-06

; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 10
; LENGTH: 8

; TYPE: PRT
; ORGANISM: Homo Sapiens

US-09-707-263A-10

Alignment Scores:

Pred. No.:	1.85e+07	Length:	8
Score:	3.00	Matches:	3
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	4	Gaps:	0

US-10-070-588A-112 (1-11) x US-09-707-263A-10 (1-8)

QY 10 AGTGCCAAA 2
Db 1 SerAlalys 3

RESULT 46

US-09-707-263A-17

; Sequence 17, Application US/09707263A
; Patent No. 6696546

; GENERAL INFORMATION:
; APPLICANT: Bond, Gareth L

; APPLICANT: Manley, James L
; APPLICANT: Prives, Carol

; TITLE OF INVENTION: A Peptide That Kills Growing But No. 6696546 Stationary Cells
; FILE REFERENCE: 63331

; CURRENT APPLICATION NUMBER: US/09/707,263A
; CURRENT FILING DATE: 2000-11-06

; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 17
; LENGTH: 8

; TYPE: PRT
; ORGANISM: Homo Sapiens

US-09-707-263A-17

Alignment Scores:

Pred. No.:	1.85e+07	Length:	8
Score:	3.00	Matches:	3
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	4	Gaps:	0

US-10-070-588A-112 (1-11) x US-09-707-263A-17 (1-8)

QY 10 AGTGCCAAA 2
Db 1 SerAlalys 3

RESULT 47

US-09-403-269-4

; Sequence 4, Application US/09403269
; Patent No. 6764844

; GENERAL INFORMATION:
; APPLICANT: ULF, Lindahl

; APPLICANT: LI, Jin-Ping
; TITLE OF INVENTION: DNA Sequence Coding for a Mammalian Glucuronyl C5-Epimerase and a

; Patent No. 6764844
; TITLE OF INVENTION: Process for Its Production

; FILE REFERENCE: 003300-589
; CURRENT APPLICATION NUMBER: US/09/403,269

; CURRENT FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: SE 9701454-2

; PRIOR FILING DATE: 1997-04-18
; PRIOR APPLICATION NUMBER: PCT/SE98/00703

; PRIOR FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 13

; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4

; LENGTH: 8
; TYPE: PRT

; ORGANISM: Human
; FEATURE:
; NAME/KEY: PEPTIDE

; LOCATION: (4)..(4)
; OTHER INFORMATION: Amino acid 4 is Xaa wherein Xaa = any amino acid.

US-09-403-269-4

Alignment Scores:

Pred. No.:	1.85e+07	Length:	8
Score:	3.00	Matches:	3
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	4	Gaps:	0

US-10-070-588A-112 (1-11) x US-09-403-269-4 (1-8)

QY 9 GTGCCAAG 1
Db 6 ValProLys 8

RESULT 48

US-09-261-894A-163

; Sequence 163, Application US/09261894A
; Patent No. 6835382

; GENERAL INFORMATION:
; APPLICANT: HUMPHREYS, ROBERT E.

; APPLICANT: ADAMS, SHARLENE
; APPLICANT: XU, MINZHEN

; TITLE OF INVENTION: IMMUNOTHERAPY BY MODULATION OF ANTIGEN PRESENTATION
; FILE REFERENCE: REH-2006

; CURRENT APPLICATION NUMBER: US/09/261,894A
; CURRENT FILING DATE: 1999-03-03

; NUMBER OF SEQ ID NOS: 167
; SOFTWARE: PatentIn Ver. 3.2

; SEQ ID NO 163
; LENGTH: 8

; TYPE: PRT
; ORGANISM: Artificial Sequence

; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

; OTHER INFORMATION: peptide
US-09-261-894A-163

Alignment Scores:

Pred. No.:	1.85e+07	Length:	8
Score:	3.00	Matches:	3
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	4	Gaps:	0

US-10-070-588A-112 (1-11) x US-09-261-894A-163 (1-8)

Oy 10 AGTGCCAA 2
Db 4 SerAlaLeu 6

RESULT 49

PCT-US95-04589-123
; Sequence 123, Application PC/TUS9504589

; GENERAL INFORMATION:

; APPLICANT: Ausubel, Frederick M.
; APPLICANT: Staskawicz, Brian J.
; APPLICANT: Brent, Andrew F.
; APPLICANT: Dahlbeck, Douglas
; APPLICANT: Katagiri, Fumiaki
; APPLICANT: Kunkel, Barbara N.
; APPLICANT: Mindrinog, Michael N.
; APPLICANT: Yu, Guo-Liang

; TITLE OF INVENTION: RPS2 GENE AND USES THEREOF

; NUMBER OF SEQUENCES: 201

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson

; STREET: 225 Franklin Street Suite 3100

; CITY: Boston

; STATE: MA

; COUNTRY: USA

; ZIP: 02110-2904

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30B

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US95/04589

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/227,360

; FILING DATE: 13-APR-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Clark, Paul T.

; REGISTRATION NUMBER: 30,162

; REFERENCE/DOCKET NUMBER: 00786/230001

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 542-5070

; TELEFAX: (617) 542-8906

; TELEX: 100254

; INFORMATION FOR SEQ ID NO: 123:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 8 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

PCT-US95-04589-123

Alignment Scores:

Pred. No.: 1.85e+07 Length: 8
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 5 Gaps: 0

US-10-070-588A-112 (1-11) x PCT-US95-04589-123 (1-8)

Oy 3 TTGGCACTA 11
Db 4 LeuAlaLeu 6

RESULT 50

PCT-US95-04589-125

; Sequence 125, Application PC/TUS9504589

; GENERAL INFORMATION:

; APPLICANT: Ausubel, Frederick M.

; APPLICANT: Staskawicz, Brian J.

; APPLICANT: Brent, Andrew F.

; APPLICANT: Dahlbeck, Douglas

; APPLICANT: Katagiri, Fumiaki

; APPLICANT: Kunkel, Barbara N.

; APPLICANT: Mindrinog, Michael N.

; APPLICANT: Yu, Guo-Liang

; TITLE OF INVENTION: RPS2 GENE AND USES THEREOF

; NUMBER OF SEQUENCES: 201

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson

; STREET: 225 Franklin Street Suite 3100

; CITY: Boston

; STATE: MA

; COUNTRY: USA

; ZIP: 02110-2904

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30B

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US95/04589

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/227,360

; FILING DATE: 13-APR-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Clark, Paul T.

; REGISTRATION NUMBER: 30,162

; REFERENCE/DOCKET NUMBER: 00786/230001

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 542-5070

; TELEFAX: (617) 542-8906

; TELEX: 100254

; INFORMATION FOR SEQ ID NO: 125:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 8 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

PCT-US95-04589-125

Alignment Scores:

Pred. No.: 1.85e+07 Length: 8
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 5 Gaps: 0

US-10-070-588A-112 (1-11) x PCT-US95-04589-125 (1-8)

Oy 3 TTGGCACTA 11

Db 4 LeuAlaLeu 6

Search completed: March 12, 2005, 11:08:45

Job time : 22 secs

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